

CGACTTCACC CCAATCATTT GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC 240  
 CGGCTTCGGG TGTACAAAC TCTCGTGGTG TGACGGGCGG TGTGTACAAG ACCCGGGAAC 300  
 5 GTATTCACCG TAGCATGCTG ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT 360  
 TGCAGACTAC AATCCGAACT GAGAACT TATGCGGAA 400

(2) INFORMATION FOR SEQ ID NO: 3690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3690:

GCnGCGTTTT AGGCCCATTC GGTTACCCCC nTTCCATAAA TGGTGCCCGG CCAGAGGACT 60  
 TGAACCCCCC AACTTACTGA TTACAAGTCA GTTGCTCTAC CAATTGAGCT AGGCCGGCTA 120  
 AGAAATGGTT CAGGACAGAG TCGAACTGCC GACACATGGA GCTTCAATCC ATTGCTCTAC 180  
 25 CAACTGAGCT ACTGAACCAT AATAAAATG TAATGATGGC GGTCTCGACG GGAATCGAAC 240  
 CCGCGATCTC tGCGTGACAG GCAGGCGTGT TAACCGCTAC ACTACGAGAC CTATAAAATA 300  
 TTGCGGGAGG CGGATTTGAA CCACCGaCtT CGGGTTATGA GCCCGACGAG CTACCGAACT 360  
 30 GCTCCATCCC GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGC 420  
 CCGTTAAGGC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGACTTGG GTATTCCTCC 480  
 ATTATTATAG GTAnATCGCT ATTAATTATA AnATTAAAT GCGGTCTCG ACGGAATCG 540  
 35 AACCCGCGGA TCT 553

(2) INFORMATION FOR SEQ ID NO: 3691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3691:

TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 60  
 50 GTTGGCTACC ATCGACGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 120  
 TCTTCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT 180

TTTGACGTTT TAGACATAAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 300  
 ATTTTGTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG TTCGGACTAC CATCGACGCT 360  
 5 AAGGGAGCTT AACTTTCTGT GTTCGGGCAT GGGGAACAGG 400

(2) INFORMATION FOR SEQ ID NO: 3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3692:

TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAAATACAG ATTGAGTATA 60  
 20 TGCATATAAG ATGTTTTTAA CATCATTTTT GGATGATAGG ATGTTGCACC ACGATGATGT 120  
 CTGAATTCAT CGAATTCCTA TCAGGTATCG TTTCAACAAT TTCATTAACA TATCGCGAAA 180  
 TATCATTTTG AGAATTCTAA CGAATTCCT ATTGGTAGTG TAAGTTGGGG TCATGTTATA 240  
 25 ATTTTATAC ATAAGGCACC TCTTTAATTT AGTTTAGTAG TATTTATTAA ATTATACGAG 300  
 GGACCCAACA CAGAAAATTC ATTTTATTGa ATTTTACATT TATGTGmCAA GTTGGGaAAA 360  
 ATGTCTTATT TTTTCAAAGT ATTTAAAAGT AAAaTTACAT GTTAATACGT 410

(2) INFORMATION FOR SEQ ID NO: 3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3693:

ACTTCATATA ATTTATGAAA TAAACCTGTC AATTTTGGAT TGATTATGCT TTGTGATTCT 60  
 TTTTATTTCT GCGTAATAAC GCTAAACCTA AAATGCTAAA TAATCCGCCG AACAACATGC 120  
 45 CGTTGTTTGT TGATTCTTCT CCACCTGTTT CAGTAGTTCA GATTTCTTAG ATTGTGCTTT 180  
 TTTAGTTGGT ACCACTGcTT TAACCTTTTC ATTGATTTCa ATAACAGGTG TTACTACTTT 240  
 ACCTTGTTCC ACTGGTTTtag AAGGTTTTTT AGGTTCTTCT TTAGCAGGTG GTaTTGGTTT 300  
 50 ACCAGGTTCA GTTGGTACCT CTGGCGTTGG CGGTGTGGT GTTTCCGGCT CGCTTGGTAC 360  
 TTCTGGTGTC GGTGGTGTG GGTGTTnCC GGCTTCGCTT GGTACTTCTG GGTGTTCCGT 420



## (2) INFORMATION FOR SEQ ID NO: 3694:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3694:

GCATCGTTGC CTGGTAAGC CGTTACCTTA CCAACTAGCT AATGCAGCGG GAGTCCATCT 60  
 ATAAGTGACA GCAAGACCGT CTTTCACTTT TGAACCATGC GGTTCAAATn ATTATCCGGT 120  
 ATTAGCTACG GTTTCCCGAA GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC 180  
 ACCCGTCCGC CGCTAACATC AGAGAAGCAA GCTTCTCGTC CCGTTCGCTC GACTTGCAATG 240  
 TATTAGGCAC GCCGCCAGGT TCCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG 300  
 ATGTTTGATT AGCTCATAAA TACTAAATAA TGTTTGTAAC TTATAGTTAC GTTTTTTGGG 360  
 AATTAAACGTT GGACATATTG TCATTCCAGT TTTCAATGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3695:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3695:

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCCCTGTGC 60  
 GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTTGAAGCG GAATCAGGGA GTGGTTCAGT 120  
 TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAAT GGTCTTTTAA 180  
 CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG 240  
 CACGGGTCTT TGTCCGACTT GGTGGTATCG TAATTTAGCG CCTTGTAATT CTAAAGTTTC 300  
 CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT 360  
 TTGGTATAAC TTAATTTChC CTTTTCCTTC ATChGGTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3696:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3696:

5 TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG 60  
 CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTTCGGAAAT 120  
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180  
 10 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 240  
 CATTTTTATA AGTCAAACGC TCACATACGG CTTTCGTTTTT ATTATTTTAA ATGCTCATTT 300  
 ACATAAGTAA ACTCTGCTTT AAAATAATTT AACTCATGTG CTGCTAAACG TTTTCTTTTA 360  
 15 TAAAAAGATT TAAACGCGTT GATTAAAnCTG TGAGTGTCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3697:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3697:

25 CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 60  
 30 ACGTTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 120  
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 180  
 TTCGACGGCT AGTCTCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 240  
 35 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA 300  
 TTACTAnCGA TTCCAnCTTC ATGTAGTCGA GTTGCAGACT ACAATCCGAA CTGAGAACAA 360  
 CTTTATGGGA TTGCTTGAC CTCGCGGTTT CGCTnCCCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3698:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3698:

50 AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

CCCCATTTCGG AAATCTCTGG ATCAAAGCTT ACTTACAGCT CCCCAGCA TATCGTCGTT 180  
 AGTAACGTCC TTCATCGGCT TCTAGTGCCA AGGCATCCAC CGTGCGCCCT TAATAACTTA 240  
 5 ATCTATGTTT CCATCCTACA GGAAACGCGT TATTAATCTT GTGAGTGTTT TTTTGAACAC 300  
 TAGCGATTAT TTCTTATGAA TTCAAGCTTA TTTAAACTC TTTATTCACT CGGTTGTGCT 360  
 TGGnAAAATC TATATTTTAC TTAATTATCT AGGTTTCAAT 400

(2) INFORMATION FOR SEQ ID NO: 3699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3699:

TTTATGGCAT ACACGCATCA TAATACAGCC CAACACCACT AATGGTGCAG TTGCAAATCC 60  
 AAATTCTTCC GCTCCAAGCG CACATGCGTA CGCTACATCT TTACCAGTTA ATAACCTACC 120  
 25 GTCTGTTTCT AACTTAACAC GACTTCTTAA GTCATTTAGT TTTAATGTTT GATGTGTTTC 180  
 TGCTAAACCA ATCTCCCAAG GAACACCGGC ATGCTGAATA CTCGTTTTGG GTGAAGCCCC 240  
 TGTAnCACCA TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCCAGA 300  
 30 TGCAATGGTA CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT 360  
 CGCATTTTTT AAATCATGTA TCAGTTGCGC TAAATCTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3700:

CGACGTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGT TCGGCATGGG AACAGGTGTG 60  
 ACCTCCTTTG CTATAGTCAC CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG 120  
 TAAGTAAAAG TnATTTTGCT TCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG 180  
 50 TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT 240  
 TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTCn GGGGGGCTTC ATGCTTAGAT 300

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA

400

## (2) INFORMATION FOR SEQ ID NO: 3701:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3701:

AACCAAGCCC AATAATGGAC TGGCCGCCTA ATAATAAAAG CTCTAAAAGT TGTATTTTAA 60  
 AAATAGTTCT TTAAATTATA TACCCACCAC ATTTGGTGGA GAACCTAAAA AAAAGCACTT 120  
 CCCAAAAATG GAAAGTGCAA GTAGTGAGCC ATAGAGGATT CGAACCTCTG ACCCTCTGAT 180  
 TAAAAGTCAG ATGCTCTACC AACTGAGCTA ATGGCTCTAA TGGCTGGGCT AGCTGGATTG 240  
 GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA 300  
 TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGnTT TACAGTCCGC 360  
 CGCGTTTAGC CAnTTcGnTA CCCCTCCAGn TTATTcATAT 400

## (2) INFORMATION FOR SEQ ID NO: 3702:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3702:

TTTAAGTCCT GTGCGTCTGC CAGTTCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA 60  
 CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTT ATTCTACCGC TGAACTACTT 120  
 CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA AGgTTAGaTC CTAAGTCTAG 180  
 TGGCTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG 240  
 ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGGCTCT TCCATGGTGC 300  
 CGGCCAGAGG ACTTGGAACC CCCAACCTAC TGGATTACAA GTCAGTTGGC TCTACCAATT 360  
 GAnGCTAAGG CCGGCAATAT GTTAAGnATn AATGGTGGAG 400

## (2) INFORMATION FOR SEQ ID NO: 3703:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3703:

	CAACTAATAA ATAGTGGCGG TGGAGGGGAT CGAACCCCCG ACCTCACGGG TATGAACCGT	60
10	ACGCTCTAGC CAGCTGAGCT ACACCGCCTT ATATAGTTTG TAAATAATAT GGTGGAACT	120
	AGCGGGATCG AACCGCTGAC CTCCTGCGTG CAAAGCAGgC GCTCTCCCAG CTGAGCTAAG	180
	CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCTG AACCTGCGAC CCCTTGGTCC	240
15	CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGCGC CCGATAGGAG	300
	TCGAACCCAT AAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG CTAACGGGCG	360
	CATATGTTTT TAATTGAAAT GGTGCCCGAG GACCGGAATG	400

20

(2) INFORMATION FOR SEQ ID NO: 3704:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3704:

30

	CTAACGCCTA CGCGTTACAT GAAAAACGGA GAACAAGCAG AACAATTATT ACGTCAGCTT	60
	ATAGAAAAAG ATGAAGCACT AGCTAAGTAT GTCATGGTTT GTGATGAAAC AGCTTGGTGG	120
35	TCATATATGG GTCAAGATAA TGATATTTTC AAAGATCAAT TAGGTCATCT AACTGTTCAG	180
	CTAAGAAAGT ATCCCGAAGT GCTAGCCAAA AATGATACGC AACAGCTAGT GTCAATGGCA	240
	GCACTCGCGG CAAATGATCG CACTTTATAT CAAATGATTT GTGGAAAAGA TAATATTTCT	300
40	AAAAATGATG TCATGACGTT ATTTGAAGAT ATCGCGCAAG TCTTTTAAA GGTAACACTA	360
	TCATTTATGC AATACGGCGC ATTACCCAGA GTTGCATGGT	400

(2) INFORMATION FOR SEQ ID NO: 3705:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 478 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3705:

55

TGACGGGGAC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT TCGAAGCAAC GCGAaGaACC 120  
 TTACCAAATC TTGaCATCCT TTGaCAACTC TAGaGATAGA GCTTTCCCCT TCGGGGGTAC 180  
 5 AAAGTGACAG GTGGTGCATG GTTGTCTGCA GCTCGTGTCTG TGAGATGTTG GGTTAAGTCC 240  
 CGCAACGAGC GCAACCCTTA AGCTTAGTTG CCATCATTAA GTTGGGCACT CTAAGTTGAC 300  
 10 TGCCGGTGAC AAACCGGAGG AAGGTGGGGA TGACGTCAA TCATCATGCC CCTTATGATT 360  
 TGGGgCTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGT GAGTCAAGCA 420  
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGACTAC ATGAAGCT 478

(2) INFORMATION FOR SEQ ID NO: 3706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3706:

ATCTTAAGTC TTGGTGAAC CGTTTTGTAG AATTAAATAA TATTACAGAG CCGCTAGCAG 60  
 TAACGATCCA AACGAATTTA CCACCATCAC GTGGATTAGG ATCGAGTGCA GCTGTCGCGA 120  
 30 TTGCTTTTGT TCGTGCAAGT TATGATTTTT TAGGGAAATC ATTAACGAAA GAAGAACTCA 180  
 TTGAAAAGGC TAATTGGGCA GAGCAAATTG CACATGGTAA ACCAAGTGGT ATTGATACGC 240  
 AAACGATTGT ATCAGGCAAA CCAGTTTGGT TCCAAAAAGG TCATGCTGAA ACGTTGAAAn 300  
 35 CTCAAAGTTT AGACGGCTAT ATGGTTGTTA TAGAnACTGG TGTGAAAGGT TCACCAAGAC 360  
 AAGCAGTAGA AGATGTTCCA TAAACTTTGG TGAGGACCCT 400

(2) INFORMATION FOR SEQ ID NO: 3707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3707:

GTCGAACTGC CGACACATGG AGCTTCAATC CATTGCTCTA CCAACTGAGC TACTGAACCA 60  
 TAATAAAAAT GTAATnnTGG CGGTCTCGAC GGGAATCGAA CCCGCGATCT CCTGCGTGAC 120  
 AGGCAGGCGT GTTAACCGCT AACTACGAG ACCTATAAAA TATTGCGGGA GGCGGATTG 180

TAAAAAATAA TGGCGGAGGA AGAGGGATTC GAACCCCCGC GGCCCGTTAA GGCCCTGTCG 300  
 GTTTTCAAGA CCGATCCCTT CAGCCGGA CT TGGGTATTCC TCCATTATTA TAGGTAAATC 360  
 5 GCTATTAATT ATAAAATTAA ATGGCGGTCT CGACGGGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3708:

GTTGCGCCAT TAAAGCGGTA CCAAGCTGGG TTCAGAACGT CGTGAGCAG TTCGGTCCCT 60  
 20 ATCnGGGGTG GCGTAGGAA ATTTGAGAGG AGCTGTCCTT AGTACGAGAG GACCGGGATG 120  
 GACATACCTC TGGTGTACCA GTTGTCGTGC CAACGGCATA GCTGGGTAGC TATGTGTGGA 180  
 CGGGATAAGT GCTGAAACAT CTAAGCATGA AGCCCCCTC AAGATGAGAT TTCCCAACTT 240  
 25 CGGTATAAG ATCCCTCAAA GATGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC 300  
 ATGTGGAGCT GACGAATACT AATCGATCGA AGACTTAATC AAAATAAATG TTTTGCGAAC 360  
 30 AAAATCCACT TTTACTTACT ATCTAGTTTT GAATGTATAA 400

(2) INFORMATION FOR SEQ ID NO: 3709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3709:

AATTTTATGG GCCCTTTATG GACTTTATAT TmCCTAAAT ACTATTAAGA AGTCCTGAAA 60  
 AATTACATT AGCAGTTGGA TTGTTCAACT TTATTAATGA TAAGTATGCA AATAATTTCA 120  
 45 CAGTGTGTTGC AGCAGGGGCA ATTATGATTG CAGTACCTAT AGCAATCGTA TTCTTGTTCT 180  
 TGCAACGCTA TTTAGTATCA GGTTTAACAA CAGGTGCGAC AAAAGGTTAG TTTGAAATT 240  
 50 GGAGTGGGGC AGAATTGATA AAGAACCACT AATGACGATA AAGATTAAAA GGAGGACGTT 300  
 ATGATGACGA TTAAAGTTGG AATCATTGGG TGTGGTGGTA TTGCGAATGG CAAGCACATG 360  
 CCAAGTTTAC AAAAAGTTGA AAATGTTGAA ATGATCGCAT TTGTGACGTG GACTTTCGAA 420

## (2) INFORMATION FOR SEQ ID NO: 3710:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3710:

```

AGTGCTCTAC CAAGCTGAGC TACTTCCCGT ATAATTAACG CGCCCGATAG GAGTCGAACC      60
CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT      120
TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGgAT      180
TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA      240
CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTa TTCTACCGCT GAACTACTTC      300
TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GcTkAGaTCC TgAAGTCTAG      360
TGCGTCTGCC AATTCCGCCA CACCCGCAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG      420
ACCCTCTGGA TTGAAAAGTh CAGATGCTCT GACCAACTGG AGCTAATGGC TCTTCCCATG      480
GTGGCCGGCC AGAAGGACTT GGAACCCCCA ACCTGATGGA TTTACAATTC AGTTGGCTCT      540
AACCAATTTG AGCTAAGGC                                     559
  
```

## (2) INFORMATION FOR SEQ ID NO: 3711:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3711:

```

AACCTTTTAG GAGCTAGCCG TCGAAGGTGG GACAAATGAT TGGGGTGAAG TCGTAACAAG      60
GTAGCCGTAT CGGAAGGTGC GGCTGGATCA CCTCCTTTCT AAGGATATAT TCGGAACATC      120
TTCTTCAGAA GATGCGGAAT AACGTGACAT ATTGTATTCA GTTTTGAATG TTTGTTTATT      180
CAAATTAATG GGCCTATAGC TCAGCTGGTT AGAGCGCACG CCTGATAAGC GTGAGGTCGG      240
TGGTTCGAGT CCACTTAGGC CCACCATTA TTTAATACCT ATTTGGGGGC TTAGCTCAGC      300
TGGGAGAGCG CCGTCTTTGC ACGCAGGAGG TCAGCGGTTG GATCCCGCTA GTCTCCACCA      360
TTATTTGTAC ATTTGAAAAC TAGATAAGTA AGTAAAATAT                                     400
  
```



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3712:

TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG 60  
 CGAnnTCATG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GCCTGAAACC nnGTGATCTA 120  
 CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTGA 180  
 AAAGTGAGCG GATGAACTGA GGGTAGCGGA GAAATTCCAA TCGAACCTGG AAATAGCTGG 240  
 TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGG ATTATTGGAG GTAGAGCACT 300  
 GTTTGGACGA GGGGCCCCCTC TCGGGTTACC GAATTCAGAC AAACCTCCGAA TGCCAATTTA 360  
 ATTTAACTTG GGGAGTCAGA ACATTGGGTG ATAAGGTCCG 400

## (2) INFORMATION FOR SEQ ID NO: 3713:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3713:

TTTTAAAGTC TGATGTGAAA GCCCACGGCT CAACCGTGAA GGGTCATTGG AAACCTGGAAA 60  
 ACTTGAGTGC AGAAGAGGAA AGTGAATTC CATGTGTAGC GGTGAAATGC GCAGAGATAT 120  
 GGAGGAACAC CAGTGGCGAA GGCGACTTTC TGGTCTGTAA CTGACGCTGA TGTGCGAAAC 180  
 GTGGGGATCA nACAGGATTA GATACCCGGT AGTCCACGCC GTAAACGATG AGTGCTAAAG 240  
 TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGTAAACGCA TTnAAGCACT CCGnCTGGGG 300  
 AGTACGnCCG CAAGTTGGAA ACTTCAAAGG AATTGACGGG GGACCCGCAC AAGCGTTGGG 360  
 AGCATGTGGT TTAATTTTCA AGCAACGGAG AGGAACCTGA 400

## (2) INFORMATION FOR SEQ ID NO: 3714:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3714:

5 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60  
 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAACGTAAAT CGACTACCAT 120  
 CGACGCTAAG GAGCTTAACT TCTGTGTTCT GCATGGGAAC AGGTGTGACC TCCTTGCTAT 180  
 10 AGTCACCAGA CATATGAATG TAATTTATAC ATTCAAACCT AGATAGTAAG TAAAAGTGAT 240  
 TTTGCTTCGC AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC 300  
 CATGTCACCA TGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAGG GATCTTATAA 360  
 15 CCGAAGTTGG GAAATCTCAT CTTGAGGGGG GCTTCATGTC TTAGCATTTT AGTCACTTAT 420  
 GCCCCG 425

## (2) INFORMATION FOR SEQ ID NO: 3715:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3715:

30 GTCCCTGCTG TTCCTATCAT ATAAATGATA GATTCAAATA GATTTGTAGG TTTGTCATGC 60  
 CCAGTTACAA GTTGCCTTAT CGTAGACACT AACATTAATA TGAAGGTAA TGTGCTGTT 120  
 AATAAACTCA TACCAAATCC TGGCATCTCT TGATCCGTAA ATTCTTTTTG TGCACCTAAC 180  
 35 GCTGAAATAT CGCCTTCTCG TGTATACGCA GACGGAATCA TTTTGTGTC ACTTTGTTAA 240  
 ATATAGGCCC TGCAATGAGT GACTGGAAT GGCAATAATC ATACCATAA GTAATACATC 300  
 TCCAACATTT GCCTTTAATT CTTTTCGAG ACTACCGGTC CTGGGATGTG GTGGTAAAAA 360  
 40 GCCATGTGTC ACTGATAAAG CTGTTACCAT AAGTAGTCCT 400

## (2) INFORMATION FOR SEQ ID NO: 3716:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3716:

55 TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG TTTGCTTGG TAAAATCTAT 60

GCAATATCAC TTTAACCAAA AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA 180  
 ATATGTCACA TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA 240  
 5 GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG 300  
 TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGnTTCGGGT GTTACAAACT 360  
 10 GTTCGTGGTG TGACGGGGCG GTGTGTTACA AGACCCGGGA 400

## (2) INFORMATION FOR SEQ ID NO: 3717:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3717:

AAAGGACGAC ATTAGACGAA TCATCTGGAA AGATAATTCA AAGAAGGTAA TAATCCTGTA 60  
 GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGGTACGAC GGAGCACGTG AAATTCCGTC 120  
 25 GGAATCTGGG AGGACCATCT CCTAAGGCTA AATACTCTCT AGTGACCGAT AGTGAACCAG 180  
 TACCGTGAGG AAAGGTGAAA AGCACCCCGG AAnGAGTTGA AATAGAACCT GAAACCGTGT 240  
 30 GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG 300  
 CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAn AAnnTGTCT 360  
 GAATAGGGCG TTTAGTATTT TGGTCGTAGC CCGAGAACCA 400

## (2) INFORMATION FOR SEQ ID NO: 3718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3718:

TAATTCATCT GCAGCATCTG GTTGATTAA GCTTTCACGT AAACACATCG CTAAAGATAG 60  
 AATCATTCCA AATGGATTGG CAACGTTTTT ACCTGCAATA TCTGGTGCTG ATCCATGAAT 120  
 50 AGGCTCATAC AATCTTGGAC CATCGTTACT AAAACTAGCA GAAGGTGATA AACCAAGTGA 180  
 ACCAGGAATC ACTGAAGCTT CATCACTTAA AATATCGCCA AATAAGTTTT CACATACGAT 240  
 GACGTCAAAT TGTTTTGGnA TTTGTGATTA AATGCATACT ACAAGCATCA ACAATAAGT 300

TTTACTAGAA GCTAATACAT TTCCTTATCA ACGGATGTnA

400

(2) INFORMATION FOR SEQ ID NO: 3719:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3719:

15	ATTTAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA AGTnGAGCTA CCATCGACGC	60
	TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC	120
	CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT	180
20	TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT	240
	CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA	300
25	GTGCGGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT	360
	CCACACATAG CTACCCAGCT AGCCGTTGGC ACGACAAnGG	400

(2) INFORMATION FOR SEQ ID NO: 3720:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3720:

40	CGTTACACCT TCCAATAAAT TTGCTGTTGC TGGATAAGGA GAAATATTGA TATATTGTCT	60
	TAAATTACTA TAATGCCAAT TTAAGTCTGG ATGATTTGTT AAGACACCAA TAGGATTATC	120
	TTTTATAACC ACTTCACCCT CTTTAAATGA AACTTCGACT GTATGTCCAG TTGCATCGGA	180
45	AACATGATAA TGCAATGGCG GAACTTCACC GATGTCATTT AAATATACAG CTACAACATG	240
	TATTTGGGAT GCTTGTTGTT TCATATCTTC AATGCTTGTT GTATATCCCA AAATCCATGT	300
	CACAATTTCA TTTTGCCTAA TATTCATCGC GTCCGCTTTG TGTGTTGGAT CCATATGGAA	360
50	CTATAACCTC GGGAAATATT GTGGTTGAAA TGGGCACGCC	400

(2) INFORMATION FOR SEQ ID NO: 3721:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3721:

	AGTCAGTTTA TAGCGATTGC TGGACTGACA GTACTTGTGC CATTATTGCC AATTTATATG	60
10	GCATCACTAC AAAATCTATC AGTCGTAGAA ATACAGTTGT nGAGTGGTAT AGCGATTGCT	120
	GCTCCAGCTG TAACGACGAT GATAGCTTCG CCGATATGGG GGAAGCTAGG TGATAAGATC	180
	AGCCGAAAAT GGATGGTGTT AAGAGCGTTA CTTGGTTTGG CGGTATGCTT ATTTTAAATG	240
15	GCATTGTGTA CGACACCATT ACAGTTTGTA CTTGTGGAGG TTATTGCAGG GACTATTTGG	300
	TGGTGTGTGT GATGCATCAA GTGCGTTTGC GAGTGCAGAA GGCGCCACTG AnAGATCGTG	360
	GGAAAGGTAT TAGGAAGACT GCAAATThCA GTTCAGCGCA	400

20

(2) INFORMATION FOR SEQ ID NO: 3722:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3722:

	TCTAAAAGTT GAACTACTCC CGCATAAACC TGGAGGCGGC AACCGGATTG GAACCGGTGA	60
	TAAAGGTTTT GCAGACCTCT GCCTTACCAC TTGGCTATGC CGCCAATAAC TGGGCTAGCT	120
35	GGATTCGAAC CAACGAGTGA CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAT	180
	TAATAATAAG GGGCGCTGAA GGGGATCGAA CCCTCGAATG TCGGAACCAC AATCCGATGT	240
	GTAAACCACT TCACCACAGC CGCCATGGCA GGGGCAGTAG GAATCGAACC CACACCAAAG	300
40	GTTTGGAGA CCTCTATTCT ACnTTGAAC TATGCCCTA TTAAAATGAT AAATGGAGGG	360
	GGGCAGATTC GAACTGCCGA ACCCGAGGGG CGGATTTTAC	400

45

(2) INFORMATION FOR SEQ ID NO: 3723:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3723:

55

GGTTCAAGTC CTCTGGCCGG CACCATTThT GGAGGGGTAG CGAATGGCTA AACGCGGCGG 120  
 ACTGTAAATC CGCTCCTTCG GGTTCGGCAG TTCGAATCTG CCCCCCTCCA TTTATTATTT 180  
 5 TTAATAGGGG CATAGTTCAA CGGTAGAATA GAGGTCTCCA AAACCTTTGG TGTGGGTTTCG 240  
 ATTCCTACTG CCCCTGCCAT GGCGGCTGTG GTGAAGTGGT TAACACATCG GATTGTGGTT 300  
 10 CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCTTATTA TTAATGGGCT ATAGCCAAGC 360  
 GGTAAGGCAA CGGACTTTGA CTCCGTCCT CGTTGGTTTCG 400

## (2) INFORMATION FOR SEQ ID NO: 3724:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3724:

CACTTTAGCA AATGGTGACA AAGTCCGTAT TGCTACAATT TTTGACTTAA TGGCAAGTCA 60  
 25 ATATGGCGTG CGTCGTTTTG ATCATAAATT AGAATCAAAA GGATACGACG ATGCAGAATC 120  
 AAAATATACA CCTGCTTGGC AAGAAGCCAT TTCAGGCGTA AAACAAAGTG TThGTCATTC 180  
 30 AAGTAGCGAA AGAATTTGCG CAAAACGCTA TCGATACTGA AGGGCGTTCA ATGATTATCA 240  
 TGGGTGCGGG TATTAACCAT TGGTTTAACT CAGATACGAT TTATCGTTCC AATCTTAAAC 300  
 TTAGTTATGT TATGTGGCTG TCAGGTGTGA ATGGTGGCGG TTGGGGCTCA CTATGTGGGG 360  
 35 ACAAGAAAAA TGTCGTCCGA TTGAAGGATG GAGTACTGTC 400

## (2) INFORMATION FOR SEQ ID NO: 3725:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3725:

CGCTATCTGA ATCTGAATCG CTATCTGAAT CTGAGTCGTT GTCTGAGTCC GAATCGCTAT 60  
 50 CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTATCTGA ATCTGAGTCG CTGTCTGAAT 120  
 CTGAATCACT GTCTGAGTCT GAGTCGCTGT CTGAGTCTGA ATCGCTGTCA GAATCTGAGT 180  
 CGCTATCTGA GTCTGAATCT GAATCACTGT CTGAGTCCGA ATCGCTATCT GAATCTGAAT 240

CCGAGTCTGA ATCGCTGTCT GAGTCTGAGT CGCTGTCTGA ATCTGAATCG CTATCTGAGT 360  
 CTGAGTCGCT GTckGAATgC GCTGTCTGAA TCTGAGTCGC TATGCTGAAT GCTGAGTnCG 420  
 5 CTATGTGAGT CTGAATGCGC TGTGCAGAAT CTGAGTGCGC TCATCTGATG TTTCTT 476

(2) INFORMATION FOR SEQ ID NO: 3726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

ATACGACCAC TGTTTAATGC GTCCATTAAA TCTGGCCAAT TATTGAATTT AACTAATTCT 60  
 20 AGTTTATATT TCGGATGATT GTATTGTGAT AATAATTTT TAGTCATCAT CAAATTAGCT 120  
 GAATGTGTAA TCGGCAAATA TCCAATTTTA ATCACTTGCT GATTTTGGGC ATTTTATAGAC 180  
 25 CGTTCTTTAG ACGTCCTTTG CCAATCACAT CCTGTAATTA TAAAGATTCC AATGATGACC 240  
 ATTATGCTTA ACCTTTTCAT CGTCACTCAC TCCTTATAAA TAATATTCAG GTTCAACTTG 300  
 ATGATGATTC AATGCAAnGT TTCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA 360  
 30 TTACGGACTG CGTGGATGTG AnGCTGTAAA TTCCATAnTG 400

(2) INFORMATION FOR SEQ ID NO: 3727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3727:

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 60  
 ATGGGCGAAC AGCAAACCCT TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC 120  
 45 GAGGTGCCAA ACCTCCCCGT CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG 180  
 GG TAGCTTTT ATCCGTTGAG CGATGGCCCT TCCATGCGGA ACCACCGGAT CACTAAGTCC 240  
 50 GTCTTTCGAC CCTGCTCGAC TTGTAGGTCT CGCAGTCAAG CTCCCTTATG CCTTTACACT 300  
 CTATGAATGA TTTCCAACCA TTCTGAGGGA ACTTTGAGCG CCTCCGTTnC CTTTTAGGAG 360  
 GCGAACGGCC CCAGTTCAAA CTGCCCCGCT GAACACTGTC 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3728:

TTGAAAAGTC ATATCAAAGC GCACATGTTT TTAAGCGTCG TCGAACACCT ATCGTGAAAG 60  
 GTGTGTCATT TGAGTGTCCTA ATCGGTGCGA CGATTGCGAT TATCGGAGAA AGTGGTAGCG 120  
 GTAAATCGAC GTTGAGTCTA TTGATATTAG GTATTGAGAA ACCGGATAAA GGTTGTGTAA 180  
 CCTTAAATGA TCAACCGATG CATAAGAAGA AAGTGAGACG TCATCAAATT GGTGCTGTAT 240  
 TTCAAGATTA TACGTCATCA TTACATCCAT TTCAGACTGT TAGAGAAATC TTATTTGAAG 300  
 TGATGTGTCA ATGTGATGGA CAACCTAAAG AAGTTATGGA AGTCCAAGCA ATTACATTGT 360  
 TGGAAGAAGT CGGTCTATCT AAGGCATACA TGGGATAAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3729:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3729:

ATCGAACCCC CGACCTCAGC GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC 60  
 TTATATAGTT TGTAATAAT ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 120  
 TGCAAAAGC CGCTCTCCCA GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA 180  
 GACAGGTTCT AACCTGCGAC CCCTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC 240  
 TTCCCGTATA ATTAACGCGC CCGATAGGAG TCGAACCCAT AACCTCTTGA TCCGTAGTCA 300  
 AACGCTCTAT CCAATTGAGC TACGGGCGCA TATGTTTTTA TTGAAAATGG TGCCGAGGAC 360  
 CGGAATCGAA CCnGTAGTGA ATCACTCACC GCAGATTTTA 400

## (2) INFORMATION FOR SEQ ID NO: 3730:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3730:

5 ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT 60  
 CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CTATGTTTCC 120  
 ACCATTTTTA TAAGTCAAAC GTTAACATGA AGTTACGTTT TTTTATAAAA AGATTTAAAC 180  
 10 GCGTTATTAA TCTTGTGAGT GTTCTTTCGA ACACTAGCGA TTATTTCTTA TGAATTCAAG 240  
 CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT TTACTTACTT 300  
 ATCTAGTTTT CAATGTACAA ATAATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT 360  
 15 GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC 400

## (2) INFORMATION FOR SEQ ID NO: 3731:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3731:

TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 60  
 30 TGGAGAATGA CGGGTTCGAA CCGCCGACCC TCTGCTTGTA AGGCAGATGC TCTCCCAGCT 120  
 GAGCTAATTC TCCGATTTAA AACTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC 180  
 GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT 240  
 35 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA TTCAAAACTA GATAGTAAGT 300  
 AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAACT GTCTTCGATC GATTAGTATT 360  
 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCTA T 401

## (2) INFORMATION FOR SEQ ID NO: 3732:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3732:

50 CATTATTAAC GGCTATGGTT TAACTGAAGC ACCTCTTGTA CTTGTTAATA CACCGGAAAA 60  
 TTCAAAACGT AAGCCAATGA GTATTGGTAA AGCAGTCATG TTCGTTGATG CACGTATCCT 120

AAATGTCACG CCAGGATATT GGAATAAACC AGCAGAGACT GCCAAAGCAT TTCATGGTCG 240  
 ATATTTATTA ACTGGTGA CT TAGCGAGATG GACAACGATG GCGATATATT TATTATTGAC 300  
 5 CGCAAAaAG AaTTAATCAT AACTGGTGGc GAAAATGTCT TACCATCCGa gTCGAAAtGC 360  
 TTaCtGaGCA TCCACTAGTA GACCGGTGTG TGGTCGT 397

## (2) INFORMATION FOR SEQ ID NO: 3733:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3733:

20 AAGTAACAAT CGTTCACCGT CGTGATGAGT TACGTGCACA GCGTATTTTA CAAGATAGAG 60  
 CATTCAAAAA TGATAAAATC GACTTTATTT GGAGTCATAC TTTGAAATCA ATTAATGAAA 120  
 AAGACGGCAA AGTGGGTTCT GTGACATTAA CGTCTACAAA AGATGGTTCA GAAGAAACAC 180  
 25 ACGAGGCTGA TGGTGTATTC ATCTATATTG GTATGAAACC ATTAACAGCG CCATTTAAAG 240  
 ACTTAGGTAT TACAAATGAT GTTGGTTATA TTGTAACAAA AGATGATATG ACAACATCAG 300  
 TACCAGGTAT TTTTGCAGCA GGnGATGTTT GCGACAAAGG TTACGCCAAA TTGTCACTGC 360  
 30 CACGGCGATG GTAGTATGCC AGCGCAAGTG CCACGGAATG 400

## (2) INFORMATION FOR SEQ ID NO: 3734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3734:

GCCGTTTACT GTGGCTTCGA TTCGTAGCTT CGCAGAAGCT AACCACTCCT CTTAACCTTC 60  
 45 CAGCACC GGG CAGGCGTCAG CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT 120  
 TTGATAAACA GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG 180  
 CACCCCTTCT CCCGAAGTTA CGGGGTCA TT TGCCGAGTT CCTTAACGAG AGTTCGCTCG 240  
 50 CTCACCTTAG AATTCTCATC TTGACTACCT GTGTCGGTTT GCGGTACGGG CACCTATTTT 300  
 CTATCTAGAG GCTTTTCTCG GCAGTGTGAA ATCAACGAcT CGAAGACACA ATGTCTTCTC 360

TAGACGTGCA ATCCAATCGG CAACGCTTCG CCTAATCCTA ACTGGCGGTC CCCCCCnAT 480

(2) INFORMATION FOR SEQ ID NO: 3735:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3735:

CGATCCCTTC AGCCGGACTT GGGTATTCCT CCAAAATTAT ATGGACCTTG CAGACTCGAA 60  
 CCTGCGACCG AACGGTTATG AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA 120  
 TAATTTTACA ACTAATAAAT AGTGGCGGTG GAGGGGATCG AACCCCGAC CTCACGGGTA 180  
 TGAACCGTAC GCTCTAGCCA GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 240  
 TGGAGACTAG CGGGATCGAA CCGCTGGACC TCCTGCGTGC AAACAGnCGC TCTCCAGCT 300  
 GAGCTnAAGC CCCATAATA ATTACAGTAT ATCGGAAGA CAGGATTCGA ACCTGCGACC 360  
 CCTTGGTCCC CAAACCAAGT GGTTTnACCA AGTTGAGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3736:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3736:

TGAGCCCGAC GAGCTACCGA ACTGCTCCAT CCCGCGATAA TAAAAAATAA TGGCGGAGGA 60  
 AGAGGGATTTC GAACCCCGC GGCCCGTTAA GGCCCTGTGC GTTTTCAAGA CCGATCCCTT 120  
 CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC GCTATTAATT ATAAAATTAA 180  
 ATGGCGGTCT CGACGGGAAT CGAACCCGCG ATCTCCTGCG TGACAGGCAG GCGTGTTAAC 240  
 CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 300  
 TTAAGCCCCT GTCGGTTTTTC AAGACCGATT CCTTCAGCCG GACTTGGGTA nTChTCCAAA 360  
 ATTATATGGA CCTTGCAGGA CTCGAACTGC GAnCGAACGG 400

(2) INFORMATION FOR SEQ ID NO: 3737:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3737:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC	60
10	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC	120
	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
15	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT GGAGCAGAAG	300
	ACGGGATTCTG AACCCGCGAC CCAACCTTG GCAAGTTGT ATTCTACCGC TGAACTACTT	360
	CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA	400

20

(2) INFORMATION FOR SEQ ID NO: 3738:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3738:

	AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG	60
	CTAATTCTCC GATTTAAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAAAGT AATCGGAnCT	120
35	ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT	180
	GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA	240
	GTGATTTTGC TTCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG	300
40	CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT	360
	TATAACCGAA GTTGGGAAAT CTCATCTTGG AGGGGGGCTT	400

45

(2) INFORMATION FOR SEQ ID NO: 3739:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3739:

55

CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAA CCGACATCTT 120  
 TAATTAATTG CTnTGACAGT TTTCTATCAA ATTTATCATT ACGTGCAAGT GATGGGAATA 180  
 5 TCATGTTATC TTCAATCGTT TCACCAAACA AGTCACTTTG CTGCATCAA TAACTGATTC 240  
 GTTGACGCAA TTCTTCCGGG TCATAATCAT TATAGGGTTT ACCTTTAAAA TAAAGTTCTC 300  
 CACTAGTTGG ACTAAACAAA TTACATATnT GCTTTTGAAA TGTACTTTTA CCACTACCTG 360  
 10 ATGGACCTAT AATGGCAATA CTCTCGCCTT TATCTACTTT 400

(2) INFORMATION FOR SEQ ID NO: 3740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3740:

ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG 60  
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTCA CTTCGCCAAG CCATTTTCT 120  
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 TGCGGCTCAT CGCATCCaTT TTTGCGCTGG CAACGTCTA CTCTAGCGGA AnTAATTGGC 240  
 30 TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT 300  
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGTTG CGCTCTTTTC TCGTTTCGTC 360  
 AGATtCAAAC GTTTTCACTT CGCCAAGCCA tTTTTClTTG TGTTTGCTTT ThA 413

(2) INFORMATION FOR SEQ ID NO: 3741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3741:

CTTAGATGCT TTCAGCACTT ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC 60  
 GACAACTGGT ACACCAGAGG TATGTCCATC CCGTCTCTCT CGTACTAAGG ACAGTCCTC 120  
 50 TCAAATTTCC TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA 180  
 GCTCGCGTAC CGCTTTAATG GGCGAACAGC CCAACCCTTG GGACCGACTA CAGCCCCAGG 240

TAAGCTGTTA TCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGCCCTTCC ATGCGGAACC 360  
 ACCGGATCAn TAAGTCCGTC TnTCGACCCT GnTGGACTTG 400

(2) INFORMATION FOR SEQ ID NO: 3742:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3742:

GTTTTGAATG TATAAATTAC ATTCATATGT CTGGTGAATA TAGCAAGGAG GTCACACCTG 60  
 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC 120  
 CGCTAGAGTA GAACGTTGCC AGGCAGTTTT AAATCGGAGA ATTAGCTCAG CTGGGGAGAG 180  
 CATCTGCCCTT ACAAGCAGAG GGTCGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 240  
 TACATATTGC CGGCCTAGCT CAATTGGTAG AGCAACTGGA CTTGTAATCA GTAGGTTGGG 300  
 GGTTC AAGTC CTCTGGCCGG CACCATGGGA AGAGCCATTA GCTCAGTTGG TAGAGCATCT 360  
 GACTTTTAAA TCAGAGGGTT CAGAGGTTnC GAATCCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3743:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

TCGCAATAAC CGCATCAAAT GTATTGCCTA AAAAGGCTGG ATTTTCCAAT GTGTCATCAT 60  
 TACGGATCTC GAAGTTCTCA TAACGCACAT CATGTAATAA CATATTCATG CGTGCTAAGT 120  
 TGTATGTAGT ATTGTTACGT TCTTGTCCGA AATAACGATA CACTTGCGTT TCTTTACCAA 180  
 CACGTAACAA CAATGAACCG GAACCACATG TTGGGTCGTA CACGTGACGT AATTTATCTT 240  
 TACCGTCTGT GACAATCTTC GCCAGTATCT TAGATACTTG TTGTGGTGTA TAGAACTCGC 300  
 CTGCTTTTTT ACCCGCTGTC GCCGCAAAGC GCCCGATTAG GAATTCATAT GCATCACCTA 360  
 ACATATCAAT TTCCATGGTC ACTGTGAACG AATGGGTAAG 400

(2) INFORMATION FOR SEQ ID NO: 3744:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3744:

10 CTACTGATTA CAAGTCAGTT GCTCTACCAA TTGAGCTAGG CCGGCAATAT GTAAGAATAA 60  
 ATGGTGGAGA ATGACGGGTT CGAACC GCCG ACCCTCTGCT TGTAAGGCAG ATGCTCTCCC 120  
 AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 180  
 15 GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG 240  
 ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTAA TACATTCAA ACTAGATAGT 300  
 AAGTAAAAGT GATTTGCTTC GCAAAACATT ATTTGATTAA GTCCTCGATC GATAGTATCG 360  
 20 TCAGCTCCAC ATGTCACCAT GCTTCCAnCT CGnACCTATT 400

(2) INFORMATION FOR SEQ ID NO: 3745:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3745:

CATAAGTAAA CTCTGCTTTA AAATAATTAA ACTCATTGTC TGCTAAACGT TTTCTTTTAT 60  
 35 AAAAAAGATTT AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT 120  
 CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA 180  
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA 240  
 40 CTGCTTTTATT nTCAAAAAAT CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTC 300  
 TTAATGCATT GTCTAACAAAC CGCTTGCTTT AAAAAGAATA GATTGnCAAG CGCTCGCATA 360  
 AGCAATATCA CTTnAACCAA AAAATA 386

45

(2) INFORMATION FOR SEQ ID NO: 3746:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 677 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

AAGGTGAAAA GCACCCCGGA AGGATGTTGA AATAGAACCT GAAACCGTGT GCTTACAAGT 60  
 AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG CGAGTTACGA 120  
 5 TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAk AACanGGTCT GAATAGGGCG 180  
 TTTAGTATTT GGTCGTACCG AnaACCAGGT GATCTACCTT TGGTCAGGTT GAAGTTCAGG 240  
 TAACACTGAA TGGAGGACCG AACCRACTTA CGTTGAAAAG TGAGCGGATG AACTGAGGGT 300  
 10 AGCGGAGAAA TTCCAATCGA ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGc 360  
 TAGCCTCAAG TGATGATTAT TGGAGGTAGA GCACTGTTTG GaCGAgGGGC CCCTCTCGGG 420  
 15 tTACCAATTc AGACAAACTC CGAATGCCAA TTAATTTAAC TTGGGgAGTC aGAACATGGG 480  
 TGATAAGGTC CGTGTTTCGAA AGGGAAACAG CCCAGACCAC CAGCTAAGGT CCCAAAATAT 540  
 ATGTTAAGTG GAAAAGGATG TGGCGTTGCC AGACAACTGA GGATGTTGGC TTAGAAGCAG 600  
 20 CCATCATTTT AAAGAGTGCG TAATAGCTCA CTAGTCGAAG TGACACTGCG CCGAAAATGT 660  
 GACCGGGCnT AAACnAT 677

(2) INFORMATION FOR SEQ ID NO: 3747:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3747:

35 GTCCAATGAT TCATATGCTT TATTATCACG GTATTGCCTT TGAATCGCAT GCACAAAATA 60  
 TGATGCTCAT TCATGAAAAT GGTTGGCCTA CACGTATTGC CTTAAAAGAT TTCCATGATG 120  
 GTGTTTCGTTT TAAGCGTGAc ATTTAAGTGA AGCTGCTTCA CACCTGACAT TAAAGCCAAT 180  
 40 GCCAGAAGCA CATAAAAAAG TGAATAGTAA TTCATTTATT GAAACAGATG ACGAACGTTT 240  
 AGTACGCGAC TTTTACATG ATGCATTTTT CTTTATTAAT ATCGCCGAAA TCATCTTATT 300  
 45 TATTGAAAAG CAATATGGTA TCGATGAGGA GCTGCAATGG cAATGGGkTa AAGGCATCAT 360  
 CGAGGCGTAT CCAGrAGcAT TTCCaGAGTT kGAATaACTA TCCAACCATT CGGTTTTT 417

(2) INFORMATION FOR SEQ ID NO: 3748:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3748:

ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG 60  
 5 CGGAACGTAA GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG 120  
 AACAGGTGTG ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA 180  
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAACAT TTATTTTGAT TAAGTCTTCG 240  
 10 ATCGATTAGT ATTTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT 300  
 CATCATCTTT GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA 360  
 15 TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3749:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3749:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60  
 30 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC 120  
 GTTTTAGGCA TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT 180  
 TGCCTGGCAA CGTCTACTC TAGCGGAAGT AAGTTGGGCT ACCATCGTCG CTAAAGACCT 240  
 35 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 300  
 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 360  
 40 GCCAAGCCAT TTTTCTTTG TGTnTACTTT TTAATTTTGA 400

## (2) INFORMATION FOR SEQ ID NO: 3750:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3750:

ATAAAAAAA GAGACCTTGC GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC 60  
 AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC 120

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 240  
 ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 300  
 5 GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGGC AACGTTCTAC TCTAGCGGAA 360  
 nTAAnTTGGG CTACCATCGA CGCTAAGAAC CTTTCTTGGA 400

(2) INFORMATION FOR SEQ ID NO: 3751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3751:

20 CACTCACCGC AGATnTTTAA GTCCTGTGCG TCTGCCAGTT CCGCCACCCC GGCACATATAA 60  
 AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC CTTGGCAAGG TTGTATTCTA 120  
 CCGCTGAACT ACTTCTGCAT ATGCGGGTGA AGGGAGTCGA ACCCCCACGC CGTAAGCTnA 180  
 25 GnATTCTTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240  
 GGATTGCAAC CTCTGGACCC TCTGATTAAA AGTCAGATGC TCTACCAACT GGAGCTAATG 300  
 30 GCTCTTTCCA TGGTGCCCGG CCAGAGGACT TGGAAACCCCC AACCTACTGA TTACAAGTCA 360  
 GTTGCTCTAA CCAATTGAGC TAAGCCGGGC AATATGTTAn 400

(2) INFORMATION FOR SEQ ID NO: 3752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3752:

45 TTAnAnAnCC GCGACATTAT AGAGCCAATC ACTAGCCTAT CTCAGAATCA CCAACGAATC 60  
 CTTCAATTATT AAGGAATCTA GGCATCTTTA CGGCGTGGTT CTAATCGCAT CTTTTTCAAT 120  
 CTAAGTGCGT TTGTGACAAC ACTTACTGAA CTTAGTGCCA TTGCAGCACC AGCAACCCAT 180  
 50 GGCGCAAGTA AGCCCAATGC AGCTATAGGG ATACCGGCAA TATTATAGCC GAATGCCCAA 240  
 AATAGATTTT GACGAATATT ACGAATGGTT GcTTTACTTG cATAAATGGC TTTAGGaATa 300  
 AGCATCAAGT cGCCACCAAG AATAGTAATA TCAGCTGCTT CAATGGGCAA CTTCTGTTAC 360

## (2) INFORMATION FOR SEQ ID NO: 3753:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3753:

```

CCTTGCGGTC TCAATGGCGG CTCATCGCAT CCATTTTGTG CCTGGCAACG TTCTACTCTA      60
GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT      120
TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC      180
TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT      240
TTACTTTTTA TTTTGACGTT TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC      300
TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTGGCTACCA      360
TCGACGTAA GAACCTTCT TGACTGGTGA CAAnCGCTTG      400

```

## (2) INFORMATION FOR SEQ ID NO: 3754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3754:

```

CTGAGCTAAG CCCCCAAATA GGTATTAAAT TAATGGTGGG CCTAAGTGGA CTCGnACCAC      60
CGACCTCAGC CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTAATTTGA      120
ATGAnCAAAC ATTCAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG      180
ATGTTCCGAA TATATCCTTA GAAAGGAnGT GATCCAGCCG CACCTTCCGA TACGGCTACC      240
TTGTTACGAC TTCACCCCAA TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGTTA      300
CTCCACCGGC TTCGGGTGTT ACAAACCTCTC GTGGTGTGAC GGGCGGTGTG TACAAAACCC      360
GGGAACGTAT TCACCGTAGC A      381

```

## (2) INFORMATION FOR SEQ ID NO: 3755:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3755:

5 AGCTCCCCAA AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCAAGGCAT 60  
 CCCCCTGCGC CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA 120  
 CATGAAGTTA CGTTCTTTTA TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCTT 180  
 10 TTCGAACATA GGCGATTATT TCTTATGAAT TCAAGCTTAT TTAAAACTCT TTATTCACTC 240  
 GGTTTTGCTT GGTA AAAACH ATATTTTACT TACTTATCTA GTTTTCAATG TACAATTTCT 300  
 TTTTAGTCAA GCGCTCGCAT ACTGCTTTAT TTTCCATAAG CAATAnCACT TTAACCAAAA 360  
 15 AATATTTGGA ATGTTnAAAT AACATnCAA AACTGAATAC 400

## (2) INFORMATION FOR SEQ ID NO: 3756:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3756:

CTACTCACAC CGGCATTCTC ACTTCTAAGC GTCACCATG TCCTTACGAT CATGCTTCAA 60  
 30 CGCCCTTAGA ACGCTCTCCT ACCATTGTCC AAAGGCATGC GCACAGCTTC GGTAATATGT 120  
 TTAGCCCCGG TACATTTTCG GCGCATGTCA CTCGACTAGT GAGCTATTAC GCACTCTTTA 180  
 AATGGATGGC TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCCAC ATCCTTTTCC 240  
 35 ACTTAACATA TATTTTGGGA CCTTAGCTGG TGGTCTGGGC TGTTCGGn GGGGnACACG 300  
 GACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCGG ATTTGTCTGA 360  
 40 ATCGGTAACC CGAGAGGGCC CnTCGTCCAA ACAGTGCTCT 400

## (2) INFORMATION FOR SEQ ID NO: 3757:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 458 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3757:

GGCAGATGCT CTCCCAGCTG AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC 60

55

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 180  
TCAAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAGT 240  
5 CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT CGAACCTATT 300  
AACCTCATCA TCTTTGAGGG aTCTTATAAC CGAArTttGG GAAtCTCATC TTGAGGGGGG 360  
gCTCATGcTt AGATGCTTcA GCACTTATCC CGTCCACACA TAGCTAnCCA GCTATGCCGT 420  
10 TnGCACGACA ACTGGTACAC CAGAnGTATG TCCATCCC 458

## (2) INFORMATION FOR SEQ ID NO: 3758:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3758:

AGCGCTCGCA TACTGCTTTA TTTTCAAAAA ATCAAATGCT CATTTACAAA AGTAAACTCC 60  
25 GCTTTAATTT TTCTTAATGC ATTGTCTAAC AACCGCTTTC TTAAAAAGA ATAGATTGTC 120  
AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA AATAAACATT 180  
30 CAAAAGTGAA TACAATATGT CACGTTATTC CGCATCTTCT GAAGAAGATG TTCCGAATAT 240  
ATCCTTAGAA AGGAGGTGAT CCAGCCGCAC CTTCCGATAC GGCTACCTTG TTACGACTTC 300  
ACCCCAATCA TTTGTCCAC CTTGACGGC TAGCTCCTAA AAGGTTACTC CACCGGCTTC 360  
35 GGGTGTTACA AACTCTCGTG GTGTGACGGG CGGTGTGTAC 400

## (2) INFORMATION FOR SEQ ID NO: 3759:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3759:

GACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG 60  
50 GTTATGAGCC GTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT TTTACAACTA 120  
ATAAATAGTG GCGGTGGAGG GGATCGAACC CCCGACCTCA CGGGTATGAA CCGTACGCTC 180  
TAGCCAGCTG AGCTACACCG CTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG 240

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 360  
 AAGTGCTCTA CCAAGCTGAA GCTACTTTCC CGTATAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3760:

CACTTAATGC CCGTACCACA CATAGCTACC CAGCTATGCC GTTGGCACGA CAACTGGTAC 60  
 ACCAGAGGTA TGTCCATCCC GGTCCTCTCG TACTAAGGAC AGCTCCTCTC AAATTTCTTA 120  
 CGCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTC TGAACCCAGC TCGCGTACCG 180  
 CTTTAATGGG CGAACAGCAA nCCCTTGGGA CCGACTACAG CCCCAGGATG CGATGAGCCG 240  
 ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTCTG GGGGAGATAA GCCTGTTATC 300  
 CCCGGGGTAG CTTTTATnCG TTGAGCGATG GnCCTTnCAT GCGGAACACC GGATCACTAA 360  
 GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3761:

TATGTATTTT ATAATGTACA GTCGTTGAn TCnTATTTTT CTTATATTA AGTGCCATTA 60  
 ATACAAAACC TAGCTCTCGT TTAACTTTAT TTATTCCTCG AACTGACATT CGAGTGAACC 120  
 CAAAATAGCC TTCATAAATC CAAAACAGG CTCTACATCA ATTTTCTTT GACTATAGAT 180  
 TTTTTTCGTT TCTGGTTCAG AAAGCTTTTG ATTAATTTGG ACTTTAAAGT ATTCCCAATT 240  
 ATAATCTTC ATGATTTTCT TATTGGATTT CGAATTTGGT TTCATGCATT GATGTCTCAA 300  
 AGAACATGAT GAACAGTCAT CACATTCATA TAGTTTGAAG TCTCGTTTAA AACCATATCT 360  
 ATCATTACGG TATGCATATC TTTAAAACC TATTCTTTTG TTATTAGGAC ATATAAATTC 420  
 ATCATTAAAGT TCGTCATATT TCCAATTTTA AGTGTTGAAA ATGTCACTTT TAACTTTCT 480

AATAGCCATA TAGTTTTGCT CACTACCATA ACCGGCATCA GCTACAAATA TACTCCGGTA 600  
 AATAACCGAG GGATTGTTGG AAT 623

(2) INFORMATION FOR SEQ ID NO: 3762:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3762:

ATTTTAAAA TAGTTCCTTA AATTATATAC CCACCACATT TGGTGGAGAA CCTAAAAAAA 60  
 AGCACTTCCC AAAAATGGAA AGTGCAAGTA GTGAGCCATA GAGGATTCTGA ACCTCTGACC 120  
 CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG GCTCTAATGG CTGGGCCTAG 180  
 CTGGATTCTGA ACCAACGAGT GACGGAGTCA AAGTCCGTTG CCTTACCGCT TGGCTATAGC 240  
 CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG GAGCGGATTT 300  
 ACAGTCCGCC GCGTTTAGCC ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT 360  
 CaAAATGGTG GaGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC 420  
 TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG 480  
 CCGTGAAAGG GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT 540  
 CGAACCTTAC GACCGATCGG TTAAACAGCC GATAGCTCTT ACCACTGGAG CTACTGTGGG 600  
 ATTAATATTA TGCCTGGGCA ACGTTCCTTAC TCTTAGCGGA ACGTTAAGTT CCGACTTACC 660  
 ATCCGACGCT AAGGAGCTTT AACTTCTnG TGGTTCCGGC ATGGGGGGAA CAGGTGGT 718

(2) INFORMATION FOR SEQ ID NO: 3763:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3763:

TnCACTCACC GCAGATTTTT AAGTCCTGTG CGTCTGCCAG TTCCGCCACC CCGGCACTAT 60  
 AAAAATGGAG CAGAAGACGG GATTCTGAACC CGCGACCCCA ACCTTGGCAA GGTGTATTTC 120  
 TACCGCTGAA CTACTTCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCT 180

AGGATTTCGAA CCTCTGGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGGAGCTAAT 300  
 GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GGAACCCCCA ACCTACTGGA TTTACAAGTT 360  
 5 CAATTGCTCT AnCAATTTGA GCTAAGGCCG GGCAATATGT 400

(2) INFORMATION FOR SEQ ID NO: 3764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3764:

TTAAAGTATT CCCAATTATA ATTCTTCATG ATTTTCTTAT TGGATTTCGA ATTTGGTTTC 60  
 20 ATGCATTGAT GTCTCAAAGA ACATGATGAA CAGTCATCAC ATTCATATAG TTTGAAGTCT 120  
 CGTTTAAAC CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA 180  
 TTAGGACATA TAAATTCATT ATTAAGTTCG TCATATTTCC AATTTTGAGT GTTGAAAATG 240  
 25 CCACTTTTAA ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGCGCTT 300  
 TTATTAAAT CATCTATAAT AGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT 360  
 ACAATATACT CTGGTAAATA ACCGaaGGaT TTTGAATCAT TGTTAAAAAT GGGATTAAATG 420  
 30 TTCTAGTATC TGTTGGGTTT TGAAATAGGT CATAGGATAA AACAAATTGr GAATTTGTCTG 480  
 CTATTTGgTA AATTGGTATC CTGGCTTAAG TTGGGCCATT TTTCCATATG GGCCTTCCTT 540  
 35 CCATTCTCCA TAAAAGTTGG CATCATGGAT CCAGATCCnG TTTTAGGAAA ACCTAATTCC 600  
 AACCTTTAAG 610

(2) INFORMATION FOR SEQ ID NO: 3765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

CTTCTTGGTG CTGCATATCC CCTACAATAA TTAAACCTTT TTTCTTATTT AAAATGTGTC 60  
 50 TTAATGCCGA TGCATCTATA CTTTTTTGAT AGTGCGGTAA AATCTTCATC TCAGAnGTTA 120  
 ACAATTCTGT TGCATTCAAA TCAGGTGTTA ACGGATCTCT AAATGGCAAG TTAAAATGAA 180



CACAATGGTC TCTTTACTAT CATCCGCAAT AGGCATATCG AACTCATAnC TTACATAATT 300  
 ATTAAACATA TTTACTTGAT TAATCGCTTG TGGTGCGCCT ACAnTTCTTA ATTCAGCGGA 360  
 5 CGGTCACTTG TTA AACCGT TTAAGGTATT CTACTAATTn 400

(2) INFORMATION FOR SEQ ID NO: 3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3766:

CnTTTAACCT TTTTAAGGAA TCCTGCTAAT GCGGGTTTGT GCATTTTCGA nTnTTTrGTA 60  
 20 tCTCACGCAA tCTTGGTGGT CATTCAAGTTC GTATATGGCA TCCATTAAGA CGCGAAGATC 120  
 AAATGGACTA TTGATGACTT CTGGAATACC ACGATCTATA TTTAGTAATT GATAAACAGC 180  
 TTCCATGGCA GTACGAACCG AATATTCTGT TGTAATACA GTGTCTCGCT CTGTTTCTGC 240  
 25 AAAGTTACCA ATAAATGCTA AGTTCTGAGA TTGATGCGGG ACGACTAAAG GTCTGTCGCC 300  
 GATAGCACGC GTCATGAAAT AAGATGTGAT ATATGGCATA TAAACAGGgA ATCGTATTAG 360  
 ATGCATGTnT TGCTAAGTCT TCAATTTTGG TCAGTTGATA CACCTAAGTG GATACAGCCA 420  
 30 TTCTTGGCAT ATTTCAATTAC CACTACATnC T 451

(2) INFORMATION FOR SEQ ID NO: 3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3767:

ACACGTGAAC GTCTTCAAAT GGAAGTACGT GACGTTCACT ACTCTCACTA TGGCCGTATG 60  
 45 TGTCCAATTG AAACACCTGA GGGACCAAAC ATTGGATTGA TTAACCTATT ATCAAGTTAT 120  
 GCACGTGTAA ATGAATTCGG CTTTATTGAA ACACCATATC GTAAAGTTGA TTTAGATACA 180  
 50 CATGCTATCA CTGATCAAAT TGAATTTTA ACAGCTGACG AAGAAGATAG CTATGTTGTA 240  
 GCACAAGCAA ACTCTAAATT AGATGAAAAT GGTCGTTTCA TGGATGATGA AGTTGTATGT 300  
 CGTTTCCGTG GTAACAATAC AGTTATGGCT AAAGAAAAAA TGGATTATAT GGATGTATCG 360

## (2) INFORMATION FOR SEQ ID NO: 3768:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3768:

CCTACGACCG ATCGGTAAAC AGCCGATAGC TCTACCACTG AGCTACTGTG GATTAATATT 60  
 ATGCCTGGCA ACGTTCTACT CTAGCGGAAn TAAGTTCGTA CTACCATCGA CGCTAAGGAG 120  
 CTTAACTTCT GTGTTCCGCA TGGGAACAGG TGTGACCTCC TTGCTATAGT CACCAGACAT 180  
 ATGAATGTAA TTTATACATT CAAACTAGA TAGTAAGTAA AAGTGATTTT GCTTCGCAA 240  
 ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT CnGCTCCACA TGTCACCATG 300  
 CTTCCACCTC GAACCTATTA ACCTCATCAT CTTTGAGGGA TCTTATAACC GAAGTTGGGG 360  
 AAATCTCATC CTGnAGGGGG CTTCATGCTT AGATGCTTTC 400

## (2) INFORMATION FOR SEQ ID NO: 3769:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3769:

CTTGACCGAA GTTCTTACCT ACATCACCTA AATTAATGAC ATGTCCACCA GTCATATACT 60  
 CTAATCCATG GTCGCCGATA CCTTCAACGA CAACATCTAC ACCACTATTT CTAATACAGA 120  
 ATCTTTCTnC TGCCTACCG TTAATAAATG CCTTACCACT TGTCGCACCA TAGAATGAGA 180  
 CGTTACCAGC AATAATTTCA TTTTGTGCTT CTTCAAAAGG TGCTTTGACA ATGACCGTAC 240  
 CACCAGATAA TCCTTTACCA ACATAGTCAT TCGCATCTCC AGTATGATGA ATCATTAAGC 300  
 CTTTCGGTGC ATATGCTGCA GGACTTTGGA CCAGCATGAC CATTCGTATA AACATTAATT 360  
 GTATTTTCAG GGAGGTCCTG CTTCTCCATA TTGTTTCGGA 400

## (2) INFORMATION FOR SEQ ID NO: 3770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3770:

5 CATTACGTAA TTAAAGATA GTCATTAAGA GAGGnTGATA ACCATGCAAG AAGCATACAT 60  
 TGTAGCTTAT GGGCGTTCAG CGCAGCGAAA CAAAGCAAGG CGCATTATTC CACGAAAGAC 120  
 CTGATGATGT CGCAGCCAAA GTATTACAAG GCGTATTGAA ACGTATTGAC GGAAAATTCA 180  
 10 ATAAGAATAT GATTGAAGAT GTCATTGTTG GTACGGCTTT TCCAGAAGGA TTACAAGGCC 240  
 AAAACATTGC ACGAACGATT GCATTGCGTG CGGGATTATC TGACACGGTA CCGGTCAAAC 300  
 AGTGAATCG CTACTGCTCA TCCAGGnTTT ACAAACCATT CGCGATTGCA GGCCAATCAA 360  
 15 ATTATGGCnG GTCCAAGGAG ATATACTTGT TAGCTGGTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3771:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3771:

ACTCTCTTGC AnTAAGGGCA GGAATGACC GATGGGATTA AAAGATCAAG CTGTTACCTG 60  
 30 GGAAGGTAT TTTCATCAAT TTCCAGAACT ATCCGATAAA GAATTTAAGA CTACACAAAA 120  
 AATTAAAGAT ATTTTAACAG AACATCATAT TAGAATATTA GACTTACCAC TTGCGACTGG 180  
 GCTTGTGCT GAAGTGGGAC AAGGTCTGAG TTGTATAGCT GTTCGGGCTG ACATTGATGC 240  
 35 TTTACCGATT CAAGAGCTTG TTGAACAGGA TTTTAAATCT GAAAATGAAG GTGTTATGCA 300  
 TCGTGTGGT CATGATATTC ACATGGCTAG nATTTTGGCT ACAGCTGGTA AAATTAAAAG 360  
 40 AGATTGAGGG CACTCTTACT GGGCGTGTTA AATCCATTG 400

## (2) INFORMATION FOR SEQ ID NO: 3772:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3772:

TTTATTTTGA CGTTTTAGAC ATAAAAAAA GAGACCTTGC GGTCTCAATG CGGCTCATCG 60

55

GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG 180  
 CTTACTCATT TAGCTCTACT AAACCTGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 240  
 5 GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTGCTTTT TTATTTTGAC GTTTTAGACA 300  
 TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT TGCCTGGGCA 360  
 ACGTTCTACT CTAGCGGGAA CGGTAAGTTC GGACTTACCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3773:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3773:

TTGATATTCC TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGGnATAGGC 60  
 GACGTGCGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG TATTAGGCAA ATCCGGTACT 120  
 25 CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT TCGAGTCGTT GATTTACACAC 180  
 TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCGTAC CGCAAACCGA CACAGGTAGT 240  
 CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA AGGAACTCGG CAAAATGACC 300  
 30 CCGTAACTTC GGGAGAAGGG TGCTCTTTAA GGTAAACGCC CAGAAGAGCC GCATGGAATA 360  
 GGCCCAACGA nGTTTATTCA AAAACACAGT CTCTGCTAAA 400

35 (2) INFORMATION FOR SEQ ID NO: 3774:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3774:

45 TACTTAGACA ATCGAAAGTG TACATTATTA AATTATCATT TCCAGTTCTA CTCTAGCGGA 60  
 ACGTAAGTTG GCTACCATCC TCGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 120  
 CTTTCTCTC CTTGCGCTCT CACTTACTCA TTTAGCTCTA CTAAACTCGT TGCGTTCTTT 180  
 50 TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCCAAGC CATTTTCTT TGTGTTTGCT 240  
 TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG CGGTCTCAA TCGGGCTCAT 300

GACGCTAAGG AGCTTAAACT TCTGTGTTTC GGCATGGGGA

400

## (2) INFORMATION FOR SEQ ID NO: 3775:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3775:

CGGTTTATCA AGAATGGAAA GAGTTGTACG TGAAAGAATG TCAATTCAAG ATACTGAGTC	60
TATCACACCT CAACAATTAA TTAATATTCG ACCTGTTATT GCATCTATTA AAGAATTCTT	120
TGGTAGCTCT CAATTATCAC AATTCATGGA CCAAGCAAAC CCATTAGCTG AGTTAACGCA	180
TAAACGTCGT CTATCAGCAT TAGGACCTGG TGGTTTAACA CGTGAACGGC TCAAATGGAA	240
GTACGTGACG TTCACTACTC TCACTATGGC CGGTGTGTCC AATTGAAACA CCTGAGGGAC	300
CAAACATTGG ATTGATTAAAC TCATTATCAG TTATGCACGT GTAAATGGAA TTCGGCTTTA	360
TTGAAACACC ATATCGTAAA AGTTGATTG GATACACAGC	400

## (2) INFORMATION FOR SEQ ID NO: 3776:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3776:

AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG	60
TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTCACC ACCATTTTATAA	120
GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA	180
CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT	240
AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACnTAG GCGATTATTT CTTATGGAAT	300
TCAAGCTTAT TTAAACTCT TTATTCACCT GGTTCCTTGCCT GGGTAAAATC TAnATTTTAC	360
TTACnTATCT AGGTTTTTCAA TGTACAAATA ATGGTGGGGC	400

## (2) INFORMATION FOR SEQ ID NO: 3777:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3777:

AATTATAAAA TTAAATGGCG GTCTCGACGG GAATCGAACC CGCGATCTCC TGC GTGACAG 60  
GCAGGCGTGT TAACCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 120  
10 ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGACTTG 180  
GGTATTCCTC CAAAATTATA TGGACCTTGC AGGACTCGAA CCTGCGACCG AACGGTTATG 240  
15 AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA TAATTTTACA ACTAATAAAT 300  
AGTGGCGGTG GAGGGGATCG AACCCCGAC CTCACGGGTA TGAACCGTAC GCTCTAGCCA 360  
GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 400

20

(2) INFORMATION FOR SEQ ID NO: 3778:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3778:

CAAATCCTGC ACCATCAGAA AGTGGGGCAG ATGTTCTGC AGTCATAGTG CCGTCAGCTT 60  
TAAATACTGT ACGTAATTTG GCTAATGCCT CCATCGTGGT GTCAGGGCGT ATAAATTCAT 120  
35 CTTGGTCAAA GATATTTGTG TGTAATTTTG GTCCTGCGTT TGTATATTCA ACTGAGTTTA 180  
CTTGATTTGG AATAATTTCA TCTTTGAACC GACCATCAGC TTGTGCGTCA TAGGCACGTT 240  
GaTGACTTCT GACAGCATAA GCATCTTGaT CTTCGCGTGA TACGTCAAAT TGGGATGCTA 300  
40 CATTTTtCAG CAGTTAAACC CATAGGATAT GACGCACCTA TATCATCaA TTGTAAGGTT 360  
GGATTGTTTG TGGGCTTCGT TnGCCACCnn TTGGTACGGC 400

45

(2) INFORMATION FOR SEQ ID NO: 3779:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3779:

CAATCTAAAT CGTTCAAATT TGGCACAACG ACAAATAAGG CTTCAACACG AATATATTCT 120  
 CTCGGTTGAA ACCTTACTTA TTCATTTATT TTTTATAAAT TAGTGACATA AACTGTATT 180  
 5 AGCATCTGCA CGATCGGTTG AAATATATGT TACATTTTCT TGCTGCTTAA TAAATGCATC 240  
 ATAGTAATCA TATTGCGACG AATGATATGT GCCATTCGAT GTATCATTTG GGTTTAGCAA 300  
 ACAGCCATAA CCTTCGTCAT ATAAATGTTC ACnGAGCATA AGGGGCGTCA TGTTTTAGAA 360  
 10 CCACCTTACC TACATAAAAT TnGCCTCCAT AGGGATCATA 400

## (2) INFORMATION FOR SEQ ID NO: 3780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3780:

ATGGnCGGTC TCGACGGGAA TCGCAACCCG CGATCTCCTG CGTGACACn CAGGCGTGTT 60  
 25 AACCGCTACA CTACGAGACC ATTAGTAAAA CGGAGGAAGA GGGATTGAA CCCCCGCGAG 120  
 CCGTTAAGCC CCTGTGGT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 180  
 AAAATTATAT GGACCTTGCA GGA CTGCGACCGA ACGGTTATGA GCCGTTAGCT 240  
 30 CTAACCAACT GAGCTAAAGG TCCTAAATAT AATTTTACAA CTAATAAATA GTGGCGGTGG 300  
 AGGGGATCGA ACCCCCGACC TCACGGGTAT GAACCGTACG CTCTAGCCAG CTGAGCTACA 360  
 35 CCGCCTTATA TAGTTTGTAATAAATATGGT GGAGACTAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3781:

AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC CGCCTGATTC 60  
 TCTAGCACGT TCATAAATAG TTA CTGATA TCCTAGTAGA TTAAGTTCTT CAGCAGCAGC 120  
 50 TAATCCTGCT GGACCGCTTC CAACGATTGC CACTTTTTCA TCTCTACGGC GACTCGGAAC 180  
 TTTCGGCGCT ACCCAACCAT TTCAAAAGC TTCATCAATA ATTGTGCGTT CAATACCTTT 240

TACACGCCCT GTAAAGTCAG GAAAGTTATT TGTTCGCTT AAGCGTCATA AGCAGTTTTA 360  
 AAATCTTGAT GATACACCAA GTCGTCCAnT CAGGATGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3782:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3782:

ACATGATGCG TGTGGTATTG GTTTTATATGC GAATATGGAT AATAAAAGGT CTCACGACAT 60  
 CATTGATAAA TCGCTTGAAA TGTGCGACG CTTAGATCAC AGGGGCGGGG TCGGCGCAGA 120  
 TGGCATCACT GGTGATGGCG CAGGTATTAT GACTGAAATA CCTTTTGCAT TTTTCAAACA 180  
 ACATGTAACG GACTTTGATA TCCAGGTGA AGGTGAATAT GCCGTGGGGT TATTTTTTTC 240  
 CAAAGAACGC ATTTTAGGTT CTGAACATGA AGTAGTTTTT AAAAAATATT TTGGAAGGCG 300  
 AnGGGTTATC AATTCTTGGT TAACGTAATG TACCAGTTAA TAAAAGATGC CATTGCCTAA 360  
 ACCATGTAGC AGATACGATG GCCAGTCATT CCACCAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3783:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3783:

AATCGGGTGA TGTTGGACGA TGATACGCAG GGAACGTTGC GTTATTCGTA TATGAAATAT 60  
 TGGATAACTG TTTTAACAAT GATGGTAGAG ATATTTTCATC ATTTGTAACA TCGTCAATTT 120  
 TGATATTGTG ATGATTTAAC ATAACGACAT CATCGATATT GAATTGGTAT GAAAAACCTG 180  
 CTGTTGCTGA ATCTGTTAAT TTGGCTCCAA TATTTAAAAT TAAATCGCTG TTGTCCACAT 240  
 AATCTCGTAT TTTATCTTCG GCAATTTTCC CATCGTAAAT ACCCATATAA TATGGATTTT 300  
 CCTCATTAAG AGCACCTTTT CCTAATGAAA GTTGTGCTAC TGGGTATCTG TGTTTGAnTT 360  
 ACAAAATCTT CnAAGTCCTG GATGGAGGTG AAAACTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3784:



- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3784:

10 GGTACTAAGA TGTTTCAGTT CTCCGGGTGT GCCTTCTGAT ATGCTATGTA TTCACATATC 60  
 GATAACATGA CATAACTCAT GCTGGGTTTC CCCATTCCGA AATCTCTGGA TCAAAGCTTA 120  
 CTTACAGCTC CCCAAAGCAT ATCGTCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180  
 15 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 240  
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 300  
 TTTAAAATAA TTAACTCAT TGTCTGcNAA ACGTTTTCTT TTATAAAAAG AnTTTAAACG 360  
 20 CGTTAATGAA GCTGTGAGTG TTCCTTCGAA CACGAGnGA 400

## (2) INFORMATION FOR SEQ ID NO: 3785:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3785:

TACTGGAATG ACATCAGATA CATGTGCACC ACCAATCCAT TTCTTTTCAC CATTGATAAC 60  
 35 CCAAGTATCG CCTTGnCGTT CAGCGACTGT TTCAAGACCT CCCGCAACGT CCGAACCGTG 120  
 TTCTGGTTCA GTTAAAGCAA AGCATGTACG CAGTTCATGT GACTGTAATT TAGGTACATA 180  
 TTTTCGCAATT TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG 240  
 40 AACACCGAGT AGGGTAGCTA AGGAAATATC AAATCGCGCG AGTAGGTAAG ACATGAAAAA 300  
 CTGAAATAGT TGACTAGGCA TTTTGCGGTT TGGACGATCC TTGTAAAGTA ATGGATTGTT 360  
 AAAATAATTT AATTCTCCCA GTCTTTAAAT AGTCCTCGGG 400

45

## (2) INFORMATION FOR SEQ ID NO: 3786:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

TCATTTGACG AATTTTCATTG TTATTCAAAA TTCTATCTAA TCGTGCTTTT TCAACATTTA 60  
 ATATCTTACC TCGTAATGGT AAAATCGCCT GCGTTCTAGA GTCACGACCA GATTTTGTAG 120  
 5 ACCCCCCGGC AGAGTCCCCT TCGACTAAGA AAATCTCACA TTCTTCAGGA CTTTACTAG 180  
 AGCAATCGGC TAATTTACCT GGAAGCTTGC TACATCTAAC GCTGATTTAC GACGTGTTAC 240  
 TTCACGCGCT TTTTTCGCAG CAACACGTGC ACGGCCGCC ATAATACCTT TTTCAACCAC 300  
 10 TGTACGTGCG ACTTGTGGGA TTTTCATATA AAAATCGTTC AAAGTGCTCT GAGAATAATT 360  
 TATCTACAAC TTGACGCACT TCAGAATTAC CTAATTTTGT 400

## (2) INFORMATION FOR SEQ ID NO: 3787:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3787:

TCTCTTCCCG TTTCGCTCGC CGCTACTAAG GGAATCGAan TTTCTTTCTC TTCCTCCGGG 60  
 TACTAAGATG TTTCAGTTCT CCGGGTGTGC CTTCTGATAT GCTATGTATT CACATATCGA 120  
 TAACATGACA TAACTCATGC TGGGTTTCCC CATTCGAAA TCTCTGGATC AAAGCTTACT 180  
 30 TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 240  
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 300  
 TTAACATGAA GTTACGTTCT TTTATAAAAA GATTTAAACG CGTTATTAAT CTTGTGAGTG 360  
 35 TTCTTTTCGGA CACTAGCGAT TATTTCTnAT GATnCAAGCT 400

## (2) INFORMATION FOR SEQ ID NO: 3788:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3788:

ATTCTCTGCT TTCATCTCAT TTGGTGACTA ATACCCTGAT TTTGTCCAAG TAAATGCTTC 60  
 50 ATAAAGTATT CTTGACCTTT TGCAGAACTT GAAATTAAGT TTGAACGCCA TATATAATGA 120  
 TTTTGATGA TTCTTTTCA AATCAGGATC TCTATTGCAA ATTGTGTTG TnTTGATTTTC 180

TCTTCTGCAA ACAACAACT ATTTTATTA AATTGTGGAT ATGATGGTAA CCAACCAAGT 300  
 CTAGCTGCTA AnACATTATA ATCAGCTGGA TGTGATGCT TTAACCTCTC TGTTTTAGCT 360  
 5 AATGGAGATT TTAAACGATC TACATTTGAC TCTTCATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3789:

CGGTTTCTTA ATTATGAACG CAACTATGAA TGGCTTATTA ACTATCACGG GCACATTGGC 60  
 AAAAGATCAG CTTGCACAAA ATGGACAAGG CATGGTGCTC GGTATACAAA CGGTTGAAAC 120  
 CGGTGTTTTT GGCGGGATTA TCACAGGTAT TATGACCGCA ATACTTCACA ACAAATATCA 180  
 CAAAGTGGTA TTACCACCGT ATTTAGGTTT CTTTGGTGGC TCTAGATTG TCCCTATTGT 240  
 CACAGCATTT GCCCAATCT TTTTAGGTGT ATTGATGTTT TTCATTTGGC CAAGCATACA 300  
 nGCCGGCATT TATCATGTTG GTGGGATTG TAACGAAAAC AGGTGCCATC GGTACTnTTG 360  
 TTTATGGGTT CATCTTAGG ATTGTTAGGT CCACTCGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3790:

ATAATGGACT GTGCCGnGTA ATAATATnGn TCTCTAAAAG TTGTATTTTA AAAATAGTTC 60  
 TTAAATTAT ATACCCACCA CATTTGGTGA kGAACCTAAA AAAAAGCACT TCCCAAAAT 120  
 GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA 180  
 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 240  
 AGTGACGGAT CAAAnGTCCG TTGCCTTACC GCTTGGCTAT AGCCaATATA TAGATGGTGG 300  
 AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC 360  
 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 420

CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGTGnTCTT 540  
 AACCGtTGAC CAAGGAGCCA TGGCTCaCCA GGTAgGACTC GAACCTACGA CCGATCGGTT 600  
 5 TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGGATTA ATATTATGCC TGGCAACGTT 660  
 CTACTCTAGC GGAACATAAG TThGAACTnA CCATCGACGC TAAAGGAGCT TAACTT 716

## (2) INFORMATION FOR SEQ ID NO: 3791:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3791:

TGTCATGACG TTATTTGAAG ATATCGCGCA AGTCTTTTTA AAGGTAACAC TATCATTTAT 60  
 GCAATACGGC GCATTACCAG AGTTGCATGG TCAAAATATA TTGTTGTCAT TTGAAGATGG 120  
 ACGTGTACAA AAATGCGTGT TACGTGATCA TGATACTGTC AGAATTTATA AACCATGGCT 180  
 25 AACAGCACAT CAGCTTTTCAT TGCCGAAGTA TGTCGTCAGA GAAGATACAC CTAATACGCT 240  
 AATTAATGAG GATTTGAAA CATTCCTTGC nTGATTTTCA AACATTAGCT GTGATCGGTA 300  
 AATCTATATG CCATTATTGA TGCAATTCCA AGATTTATTT GGTGTGAAGT GnAGCATGAA 360  
 30 CTTATGTCGT TGTTAAAACA AATTTTGAAA AAAGGAAGTG 400

## (2) INFORMATION FOR SEQ ID NO: 3792:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3792:

TTTTACACA ATACATGGAC ACCATGGTTC AATGCTTCTA TAGAAAGATC AGCATGGAAT 60  
 45 TTATTAGGTG TACAAATGAC CACCGCATCA ACAAGTTTAA ACAGCTCGCT AGGTGTCTCA 120  
 ACTGCATGAG GTATATTAAA GCGCTTCGCA ACATCAATCA TCTGCACTGT ATTAATATCT 180  
 TGTACTGCAA CTAATGAGAC TGTGTCTTTG AGTTTCAGCA ATGCTGGAAT ATGACGGTCT 240  
 50 TGTGCAATAC CACCAACACC TATCACACCA ACTTTTAATT TTGTCATGAT GTGCCTCCTT 300  
 ACCGTATGAT GTtATTCAAA GTAAATTGCT TTGCCTGATT TkGCAGACTG ATaAATyGCT 360

TACCA

425

## (2) INFORMATION FOR SEQ ID NO: 3793:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3793:

15 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 60  
 AGTGACGGAG AAAAGGTCCG TTGCCTTACC GCTTGGCTAT AGCCCAATAT ATAGATGGTG 120  
 GAGGGGGGCA GATTCGAACT GCCGAACCCG AAGGAGCGGA TTTACAGTCC GCCGCGTTTA 180  
 20 GCCACTTCGC TACCCCTCCA GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG 240  
 ACGGGTTCGA ACCGCCGACC CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT 300  
 25 CTCCAAATA ATGACTCCTA CGGGACTCGA ACCCGTGTTA CCGCCGTGAA AGGGCGGTGT 360  
 CTTAACCGCT TTGACCAAGG AGCCATGGCT CCACAGGTAG 400

## (2) INFORMATION FOR SEQ ID NO: 3794:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3794:

40 ATCAGCAGGG TTGAAAGTAC CTGCTGCAAC AGTAATACCA TTATTAGTTC CAGCAATACC 60  
 TGCTACAGTT GCTGCAGATG CTTCTTTCAC CCATGGACTC GTATTATTGC GACGTGTAAA 120  
 TGTATCACAA CGTTACCATT ACGTTTAATA ACTAATTTAT CAGCGTATGT CGTTACGTTA 180  
 45 CCGGCATGTG TATTCAGTGT TTGGTTTGCT CCAGGTGCAA TTGTAATCGC TCCTGCCGCT 240  
 GTTTCAGTCA CAGTTGGTTT CGCTGGTTGC ACATCTTTTA CTACAAATTT CGCTGGTAAA 300  
 GATGTTGCAA AAGTATGTCC GTTATAGATG ACGTCCATAT TTTGCGTTAA CGACTTTAGC 360  
 50 CACATTCGGT TTATTCATAG CGGACCAGTT TCGTCCATT 400

## (2) INFORMATION FOR SEQ ID NO: 3795:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3795:

GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACAA 60  
10 TGGTAGGAGA GCGTTCTAAG GCGGTTGAAG CATGATCGTA AGGACATGTG GAGCGCTTAG 120  
AAGTGAGAAT GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT 180  
AAGGTTTCCA GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTAAGC TGAGGCCGAC 240  
15 AGGCGTAGGC GATGGATAAC AGGTTGATAT TCCTGTACCA CCTATAATCG TTTAATCGAT 300  
GGGGGACGC AGTAGGATAG GCGAACGTGC CATTTGATTG CACGTCTAAA GCAGTAAAGC 360  
TGAGTATTAG GCnAATCCGG TACTCGTTnA AGGCTGAACT 400

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(2) INFORMATION FOR SEQ ID NO: 3796:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3796:

GCACATGTTG CCATgCTTGA GCTAAATTAC CTTGCATCAT TGCTAGCTTT TCTTGTATTA 60  
ACTGATATTT ACTAATTGGT TTGCCGAATT GCTTACGCTC AGTGACATAA TCTAATGTGG 120  
35 CACGTAAAGC GCCACCATAC CACCTGTAGC CATATAAGCA ACGsCTGCTC TCGTTGAATA 180  
AAGAAATTTTG GCAATATCTT TAAAGCTTGT TATGTTTTGT AAGCGATCCG CTTCATCTAC 240  
40 TTTGACATTA GTTAATTTAA TTAGGGCGTT AGGAACAATG CGAAGTGCGA TTTTATTATC 300  
AATGACTTCA ATATCGACGC CATCTTGTTT TGGTCTGACT ACAAAGCAAT GGGGTTTGCC 360  
AGTTTCnGTT ATTTACTGCG AATACTGGGG GGGnGnGGTT 400

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(2) INFORMATION FOR SEQ ID NO: 3797:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3797:

GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG ACGCTGATGT GCGAAACGTG 120  
 GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT AAACGATGAG TGCTAAGTGT 180  
 5 TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA AGCACTCCGC CTGGGGAGTA 240  
 CGACCGCAAG TTGAAACTCA AAGGAATTGA CGGGGACCCG CACAACGGTG GGAGCATGTG 300  
 GTTTAATTCTG AAGCAACGnA GAGAACCTTA CCAATCTTTG ACATCCTTTT GACACTCTAG 360  
 10 GAGATAGAGC CTTCCCTTCG GGGGGACnAA GTGACAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 3798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3798:

CACAAAACAA GCCAAGCAAA ACAAAACGCAT ATAACGTAAC AACACATGGA AACGGCCAAG 60  
 25 TATCATATGG CGCTCGCCCA ACACAAAACA AGCCAAGCAA AACAAATGCA TACAACGTAA 120  
 CAACACATGC AAACGGTCAA GTGTCATACG GAGCTCGCCC GACATACAAG AAGCCAAGTA 180  
 30 AAACAAATGC ATACAAATGTA ACAACACATG CAGATGGTAC TGCGACATAT GGGCCTAGAG 240  
 TAACAAAATA AGTTTGTAAC TCTATCCAAA GACATACAGT CAATACAAAA CATTACGTAT 300  
 CTTTACAACA GTAATCATGG CATTCTATGG ATGCTTCTAA CTGGAATTAA AGCATCGGAA 360  
 35 CAATCGGGAn GCATATTTCT AAAATTATTT ATTCCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 3799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3799:

CTTCGCCGAT ATGGGGGAAG CTAGGTGATA AGATCAGCCG AAAATGGATG GTGTTAAGAG 60  
 50 CGTTACTTGG TTTGGCGGTA TGCTTATTTT TAATGGCATT GTGTACGACA CCATTACAGT 120  
 TTGTACTTGT GAGGTTATTG CAGGGACTAT TTGGTGGTGT TGTTGATGCA TCAAGTCCGT 180  
 TTGCGAGTGC AGAGGCGCCA CTGAAGGATC GTGGAAAGGT ATTAGGAAGA CTGCAAAGTT 240

TTTtagTGCg TtACTGATGA GTATTGCCGT TATTACTTTT ATTGTCTGTn TTTTCGGTGc 360  
 CATTAAaATG ATTGAAACGA CACATATGGC CAAAnnCACA 400

(2) INFORMATION FOR SEQ ID NO: 3800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3800:

GGAATCTATT ATATTAGATG TAAAAAATTT CGCGCAAAAT GTGTTAGGTA AAGGTGTCAT 60  
 TGTCGTCAAT GATGTGCCCTG GCTTTGTGCGC AAATAGAGTC GGCACGCAAA CAATGAATGA 120  
 TATTATGTAT CGCGCCGAGC AACACAAGAT AAGCATTGTA GATGTGGATG CTTTAACTGG 180  
 GCAAGCGATT GGTCGTCCTA AAACAGGTAC ATATGCGCTA TCTGACCTAG TCGGTTTAGA 240  
 TATTGCAGTG TCTGTAAATT AAAGGCATGC AACAAGTACC TGAAGAAACA CCTTATTTTC 300  
 ATGATGTCAA AATGTAAATA CGTTGTTTGA CCATGGGCGC ACTCGGACGT TAAnnCGnAA 360  
 ACCAAGGGTT TTTACCAAAA AGGGTTAAAG GGnAACTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3801:

TGCAGGCGTT TCTGGTCTGC ATAGTTTACG CATACGACCT GCGCGATCCT TATCTGGTAA 60  
 TAAATTGTAA AACGATAGTT CCCGTTGTTC CTAATAGTTG TATTCTATCT GACGCATAAT 120  
 GTGAAAAATA ACCTGCCATC TCTAAGCCCG GTCTTGATAT ATCAGCATTT TTAATTGGCT 180  
 TCGATAGTCC TTCTTCACCA GCGATTAAAT CTAACTTTAA TGTTTCAACT AGTTTTTCTG 240  
 TCGTTAACAT GGGTTCACCT CAATTGTATT TACCCTACTC TTACATCTCT TCTTATCATA 300  
 TCAAAAATAT AACACCAATC TACATTGAAA AGCTAAAnTA AATATTAATG TTCATTATTG 360  
 TTATnATTTT ACAAGTCAAT ATCATCATAA TTTATTGCTG 400

(2) INFORMATION FOR SEQ ID NO: 3802:



- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3802:

10 TTTCAC TTTT GAACCATGCG GTTCAAAATG ATTATCCGGT ATTAGTCCG GTTCCCGAA 60  
 GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC ACCCGTCCGC CGCTAACATC 120  
 AGAGAAGCAA GCTTCTCGTC CGTTCGCTCG ACTTGCATGT ATTAGGCACG CCGCCAGCGT 180  
 15 TCATCCTGAG CCAGGATCAA ACTCTCCATA AAAATTATGA TGTTTGATTA GTCATAAAT 240  
 ACTAAATAAT GTTTGTAAGT TATAGTTACG TTTTTTGGAA TTAACGTTGA CATATTGTCA 300  
 TTCAGTTTTT AATGTTCAAT TTTCTTACCG ACAAGAATTA ATTATACATT TTATTAACAT 360  
 20 TTAAGTCAAT AACTTTnTTT ATCCTGTCCA TTTnATTTTT 400

## (2) INFORMATION FOR SEQ ID NO: 3803:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3803:

TAGTACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 60  
 35 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 120  
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 180  
 AACCGAAGTT GGGAAATCTC ATCTTGAGGG GGGCTTCATG CTTAGATGCT TTCAGCACTT 240  
 40 ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC GACAACTGGT ACACCAGAGG 300  
 TATGTCCATC CCGGTCCTCT CGTACTAAGG ACAGCTCCTn TCAAATTTCC TACGnCCAnG 360  
 45 ACGGATAGGG ACCGAACTGT TTTCACGACG GTnCTGAACC 400

## (2) INFORMATION FOR SEQ ID NO: 3804:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 457 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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AGTnCACTCA CnCCAGATGT TTAAGTCCTG TCGTCTGCC AGTTCGCCA CCCCGGCACT 60  
 ATAAAAATGG AGCAGAAGAC GGGATTGCAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 120  
 5 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 180  
 TTAGwATCCT AAGTCTAGTG CGTCTGCCAA TTCCGCCACA CCCGCAAATG GTGAGCCATA 240  
 GAGGATTGCA ACCTCTGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG 300  
 10 GCTCTTCCAT GGTGCCGGCC AGAGGACTTG AACCCCCAAC CTACTGATTA CAAGTCAGTT 360  
 GCTCTtACCA ATTGaGCTAG GCCGGCAATA TGTaAGAATA AATGGTGGAG AATGACGGGT 420  
 15 TTCGAAACCG CCGnACCCTC TGGCTTGTTA AGGGCAG 457

## (2) INFORMATION FOR SEQ ID NO: 3805:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3805:

ACTTTTTATT TTGACGTTTT AGACATAAAA AAAGCTCACG GTCTCAACTT GCCTGGCAAC 60  
 GTTCTACTCT AGCGGAACGT AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120  
 30 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180  
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTTCACTTCGC CAAGCCATTT 240  
 35 TTCTTTGTGT TTTACTTTTIA TnTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300  
 TCAATGCGGC TCATCGCATC CATnTTTTGC CGGGCAACGT TCTACTCTTA GCGGAACGTA 360  
 AGTTGGCTAC CATCGTCGCT AAAGACCTTT TTGACTGTG 400

## (2) INFORMATION FOR SEQ ID NO: 3806:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3806:

GTTATGAAAG TCGCGCTTAA AATGCGTTAA TGTGACAAGG ATAATTCAAC ATCGTTTCAT 60  
 TTTACTGAGT CATTGCACTT ATCATACACA TTATATTTAG CATGAGTTAT ATTACTAAAA 120

TCATTGGCTT AATATTTACA GCGCTTGGTA TTGCAGGTGC CGTATTACCT TTA CTGCCAA 240  
 CGACCCCTTT TTTACTCGTA GCAGTTTTTT GCTTTGCTCG AAGTTCAGAT CGCTTTTACA 300  
 5 ATTGGGChnA TTAATCAAAA AATTTATAAA GAATATGTAG AAAACCTTTn TTTGACATCG 360  
 AGGCTACACG CTACAACAGA AAATTGAAAA TTTAATTAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3807:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3807:

20 AGGAGAACAT GCTGTTACAT TTGGAGAGCC TGCTATTGCA GTGACCGTTT AACGCAGGTA 60  
 AAATCAAAGT TTTAATAGAA GCCTTAGAGA GCGGGA ACTA TTCGTCTATT AAAAGCGATG 120  
 TTTACGATGG TATGTTATAT GATGCGCCTG ACCATCTTAA GTCTTTGGTG AACCGTTTTG 180  
 25 TAGAATTAAA TAATATTACA GAGCCGCTAG CAGTGAACGA TCCAAACGAA TTTACCACCA 240  
 TCACGTGGAT TAGGATCGAG TGCCAGCTGT CGCGGTTGCT TTTGTTCTGT CAAGTTATGG 300  
 ATTTTTTAGG GnAAATCATT AACGAAAGnA AGAACTCATT GGAAAAGGCT nATTGGGCCA 360  
 30 GAAGCAAATT GCCACATGGT AAAACCAA 388

## (2) INFORMATION FOR SEQ ID NO: 3808:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3808:

ATGCGCAGAG TATATGGAGG AACACCA GTG TCGAAGCGCA CTTTCTGGTC TGTA ACTGAC 60  
 45 GCTGATGTGC GAAACGTGkG GGATCAAACA GGATTAGATA CCCTGGTAGT CCACGCCGTA 120  
 AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG TGCTGCAGCT AACGCATTAA 180  
 GCACTCCGCC TGGGGAGTAC GACCGCAAGT TgAAAACTCA AAGGrATTGA CGGGGACCCG 240  
 50 CAcAAGCGTG GGAGCATGTG GtTTAATTCTG AaGCAACGnn GAGGAACCTT ACCAAATCTT 300  
 GACATCCTTT GACAACTCTA GAGATAGAGC CTTCCCCTTC nGGGAACAAA TGACAGGTGG 360

ACCCTTAAGC TTATTGCCA TCATTAA

447

## (2) INFORMATION FOR SEQ ID NO: 3809:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3809:

CCAACTGAGC TACTGAACCA TAATAAAAAT GTAATGACTG GCGGTCTCGA CGGGAATCGA 60  
 ACCCGCGATC TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACTACTACGA GACCTATAAA 120  
 ATATTGCGGG AGGCGGATTT GAACCAACCGA CCTTCGGGTT ATGAGCCCGA CGAGCTACCG 180  
 AACTGCTCCA TCCCGCGATA ATAAAAAATA ATGGCGGAGG AAGAGGGATT CGAACCCCGG 240  
 CGGCCCCGTTA AGGCCCTGTC GGTTTTC AAG ACCGATCCCT TCAGCCGGAC TTGGGTATTTC 300  
 CTCCATTATT ATAGGTAAAT CGCTATTAAT TATAAAATTA AATGGCGGTC TCGACGGGAA 360  
 TCGAACCCGC GATCTCCTGC GTGACAGGCA GCGGTGTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3810:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3810:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA ATAATGGTGG 60  
 GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT AACCAGCTGA 120  
 GCTATAGGCC CATTTTTTTT AATGTTAAAT AAACATTCAA AACTGAATAC AATATGTCAC 180  
 GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG AGGTGATCCA 240  
 GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTT GTCCACCTT 300  
 CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC TCTCGTGGTG 360  
 TGACGGGCGG TGTGTACAAG ACCCGGGAAC GATTTCACCG 400

## (2) INFORMATION FOR SEQ ID NO: 3811:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3811:

	GCTTCATGCT TAGATGCTTT CAGCACTTAT CCCGTCCACA CATAGCTACC CAGCTATGCC	60
10	GTTGGGCACGA CAACTGGTAC ACCAGAGGTA TGTCCATCCC GGTCTCTCTG TACTAAGGAC	120
	AGCTCCTCTC AAATTTTCCTA CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC	180
	TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTGGG ACCGACTACA	240
15	GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGGAACTCT	300
	TGGGGGAGAT AAGCCTGTTA TnCCCCGGGT AGCTTTTATC CGTTGAGCGA TGGnnCTTCC	360
20	ATGCGGGAAC CACCGGGATT	380

(2) INFORMATION FOR SEQ ID NO: 3812:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3812:

	GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA TGCTTAGATG	60
	CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTAGC ACGACAACCTG	120
35	GTACACCAGA GGTATGTCCA TCCCGTCTCT CTCGTACTAA GGACAGCTCC TCTCAAATTT	180
	CCTACGCCCA CGACGGATAG GGACCGAACT GTCTCACGAC GTTCTGAACC CAGCTCGCGT	240
	ACCGCTTTAA TGGGCGAACA GCAACCCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA	300
40	GCCGACATCG AGGTGCCAAA CCTCCCGTCT GntGTGAACT CTTGGGGGAG ATAAGCTGTT	360
	ATCCCCGGGT GAGnTTTnTC CGTTGA	386

(2) INFORMATION FOR SEQ ID NO: 3813:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3813:

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CTTGGTACTT CTGGTGTGG TGGCGTTGGT GTTCCGGCT CACTTGGTAC TTCTGGTGTC 120  
GGTGGCGTTG GTGGCACGAT TGGAGGTGTT GTATCTTCTT CAATCGTTTG TTGACCTTCA 180  
5 TTTTGGCCGC TTACTTTTGG AAGTGTATCT TCTTCAAAGT CAACACTATT GTGTCCACCG 240  
AATTGATAAC TTGGTTTATC TTTATTTGTA TCTTCTTCAA TAATTTTCACT GTGCTTATTG 300  
AATCCGTGAA TATGTGGCAC nTGGTCGAAG TCGATATCAA TGATGTTACC GCCATGTTCA 360  
10 TACTTAGGTT TGTCTTTTTT TGTAnCTTCC TCGAATGACT 400

## (2) INFORMATION FOR SEQ ID NO: 3814:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3814:

TAATTGGGCT ACCATCGTCG CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
25 TCCTCTCCTT CGGCTCTCGC TTAATCATTT AGCTCnACTA AACTCGTTGC GCnCTTTTCT 120  
CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
TATTTTGACG TTTTAGGCAT AAAAAAAGA GACCTTGCGG TCTCAATGCG GCTCATCGCA 240  
30 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGGCT ACCATCGTCG 300  
CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 360  
TTACTCATTT AGCTCTACTA AACTCGGTGC GCTCTTTTCT 400

## (2) INFORMATION FOR SEQ ID NO: 3815:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3815:

TTCTTTTATA TGATTTTTTA GATTTTAGTA AGTCAATAAA GCCAATTTTC TCCAACGATT 60  
GAATGTAACG TTGATTGATA AATGTATTTT TTGGTAAATC ACCACCCGCT AAAATTGTGG 120  
50 CGATATTTAA GGCAATATGA TAATCATGGT CGCTAATAAA ATGACCCCGT CTTTGCGCAT 180  
CTAATTGTCC TTGGATCAAT GCTTTGAAGT CTTACCTAA AGCGATATAT TGATGTCTAG 240

GTTGTGCTGT ATTGAAAATA ATCGTATCTG GTATCACGTA AATnACCATA ACGACGTGCC 360

TCCAAAGGCA TTTGGTAnGA GCCTTCGGCA ATGCCGATAA 400

(2) INFORMATION FOR SEQ ID NO: 3816:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3816:

CCAATATTTA TATTAATGAA AATAAGATGT TATATTCATT GTTAATTTAA CACATAGTAA 60

GAnAAACAGT CATAAATTGA TTTCTAATTG AAATCATCTT ATGACTGCTT TTTATTATAC 120

TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TCTTTCTTTG 180

TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240

CTCATCGCAT CCACTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA GTCGGACTAC 300

CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG GAACAGGTGT GACCTCCTTG 360

GCTATAGTCA CCAGACATAT GAATGTAAAT TCATACATTC 400

(2) INFORMATION FOR SEQ ID NO: 3817:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3817:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGGG GGGnATTATG AAGCGATGCA 60

TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120

ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180

GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240

TACCGAACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCATGATAAT TTCTTTGAAT TAGGTGGCCA TTCATTAAAA GCAACGTTAT GGnTGGAATC 360

GGATAGAGGC ATCTACTGGG GAAACGATTA CCAATTGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3818:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3818:

10 TCGGAATCTG GGAGGACCAT CTCCTAAGGC TAAATACTCT CTAGTGACCG ATAGTGAACC 60  
 AGTACCGTGA GGAGAAGGTG AAAAGCACCC CGGAAGGAAG TTGAAATAGA ACCTGAAACC 120  
 GTGTGCTTAC AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA 180  
 15 CCGGCGAGTT ACGATTTGAT GCAAGGTTAA GCAGTAAATG TGGAGCCGTA GCAnAACATG 240  
 TTCTGAATAG GCGGTTTAGT ATTTGGTCGT AGCCGnAAAC CAGGTGATCT ACCCTTGGTC 300  
 CAGGTTGAAG TTCAGGTAAC ACTGGAATGG AGGACCGAAC CGACTTACGT TTGAAAAGTG 360  
 20 AGCGGATGAA CTGAAGGTAG CGGAGAAATT CCCAATCGAA 400

## (2) INFORMATION FOR SEQ ID NO: 3819:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3819:

CAACGAGAGA CTCGGTGAAA TCATAGTACC TGTGAAGATG CAGGTTACCC GCGACAGGAC 60  
 35 GGAAAGACCC CGTGGAGCTT TACTGTAGCC TGATATTGAA ATTCGGCACA GCTTGTACAG 120  
 GATAGGTAGG AGCCTTTGAA ACGTGAGCGC TAnTTACGTG GAGGCGCTGG TGGGATACTA 180  
 CCCTAGCTGT GTTGGCTTTC TAACCCGCAC CACTTATCGT GGTGGGAGAC AGTTTCAGGC 240  
 40 GGGCAGTTTG ACTGGGGCGG TCGCCTCCTA AAAGGTAACG GAGGCGCTCA AAGGTTCCCT 300  
 CAGAATGGTT GGAAATCATT CATAGAGTGT AAAGGCATAA GGGACTTGAC TGCGAGACCT 360  
 45 ACAAGTCGAG CAGGTCCAAA AACGGACnTA GTGATnCGGT 400

## (2) INFORMATION FOR SEQ ID NO: 3820:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55



TGGCTCGAAC CACCGACCTC ACGCTTATCA GGCCTCGCTC TAACCAGCTG AGCTATAGGC 60  
 CATTAAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120  
 5 TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180  
 ATACGGCTAC CTTGTTACGA CTTCAACCCCA ATCATTGTGC CCACCTTCGA CGGCTAGCTC 240  
 10 CTAAAAGGTT ACTCCACCGG CTTCCGGGTGT TACAACTCT CGTGGTGTGA CGGGCGGTGT 300  
 GTACAAGACC CGGGAACGTT ATTCAACGTA GCATGCTGAT CTACGATTAC TAnCGATTCC 360  
 AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

(2) INFORMATION FOR SEQ ID NO: 3821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

TATTAAATTA ATGGTGGGCC TAAntGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT 60  
 GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA 120  
 30 ATACAATATG TCACGTTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180  
 AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240  
 ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTAC 300  
 35 AAACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360  
 GCTGATCTAC GATTACTnAG CGnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTCTGAAC CAACGAGTGA 60  
 CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAA TATATAGATG GnGGAGGGGG 120  
 GCAGATTCTGA ACTGCCGAAC CCGAAGAGCG GATTTACAGT CCGCCGCGTT TACCACTTCG 180

GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCAAAA 300  
 TAATGACTCC TACGGACTCG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCGC 360  
 5 TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AAC TTGCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60  
 20 ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120  
 CATAACCACT CTTACTTTCA ACTGCAnGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT 180  
 GCTCTGCTTT TTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATT ACGGTAGATA 240  
 25 ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300  
 TCTCATGTTC TCGAGATCCA CCAAATGTnA AATGGGGTAT GTGGCATCTA CTAAGCCGGG 360  
 GGACACTAnC TTTCCCACTA GGCATCAATC G 391

(2) INFORMATION FOR SEQ ID NO: 3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTTCGGAAAT CTCTGGATCA 60  
 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120  
 45 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180  
 ACGCGTTATT AATCTTGTTG AGTGTTCCTT CGAACACTGA GCGATTATTT CTTATGAATT 240  
 CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300  
 50 ACnTATCTAG TTTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360  
 TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC 60  
 TTACTTACAG CTCCCCAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC 120  
 CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC 180  
 GTTATTAATC TTGTGAGTGT TCTTTTGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 240  
 TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAAA TCTATATnTT ACTTACTTAT 300  
 CTAGTTTTCA ATGTACAATT TCTTTTTAGT CAAGCGCTCG CATAAGCAAT ATCACTTTAA 360  
 CCAAAAAATA TTTGAATGTn AAATAAACAT TCAAAACTGA 400

(2) INFORMATION FOR SEQ ID NO: 3826:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

TCACTCACCG CAGATTTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA 60  
 AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT 120  
 ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT 180  
 TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240  
 GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC 300  
 TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG 360  
 CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3827:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACCTTTAG AGAAGACCAA AAGAAGAAAA 60  
 5 GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AAACAGAGAA AATATAAAGA 120  
 AATGGTTTGG AAATGCTTGG GACGGCGTAA AAACATAAAC TGCTGAAGCC TTTAGTAAAA 180  
 TGGGCAGAAA TGCTAATCAT TTTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG 240  
 10 GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA 300  
 CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGGG AAAGCTTGGC CAATCTGTTA 360  
 15 AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCAAA 400

## (2) INFORMATION FOR SEQ ID NO: 3828:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

TCTCAGTTCC AGTGTGGCCG ATCACCTCT CAGGTCGGCT ATGCATCGTT GCCTTGGTAA 60  
 GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC 120  
 30 GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG 180  
 AAGTTATCCC AGTCTTATAG GTAGGTTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA 240  
 TCAGAGAAGC AAGCTTCTCG TCCGTTGCT CGACTTGCAT GTATTAGGCA CGCCGCCAGC 300  
 35 GTTCATCCTG AGCCAGGATC AAACCTCCA TAAAAATTAT GATGTTGANT AGCTCATAAA 360  
 TACTAAATAA TGTTGTAAC TATAGTACGT TTTTnGAAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3829:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA 60  
 GATTCGTGGC ATGCATACGC AAACCATTTT CTTCAATTAC TTCACCAAGG CGTTTAAAAAT 120

ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240  
 TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTTCGATT 300  
 5 CAAGTGGGA<sub>r</sub> sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCATT CTGCAAATnC 360  
 ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTC 400

## (2) INFORMATION FOR SEQ ID NO: 3830:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60  
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCCG AAATCTCTGG ATCAAAGCTT 120  
 ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180  
 25 GGATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTTA TAAGTCAAAC 240  
 GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT 300  
 TTAAATAAAT TTAACTCATT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG 360  
 30 TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

## (2) INFORMATION FOR SEQ ID NO: 3831:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 60  
 45 TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTA CAATCGCTTG CTTCTTTCCT 120  
 CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT 180  
 TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTGTGTTT ACTTTTTATT 240  
 50 TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300  
 TTTTTTGCCT GGGCAACGTT CTACTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

## (2) INFORMATION FOR SEQ ID NO: 3832:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

AGCTTATTTT AAAACGTCGT TTATTCACCTC TGGTTTTGCT TGGTAAAATC TATATTTTAC 60  
 TTACTTATCT AGTTTTCAAT GTACAATTTC TTTTITAGTCA AGCGCTCGCA TAAGCAATAT 120  
 CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 180  
 ACATTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 240  
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 300  
 TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 360  
 TGTGACGGGC GGTGTGTACA AGACCCGGA ACGTATTTCA 400

## (2) INFORMATION FOR SEQ ID NO: 3833:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

TTTTCTTCTG GTAAAATATC TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT 60  
 TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCAT ATCATGCAAT 120  
 TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCnAT GATACCAGTT 180  
 AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTTCATA ATGTGTTAAA 240  
 TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTGAG CCATTAATnT ACGGGTTACC 300  
 AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTTnAA 360  
 AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA 400

## (2) INFORMATION FOR SEQ ID NO: 3834:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

5 nAATTATATG GACCTTGCAG GACTCGAACC TGC GACCGAA CCGTTATGAG CCGTTAGCTC 60  
 TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA 120  
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 180  
 10 CGCCTTATAT AGTTTGTAAA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC 240  
 TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC 300  
 GGAAGACAG GATTGGAACC TGCGACCCCT TGGTCCCAAA CCAAGTGCTC TACCAAGCTG 360  
 15 AGCTACTTCC CGTATAATTA ACGCGCCCGA TAGGAGTCGA 400

## (2) INFORMATION FOR SEQ ID NO: 3835:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT 60  
 30 CGCAACATAA CCAAATGTTA TAATAATCT ATTACACAAA GAGATAAATT ACTTATGCAA 120  
 AGGCGGAGGA ATCAGATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT 180  
 AAAAAATTAT GGTGATTGTC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCCGT 240  
 35 AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT 300  
 GCAGATGCCT TGTCAGGTGA AGACATCACG TATCnAGAAG CGTGCGCAGA TGAAGAATAT 360  
 40 CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG 400

## (2) INFORMATION FOR SEQ ID NO: 3836:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

CTAATCGCAT CTTTTTCAAT CTAAGTTCGT TTGTGACAAA CTTACTGAAC TTAGTGCCAT 60

ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180  
 ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240  
 5 AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300  
 GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360  
 10 CAATTGTGGC AGCTTTTTnC TTCCGGnGAA AATATCnGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3837:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TATTCATATA 60  
 ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG 120  
 25 GCAGATGCTC TCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180  
 CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGGA CCAAGGAGCC ATGGCTCAAC 240  
 30 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300  
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGGAAGTAAn TCGGACTACC 360  
 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3838:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC 60  
 GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTT 120  
 50 TTTGTGTTTA TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240  
 GCTACCATCG ACGTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 300



TCAGATCCAA ACGTTTTCA<sub>n</sub> TCG<sub>n</sub>CCAAGC CAATTGCTT

400

(2) INFORMATION FOR SEQ ID NO: 3839:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 416 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGAC<sub>r</sub>C GACTCCTCTT 60  
 AACCTTCCAG CACCGGGCAG GCGTCACCTT gATAcATCAC CTTACGGTTT AGCAGAGACC 120  
 TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCACTGCG GCTCTTCTGG GCGTTAACCC 180  
 TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCATTTTG CCGAGTTCCT TAACGAGAGT 240  
 TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACCTGTG TCGGTTTGCG GTAGGGcACC 300  
 TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACTcGAg GACACAATGT 360  
 CTTCTCCCCA TCACAGtTCA GCCTTgAACG rGTaCCGGAT TTG<sub>n</sub>CTAATG ATTCAG 416

(2) INFORMATION FOR SEQ ID NO: 3840:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
 TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAAAC<sub>T</sub>TG CCTGGCAACG 240  
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300  
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 360  
 CTCGTTGG<sub>n</sub>G CTCTTTTCTT CGGTTT<sub>n</sub>GTC AGAnTTCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3841:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

	CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA	60
10	ATTCTTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA	120
	TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG	180
	ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG	240
15	CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAATTGCT	300
	AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTTG TAGTGGTGAA	360
	GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA	400

20

(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

	TCGCGATTCTG CGTGTTTCTAGA AATCATCGGC ATCGCGTCAT TCAATGATTC ATATGCATCT	60
	AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA	120
35	TGATGTTCTG CTACCGCAAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT	180
	CCTTGCTCTGA CATTGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT	240
	GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA	300
40	CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTTT	360
	AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG 120  
 ACCTTAGCTG GTGGTCTGGG CTGTTTCCCh GTCGAACACG GACCTTATCA CCCATGTTCT 180  
 5 GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG 240  
 GGCCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG 300  
 10 CTATTTGCGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAGT 360  
 TCATCCGnTC ACTTTCAACG TAAnTCGGGT CGGGTCTCCA 400

## (2) INFORMATION FOR SEQ ID NO: 3844:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 469 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT 60  
 25 TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT 120  
 CGCCTTGCCA GAATTACTTT TGTTTGTAGC GTCATTTGAA TGTTTCTTAG CTTTAGAAGC 180  
 30 AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT 240  
 TTTACCATTA TGATGTTCTT TAGGTTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG 300  
 TTCATTTTTT GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG 360  
 35 AGATTGTTCA GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTTAT TTTCTGCATT 420  
 TTTAATAGTA TCGTGTTTAn CCATTGTCCT CGAATGGGTT CnGGATGTG 469

## (2) INFORMATION FOR SEQ ID NO: 3845:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

GCTTCACTAC CAAGTGAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA 60  
 50 GAAGGCGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TCGTAGAGC AATTGCGnAA 120  
 CATGGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT 180

TTAACATTCT TACCTTATGT TGTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300  
 CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360  
 5 CGGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

(2) INFORMATION FOR SEQ ID NO: 3846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTG TG ACAATCGCTT GCTTCTTTCC 60  
 20 TCTCCTTCGG CTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 120  
 TTCGTCAGAT TCAAACGTTT TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTTAT 180  
 TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240  
 25 ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT GACTTGTGAC 300  
 AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCnTACT CATTAGCTC TACTAAACTC 360  
 30 GTTGGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 3847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG ACAAAAAAGG TATTACGATG 60  
 GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120  
 45 GCACGTCCAT TAAGACGTAT TGTGAACAG CAAGTACGTG ACAAATTAC AGATTACTAT 180  
 TTAGATCATA CAGACGTTAA ACATGTGGAT ATAGATGTTG AGGGATAACG AATTAGTCGT 240  
 AAAAGGTAAA TAACGACACT TTAACATATC GCGCATCAAA AATGAGCATC AGGTCGCCCT 300  
 50 TGCCTGTGGC TCATTTTTTT GAATTATTTT CCTGGGAAAA TGATTCGCTG TGTGCTGTTC 360  
 TGTnCCACA ACAATCACGA TTGAATGTGC ACATGTGACC 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

TTTAAAACTC TTTATTCAC TCGTTTTGCT TGGTAAAATC TATATTTTAC TTAATTATCT 60  
 AGTTTTCAAT GTACAAATAA TGGTGGGCCT AAGTGGACTC GAACCACCGA CCTCACGCTT 120  
 ATCAGGCGTG CGCTCTAACC AGCTGAGCTA TAGGCCCAT TTTTGAATG TTAAATAAAC 180  
 ATTCAAAAC TGAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA 240  
 TATATCCTTA GAAAGGAGGT GATCCAGCCG CACCTTTCCG ATACGGCTAC CTTGGTnACG 300  
 ACTTCACCCC AAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTAATCCACC 360  
 GGCTTCGGGn GTTACAAACT CTCGTGGGTG TGACnGGCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3849:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 60  
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 120  
 TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 180  
 TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 240  
 AAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG 300  
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 360  
 GACAATCGCT TGCTTCTTTC CTnTCCTTCG GCTCTCGCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3850:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

5 GTCTACTAAT GTTACAACCA CACCTGATTA ATTGCTTTTT TAGCAGTAAT TGCCACATCT 60  
 GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC 120  
 ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA 180  
 10 TGGTTCAATG CTTCTATAGA AAGATCAGCA TGAATTTAT TAGGTGTACA AATGACCACC 240  
 GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC 300  
 TTCGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG 360  
 15 TCTTTGAGTT TCAGCAATGC TGAATATGA CGGTCTTGTT CAATACCACC AACAACTATG 420  
 CACACCAACT TTAAAnTTTG TnCATGATGT GCCnGCTTnA CCG 463

## (2) INFORMATION FOR SEQ ID NO: 3851:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 628 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

30 TATGCTCTAA TGCTGGGCTT AGTGGAATCG ACCAACGAGT GACGnAGTCA AAGTCnGTTG 60  
 CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCG 120  
 AACCCGAAGG AGCGGATTTA CAGTCCGcG CGTTTAGCCA CTTGCTACC CCTCCAGCTT 180  
 35 ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT 240  
 GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG 300  
 ACTCGAACCC GTGTTACCGC CGTGAAAGGG CGtGTcTTAA CCGCTTGACC AAGGAGCCAT 360  
 40 GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTAA CAGCCGATAG CTCTACCACT 420  
 GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG 480  
 GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA 540  
 45 CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAAnTAGn 600  
 TTAGTAAGTA AAAGTGGATT TTGGnTTn 628

## (2) INFORMATION FOR SEQ ID NO: 3852:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

5 TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTCGAATT GGCCGTGTAG TAGCCGATAT 60  
 ATTTGCCAAT GGTATACAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120  
 GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180  
 10 ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTTAAA 240  
 CATTTTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300  
 GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTGn TTACGTATGG 360  
 15 ATTTGGAACG GCAAACTTTT TCCCAAGTGG TCCAAAGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3853:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

25 TCTTAAACAT TAGCCACAGC TAATTGTGAC TTAAAAATAG GAATACATGA GTAAAACTCA 60  
 30 TCATAAGAAA TACTAATTTT TATAGAAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120  
 TGCACATTAT TGTAAGCTGA CTTTCCGCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180  
 CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTTGCACATT 240  
 35 ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAACTTG CATTGTCTGT 300  
 AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCA CA CCAACTnC GCATTGCCTG 360  
 TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGGCCCA 400

## (2) INFORMATION FOR SEQ ID NO: 3854:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

50 GTGCAATCTG CGTTAACAAA TGTAATCGT GTCAATGAGC GATTAACGCA AGCAATTAAT 60

55

GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180  
 AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240  
 5 GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300  
 TTAAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAnCT 360  
 CAGTTGCAAA TGnTATTGTC AGCCACGAGT ACGGCTGGTA 400

10 (2) INFORMATION FOR SEQ ID NO: 3855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60  
 AAATCAACAG GTAAAAAATT AACAATAGGT TATCAAAATC GTTCCGAGC AGATAGTCAA 120  
 25 TTTTACATC AAGCAGCGCA ACGTGGCGAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180  
 GCCATTTCGTC GTCGAGCAGT ACCAACATGG GGTGTCCTTC TAGACGTAGT AAGCTCAAGG 240  
 TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300  
 30 TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATTnAA TAAACAGCCT 360  
 CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

45 CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60  
 CTATTTCTTC TATTGTTAAA TCGCTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120  
 CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTTTCGAT TCGTGATTTT 180  
 50 GAATACTTTT CTTCCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240  
 CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAACTGAA 300



TATAAGAAGG nGGTTGGAnC nTGAGCGAAC CACAnCATCC

400

(2) INFORMATION FOR SEQ ID NO: 3857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTTTGA 60  
 AGTTGTGAAT GCACATGGTA AACATTTTTG TGCATTACCA CGTGAAGATG AAGATATTGC 120  
 AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA 180  
 TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT 240  
 AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTTG TCATTAnATC 300  
 TATGATTTAG TCGGACTGGG ACATCATTG CAnCATATTA CATCGnCCTT GCCGAGTAAT 360  
 TGTCAAATGT ACTATGCAAT G 381

(2) INFORMATION FOR SEQ ID NO: 3858:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

GCATGAAGCC CCCCTCAAGA TGAGATTTC CAACTTCGGT TATAAGATCC CTCAAAGATG 60  
 ATGAGGTTAA TAGGTTGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT 120  
 CGATCGAAGA CTTAATCAAA ATAAATGTTT TCGGACAATT CACTTTTACT TACTATCTAG 180  
 TTTTGAATGT ATAAATTACA TTCATATGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT 240  
 TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC 300  
 GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA 360  
 GGnCTnTTTG TTTTTTATGT CTAAAACGTC CAAATTAAnA 400

(2) INFORMATION FOR SEQ ID NO: 3859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

	GTTTATTAAT CGTGTCAATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA	60
10	ATGTTAAATC TGTTTTAACA TTATTTTGAA TTTCAATTCAT GCATCTGAAT CTGAATCGCT	120
	ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCTGAGT CGCTGTCTGA	180
	ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA	240
15	ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT	300
	ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA	360
	ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA	420
20	ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC	480
	CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG	540
25	CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG	573

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

	GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG	60
40	CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA	120
	CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT	180
	ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT	240
45	CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA	300
	AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT	360
	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGnGC	400

50

(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:

55	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

5 TGTTGCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60  
 ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120  
 CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTT CACCTAAACG 180  
 10 AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAACA nGTCCAGATT GCGCACTGAT 240  
 AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300  
 AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnt 360  
 15 CAATAAAAGG TACTTCCATG TCCGACGTTT CGATGGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3862:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60  
 30 GGTACTTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATTT TGGCATGAAG 120  
 GTCACCTTAA ATGTACATTG TTGTAATAAA ATTCCTATA AATTTTTAGC ACATAAAATA 180  
 AGAGGAGCCA ACCATTGTGA GACTATAACA ACGGTTGGCT CTTTAATTGT AAAAAGAAAA 240  
 35 CCATACGCTA TCGGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300  
 CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360  
 ATGTCCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

40 (2) INFORMATION FOR SEQ ID NO: 3863:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

TCGGCAAGCC ATTTTCTTT GTGTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 60

CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180  
 GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG 240  
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 300  
 TGTTTGCTTT TTATTTTGAC GTTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG 360  
 10 CGGCTCATCG CATnCATnT TGCCGGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTACTATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60  
 GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGT TATGGGAAAT GAATTAATGT 120  
 25 AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180  
 TGACGCTCAA TCAACTAATT TACAACCGTA TTTTATAAT CAACCATAAA GGAGGAGATA 240  
 30 GAAAATGAAT AGTGCAAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300  
 GCAAATCGAT CCAAATCATC GATGAAGCGA AGCATACCAT TTAAATCTG TATGTGTGAA 360  
 TCCAACGCAT GTTAAAnGTG CCAGCAGAGC GACTAGCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATTCAAC GCATGTAGTA CCACATCTTC 60  
 AAAGCTTGAT AGTTC CATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120  
 50 GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCACATG 180  
 TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTAACTCTA GTTGGTCCGC 240  
 TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT

400

## (2) INFORMATION FOR SEQ ID NO: 3866:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

AAGTCAATAA CTTTTTTTAT CTTGTCCATT TTATTTTTTA ACCAAAATTT GATTAAAAAA 60  
 CTGCCTGGCA ACGTCTACT CTAGCGGAAC GTAAGTTGCA nCTACCATCG ACGCTAAGGA 120  
 GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA 180  
 TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA 240  
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300  
 GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT 360  
 TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG 400

## (2) INFORMATION FOR SEQ ID NO: 3867:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT GnCGATTGGA 60  
 TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC 120  
 TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTGTTGAT TTCACACTGC CGAGAAAAGC 180  
 CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT 240  
 CTAAGGTGAG CGAGCGAACT CTCGTTAAGG AACTCGGCAA AATGACCCCG TAACTTCGGG 300  
 AAGAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT 360  
 GTTTAnTCAA AACACAGTCT CTGCTAAACC TAAGGATGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3868:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

	TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTTGA TCACTGTTTA	60
10	GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT	120
	GTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT	180
	GACAATGTTA ACTTTGATTA TCTATTTGCC GCAATTGGTG GTGGCGGTTT AATTTCAGGT	240
15	ATTAGTACTT ACTTTAAAAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA	300
	GGTGCCAAGT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA	360
20	AnTCGATAAA TTTGTGGACG GTG	383

(2) INFORMATION FOR SEQ ID NO: 3869:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

	CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA	60
	CGACAACCAC CACCTGTCAC TTTGTCCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA	120
35	GGATGTCAAG ATTTGGTAAG GTTCTTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG	180
	nTTGTGCGGT TCCCCGTCAA TTCCTTTGAG TTTCAACCTT GCGGTCGTAC TCCCCAGGCG	240
	GAGTGCTTAA TGC GTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC	300
40	ATCGTTTACG GCGTGGAATA CCAGGGTATC TAATCCTGTT TGATCCCCAC GGTTTCGCAC	360
	ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTGCGCAAT	400

45 (2) INFORMATION FOR SEQ ID NO: 3870:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 377 base pairs
50	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:

55

GTGTGCCTTC TGATATGCTA TGTATTACACA TATCGATAAC ATGACATAAC TCATGCTGGG 120  
 TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180  
 5 GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC CCTTAATAAC 240  
 TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCTTTTCGAA 300  
 CATGAGCGAT TATTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 360  
 10 GCTTGGTAAA AGCnnGn 377

## (2) INFORMATION FOR SEQ ID NO: 3871:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCTCCCATG TATATCCTAC CCAAACATGA CCATCTTGTA ACATCACTTC 60  
 25 TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAATGG 120  
 CCCCACTTTT CTTACTGTGA TTGGTTGATT GCCGTTTGTG AATCTAGCAC TTTCTTCCAT 180  
 GTAGTAAGTA CCATATTTAT TACGTTTCCA TGCACTTGCA ACTGGTTTAA CTGTATTACT 240  
 30 TGAAGCGCTT GACTCATTAG AGACAGTGGC AACC GGTTATT TTACCATCCA TGTACGCCCT 300  
 AAATCTGCTT GATAAAGTAG TCTTTTAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360  
 35 GCGAGTTACn GGGGTCCAAA CCnTGGTGT AAAAnCGAAC 400

## (2) INFORMATION FOR SEQ ID NO: 3872:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAAACGC AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60  
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120  
 50 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180  
 CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAACTAA TAAATAGTGG CGGTGGAGGG 240

GCCTTATATA GTTTGTAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360  
 CTGCGTGCAA ACGGGCGCTC TTCCCAGCTG nAGCTAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

ACAGCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60  
 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120  
 GTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGTT TCGTCAGATT 180  
 CAAAnGTTTT CatTCGCCAA GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA 240  
 GGCATAAAAA AAAGAGACCT TGCGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTTGCCT 300  
 GGCAACGTTT TACTCTAGCG GAAnTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360  
 GACTTGTGAC AATCGCTTGC TTCTTCTCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 420  
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACITCGCCAA 480  
 GCCATTTTTT TTTGTGTTTA CTTnTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540  
 TGCGGTCCAA ATGCGGGCTC ATCGCATCCA TTTTTTGCCT GGGC 584

(2) INFORMATION FOR SEQ ID NO: 3874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

TTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAnTTGG CTACCATCGT CGCTAAAGAC 60  
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 120  
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180  
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA 240  
 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300



GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT

400

## (2) INFORMATION FOR SEQ ID NO: 3875:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60  
 GTCGATTCAT CTAATAAAAG AATATCCGGT GTATACATCA GTTGGCGCGC TATAGCAATT 120  
 CTTTGCCGCT CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAA 180  
 CCGACATCTT TAATTAATTG CTTTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240  
 GATGGAATA TCATGTTATC TTCAATCGGT CACCAAACAA GTCACTTTGC TGCATCAAAT 300  
 AACTGATTCG TTGACGCCAA TTCTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360  
 TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

## (2) INFORMATION FOR SEQ ID NO: 3876:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60  
 TGGTGATCCT CAATTGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCGTCA 120  
 AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATTT TTATATGAAA ATCCACAAGT 180  
 CGCACGTACA GTGGTTGAAA AAGGTATTAT GGCGGCACTG CACGTnTTGC TCGAAAAAAA 240  
 GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300  
 AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360  
 CCGGGGGGTC TACAAAATCT GGTCGTGACT CTAGACCGCA 400

## (2) INFORMATION FOR SEQ ID NO: 3877:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

	ACCAATTTCT CCTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC	60
10	CATCATGTTA TGTGATTGGA ATACTTTTTC AAAATCATAT TTAATACCTG GAGGGAATTT	120
	ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT	180
	TACTTCTGGG AATTCTTTAA AACAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT	240
15	ACGnTTTAGA AAATCGCCAT CTTTGGTGGT ACACCTTCTGG GnGTATCAAA ATGnTGCAAT	300
	GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC	360
20	TCAACACCTT AGGGGTAAAC TTCGGCCATA TCCCTTTTGG	400

(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

	ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCGTATTA CAAAAGAAGA TG TAGATGCA	60
	TACTTAAATG GTGGTGCACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAAGTGAA	120
35	GAAGTTGCTG AAACCTCTGC AGCACCTGCh GCAGTTAACA TTAGAAGGCG ACTTCCCAGA	180
	AACAACTGGA AAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC	240
40	TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG	300
	GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA	360
	CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT	400

45

(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:

TTGTGTTTAC TTTTATTTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120  
 TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180  
 5 GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240  
 CTTGCGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCCTCTTTT TCTCGTTTCG 300  
 TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTTCCTTG TGTTGCTTTT ATTTGACGTT 360  
 10 TAGACATAAA AnAAGAnCCT TGCGGnCTCA ATGCGGCCAT 400

## (2) INFORMATION FOR SEQ ID NO: 3880:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAA TCCTGCGATT CGATCTGGAC CATATTTTTT TATGTATAC AGTAATTGTG 60  
 25 CTGCGATTAT CTCTGTAACG TCTTTCGAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120  
 CTTGCTTATA TTGTTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCAT GCAGCAACGC 180  
 GATTACCATT GTTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240  
 30 ATGGATATTG ATTCGAAGCG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300  
 CTCTCGGTCA TATTCAGGCA TATCCGGACA CAACTTGGAT AGCAGTTGTG ATTTCCCAGG 360  
 35 AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3881:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60  
 50 GCTCGTCCGC TCTGGGTTAG TCGGGTCTTA AGCTGAGGCC GACAGnTAG GCGATGGATA 120  
 ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCAGTAGGA 180  
 TAGGCGAACG TGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240

TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360  
 ACAGGTAGTC CAAGATGGAG AnTCTnAAGG TGGAGCGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3882:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60  
 ACCCCAACTC GCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGCCCCCTGA 120  
 CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTT AGTCAACTAC TGCCAATATA 180  
 ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240  
 ATATTTAATT TCGGTTTATA CCGTCAAAC TCACTTTAGC TTTGTCAAAC CCCTTTCTAT 300  
 TAAGTTTTC AAAATAAACC TATCTTAAAA TATAAAAAAA TCGAGAATTC GTAGTTTAAT 360  
 AACGAAATTC TCGTTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAACAAGT 420  
 AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACTAAA 480  
 CTTTATTAGT TATCTTTnTT CTCTATATTT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540  
 AGATTCATAA TCTTCTTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600  
 CGGAGTCAA 609

(2) INFORMATION FOR SEQ ID NO: 3883:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60  
 CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA ACACTTTCAC CAATAGATAG 120  
 TTATTTGTTG TTACGTGGAC TTAAACTTTT GCATTTACGC ATTGAGCGTG CGCAATCAAA 180  
 CGCTAGAAAA CTTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

GAAAATTTAG ACATTTGcAT TTTTGCAGAA AGTTTAGGAg GTACKGAAAC ATTAGTGACC 360  
 TTCCCTTACA CCCAAACACt GTTGATATGC CAGT 394

(2) INFORMATION FOR SEQ ID NO: 3884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTAATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60  
 TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAGA 120  
 ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTGATTAG CGTAACAAAA TATGGACCTG 180  
 TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240  
 ATCCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300  
 CAATAACGAC GCCAACACTA AAAAnTCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360  
 AAAGAGGAAT CACAAAAGTT CCnTTTATGA TTAACAGATA 400

(2) INFORMATION FOR SEQ ID NO: 3885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120  
 CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG TCGCTCTAA CCAGCTGAGC 180  
 TATAGGCCCA TTTTTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240  
 TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300  
 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360  
 GACGGCTAGC TCCCAAAGG GTACTnCCAn CGGGnTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

10 TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60  
 TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCATTGGA AACTGGAATn 120  
 CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180  
 15 GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240  
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300  
 20 GTTAGGGGGT TTCCGCCCTT TTAGTGCTGC AGCTAACGCA TTTAAGCACT CCGCCTGGGG 360  
 GAGTTACGAC CGCAAAGTTT GGAAACTCAA AGGGAATTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3887:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

35 ATTTTTTAAT TTTCATGCAA ATTTTAAAGC ACCATATAAT GCCTACCAA TTTCAATAAT 60  
 CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAAC TAGT CGAAAATAAA 120  
 GGGAGTnGGA CATAAATCCC TAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180  
 40 CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240  
 GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAATACT 300  
 ACGTATTAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAACT 360  
 45 TACACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

## (2) INFORMATION FOR SEQ ID NO: 3888:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAACTG GAACTTACAA 60  
 GTCTAGTTTCG AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120  
 5 ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTTCGATTCA TAAAATTAAA 180  
 ACAATGATTA AAATTAGACG TGTAATGTG AAATTCTAAA ACGGAAATAA CCACCATCCC 240  
 10 ATTAAACCAC TTTnATnGTT CAATCACTAT ATTTACACA GCTTCATTAA TAAAACGACT 300  
 TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360  
 AACGAATCCG CTTCATCCAA AATCAnCCAT TCTAACGCAC 400

(2) INFORMATION FOR SEQ ID NO: 3889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGChAGA CGCATACATT GTaGCTTATG GgCGTTCAGC gCAGCGAAmG aaAGCAAGGC 60  
 GCATTATTCC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120  
 30 CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180  
 CCAGAAGGAT TACAAGGCCA AAACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240  
 GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300  
 35 ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTAgCTGG TGGCGTTGAA 360  
 TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420  
 tGaTGATATA GGTGCGTCCA TATnCTATG GGTTTnAaNT GCTGGAAAAT GTTAGCCTnC 480  
 40 CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

AGGCAGATGC TCTCCCAGCT GAGCTAATTC TCCAAAATAA TGACTCCTAC GGGACTCGAA 60

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180  
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTA CTCTAGC GGAAnTGAAT TCGGACTACC 240  
 5 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300  
 ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360  
 10 GGTTTTGChT CGCAAAACAT TTATTTTGn 389

## (2) INFORMATION FOR SEQ ID NO: 3891:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60  
 AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120  
 25 TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180  
 TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG GATTCTGAACC 240  
 30 TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTTCCATGG 300  
 TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360  
 ATTGGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3892:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60  
 CAGGTGTGAT TGAACCCCT AGTGCTTCAC CGGTTATAAT CGAGGATGAT GTATTAATCG 120  
 50 GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGCAGCTG 180  
 GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240  
 TGATTAAGCA AGCTTCTGAA GTACAAGATA CTAAAAAAGA GATTGTAGCA GCATTAAGAA 300



CCACCnTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC

400

## (2) INFORMATION FOR SEQ ID NO: 3893:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT	60
GGAGTTGAAG TAACTAAATC TAAAGTACGT CGTGAAAGAA TGGGTCACAT TGAACCTGCT	120
GCTCCAGTTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT	180
TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCTTATG TGTGTAGAT	240
CCAGGTCCAA CTGGTTTAGA AAAGAAAACCT TTATTATCTG AAGCTGAATT CAGAGATTAT	300
TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAAATGGG TGCCAGAAGG TCATTAAAAG	360
ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAACCTnA	400

## (2) INFORMATION FOR SEQ ID NO: 3894:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCTTG	60
ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT	120
TAGTACGTGT ATATATCGTT CAAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC	180
GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCTGA AGAAGATATG CCTTACTTAC	240
CAGATGGACG TCCGATCGAT ATCATGTAA ATCCTCTTGG TGTACCATCT CGTATGAACA	300
TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG	360
cATCACCAGT ATTTGaCGGT GcAaACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG	420
GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCCnTCCGA	480
TAACC	485

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 507 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

GAACAACATA CCTTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTTCTT 60  
 AGATTGTGGT TTTTAGTTG GTGCCACTGc TTAAACCTTT TCATTGATT CAATAACAGG 120  
 TGTTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG 180  
 TGGTACTGGT TTACCAngTT CAGCTGGTAC CTCTGGTGTG GCGGTGTGTG GAGTTTCTGG 240  
 CTCCTCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTCG GGTCACTTG GTACTTCTGG 300  
 TGTTGGTGGc GTTGGTGTTC CCGGCTCACT TGGTACTTCT GGTGTCGGTG GCGTTGGtGG 360  
 CACGATTGGA gGTGTTGTAT CTTCTTCAAT CGTTTGTGA CCTTCATTTT GGGCCGCTTA 420  
 CTTTGGGAA GTGTATCTTC TTCAAAGTCA AACTAATGT GGTCCACCGG AATTGATAAC 480  
 TGGGGTTAAC CTAAATTGG AACCTCC 507

(2) INFORMATION FOR SEQ ID NO: 3896:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGgNgACTTG TGACAATCGC 60  
 TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 120  
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTCACTTCG CCAAGCCATT TTTCTTTGTG 180  
 TTTACTTTTT ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG 240  
 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC 300  
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 360  
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 400

(2) INFORMATION FOR SEQ ID NO: 3897:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

	TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT	60
10	CAGAAACAGT TCGTCACATG GGTAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC	120
	ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAACTTC TAAATTGGGT	180
	CAATACGCAT GTTAACGATC GAATGCTTAA TGTCCCGGGA AATAAATCTA TCATAAGTTA	240
15	CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGAnTTGAC	300
	AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TCGGCACATG CTCCTATCAA	360
20	ATGGTGTGGG CAATGGTCAA CGGGTTGCCT TGGTGACAG	400

(2) INFORMATION FOR SEQ ID NO: 3898:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

	GAAATCAGTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT	60
	GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA	120
35	TTCCAACAAG CAGTCGCATG CGGTACTGCC ACGGCATTG ATGAGGACTT AGCAACACGG	180
	GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA	240
	TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATTTA ATGGCAAATG	300
40	ACAAAAATGG TGTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG	360
	ATGTCGCGTC ATTTAAAnGGA AGCGATTAC CATCGnGATC	400

45

(2) INFORMATION FOR SEQ ID NO: 3899:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

55

CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120  
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG 180  
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 240  
 TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA nACCTCACGG TCTCAACTTG 300  
 CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360  
 10 TTCTTGGAAT TGTGGACAAT CGGCTTGGCA nTCTTTnCTC 400

## (2) INFORMATION FOR SEQ ID NO: 3900:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60  
 25 ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120  
 TAATGTTATT TGTTCATTCA CTTTCATTCC AACATACCA TCACATCCTC ATTCATTTTTT 180  
 CATATAATTC TGTAAATTAT CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240  
 30 TTTGTTGTCC TTCCCCAACT TGCAATGCTT GTAGAATTC TTTTCGAAAT TCTCTATGTT 300  
 GGGGCCCCGn AACTTGCATT GTCTGTAGAA ATTACGGACC CAATTTCTCT AGGTGGGGCC 360  
 CATCCCCAAC TTGCACATTA ATnGCAAGCn GACTTTCCGT 400

## (2) INFORMATION FOR SEQ ID NO: 3901:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA 60  
 TTAAATAAT CAAAAGTGCA CATTATTAAA ATATCAATTT CACACTCAAT GCGGCTCATC 120  
 50 GCATTCAITTT CTTGTCTCAA CGTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180  
 TAAGAACCTT TCTTGACTTG TGACAAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

TTTCACTTCG CCAAGCCATT TTTCCTTGGT GGTTTACCTT TTAATTTGGA CGGTTTAGAC 360  
 ATnAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3902:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60  
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120  
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180  
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTTCACTTCGC CAAGCCATTT 240  
 TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300  
 TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360  
 AAGTTGGGCT ACCAnCGGCG GCTAAAGACC TTTCCTGGAC 400

(2) INFORMATION FOR SEQ ID NO: 3903:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAAACCATT AATAGATTTT TATTTGGTGA TTTCAAATCA TGAGACTGGG 60  
 ACAGAAATGA TGTTTTCATA AAAATTATTT CGTTGTCCA CTCTCATGAT TTTTTTGATG 120  
 AACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180  
 TTCACACTGA AAATTTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240  
 ATATTGTTAA ATAATTTTAC CTAATCTTAA CATTAAATTT ACAATTATAA GCGATAATCT 300  
 AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360  
 CTTTTTAGGT GGGTTTAGGG AATTTCCnTT ACGGCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3904:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

10 CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG 60  
 TAGGATGGAA ACATAGATTA AGTTATTAAG GCGGCACGGT GGATGCCTTG GCACTAGAAG 120  
 CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC 180  
 15 AGAGATTTCC GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC 240  
 ATAGCATATC AGAAGGCACA CCCGGAGAnC TGAAACATCT TAGTACCCGG AGGAAGAGAA 300  
 AGAAAATTTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCAAA CCAnCAAGCT 360  
 20 TGCTTGTTGG GGTGTAGGG CACTCTATAC GGAGTTACAA 400

## (2) INFORMATION FOR SEQ ID NO: 3905:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA 60  
 35 TGgTAAATGA ACAAATCATT GATATTTTCAG GTCCGTAAAA GGGCGAAATA GAAGTGCCGG 120  
 GCGATAAGTC AATGACACAC CGTGCAATCA TGTGGCGTC GCTAGCTGAA GGTGTATCTA 180  
 CTATATATAA GCCACTACTT GGCGAaTtCG TCGTACgATG GaCATTtTCC gACTGTtTAGG 240  
 40 TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT 300  
 TAACACGCCA CATCAAGTnT TGTnTACAGG TAATTCCGGG TACGACAACA CGATTGATAG 360  
 TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG 399

45

## (2) INFORMATION FOR SEQ ID NO: 3906:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTcAGCAGT AGAAGAGGGA 60  
 ACATTCTAAA CTAAATTTGC TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120  
 5 GCACAGCGTA TTTTACAAGA TAGAGCATTc AAAAATGATA AAATCGACTT TATTTGGAGT 180  
 CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAAGTGG GTTCTGTGAC ATTAACGTCT 240  
 ACAAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300  
 10 AACCATTAAc AGCGCCATTT AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360  
 AAAGGTGGAT TGGCCAC 377

(2) INFORMATION FOR SEQ ID NO: 3907:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

25 AATTAGGTAA TTCAAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60  
 CATAACCCGA AGTCGGtGGT TCAAATCCGC CTCCCGCAAT ACATAGTTTT TAATTTAATA 120  
 GGTCTCGTAG TGTAGCGrTT AACACGCCTG CCTGTCACGC AGAGATCGCG GGTTCGATTc 180  
 30 CCGTCGAGAC CGCCATTATT ATTACCATTA CGGTTcAGTA GCTCAGTTGG TAGAGCAATG 240  
 GATTGAAGCT CCATGTGTcG GCAGTTCGAC TCTGTCCTGa ACCATTCTTA ATTCATGGCG 300  
 GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTcGAGGG TTCGATCCCC 360  
 35 TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420  
 TCCAAGCTGA TGTTGTGGGk TtCGrTTCCC AtCAmCCnGy TCCaTaATTT CnAAnAATTC 480  
 40 CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

TAAGTATCAT ATTGTCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180  
 AAAAGATATA GGGATTATAT TGCCTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240  
 5 AGCAGAGGCA TGTAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTTGGGGG 300  
 TATCATCATT TGTGGGCTA TTTAAAAGGG AAAAAGTAGT TTAATGGATA TTTGGATAGA 360  
 CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

(2) INFORMATION FOR SEQ ID NO: 3909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAATGC GGTATATTCA 60  
 GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120  
 25 CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180  
 GATATTTTAG ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240  
 AAAAGGCTAA GTTGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAAGCG 300  
 30 TTTAAATTTT GCAGCTGGAT GACGTGCCAC GcGTTCCTT AAAATTAATC CAGGGCTTAA 360  
 CATTGCGAGT CCAGGTATTG GtTCCAAGCT AATGGGGCCG 400

(2) INFORMATION FOR SEQ ID NO: 3910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

TTACCCGATA TCGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60  
 GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120  
 AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAGAAGAA GGTACAGTAG 180  
 50 CTGTAGTTGG TGACGTTATT GTTAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240  
 AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCTGC GAAAGAGGGA AGCGCCACAG 300



GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGGAAAAG

400

## (2) INFORMATION FOR SEQ ID NO: 3911:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

CGTGTAnCTC AAGTTATGGG TCCTGTAATT GATGTTTCGAT TTGAACATAA CGAATTCCTA 60  
 AAATTAATAA CGCCTTGTT ATTGATGTGC CTAAAGAAGA AGGTACAATA CAACTAACAT 120  
 TAGAAGTTGC GCTGCAATTA GGTGACGACG TTGTTTCGTAC AATTGCGATG GATTCAACTG 180  
 ATGGTGTCCA AAGAGGCATG GATGTAAAG ATACAGGCAA AGAAATTAGT GTACCTGTTG 240  
 GTGACGAAAC ATTAGGTCGT GTATTTAATG TACTAGGTGA AACAATTGAC CTAAAGAAG 300  
 AAATTAGTGA TTCTGTTCGC CGCGATCCTA TCCATCGTTC AAGCACCAGC ATTCCGATGG 360  
 AACTTTTCAA CAGAAGTTCC AAATTTTTAG GnACAGGGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3912:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

TTGTACAAGT TGAAGAAAAA TCAACACAAC CAAAAGGTAG AAAATTCAAA GATTTCACTA 60  
 GTAAATTTAA TATAGCATCA GAAGCTAAAG AAAATGAACC TATATCAGTC ATTGGTTATC 120  
 CAAATCCTAA TGGAAATAAA CTACAAATGT ATGAATCAAC TGGTAAAGTA TTATCAGTGA 180  
 ATGGGAATAT AGTGTCATCG GATGCAATTA TTCAGCCTGG TAGCTCTGGT TCACCTATAT 240  
 TAAATAGTAA ACACGAnGCT ATTGGTGTA TCTATGCCGG TAATAAGCCA TCAGGTGAAA 300  
 GCACCAGAGG GATTTGCTGT TTATTTCTCT CCTGAAATTA AGAAATTCCA TTGCAGATAA 360  
 TTTAGATAAA TnATTAAGAC CTAnGACATT CACCCAATCC 400

## (2) INFORMATION FOR SEQ ID NO: 3913:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

ACTCATTTAG	CTCTACTAAA	CTCGTTGCGC	TCTTTTCTCG	TTTCGTCAGA	TTCAAACGTT	60
TTCAC TTCGC	CAAGCCATTT	TTCTTTGTGT	TTACTTTTTA	TTTTGACGTT	TTAGACATAA	120
AAAAAAGAGA	CCTTGCGGTC	TCAATGnGGC	TCATCGCATC	CATTTTTTGC	CTGGCAACGT	180
TCTACTCTAG	CGGAAGTAAG	TTGGCTACCA	TCGACGCTAA	GAACCTTTCT	TGACTTGTGA	240
CAATCGCTTG	CTTCTTTCCT	CTTCTTCGGC	TCTCGCTTAC	TCATTTAGCT	CTACTAAACT	300
CGTTGCGCTC	TTTTCTCGTT	TCGTCAGATT	CAAACGTTTT	CACTTCGCCA	AGCCATTTTT	360
CTTTGGGGTT	TGCnnTTTGA	ATTTGGACGT	TTTAGACATA			400

20

(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

30

TGGAATGAGC	GGATATAAGC	ATCTTTAGAT	AATGCACCAT	CAACTAATGG	ATATTTATGT	60
CCAGTTGGAC	GCCAGAAATC	ATAAACGTCT	TCAGTGTAAG	CAACAGCATC	TTCATTTAAT	120
GCCAAAATGC	TTGGATTATG	TGCAATAACC	ATCGCAACTG	nGCCACACCT	TGTGTTGGCT	180
CGCCGCTGA	ATTCAATCCA	TAACGTGCTG	TATCTGTAGC	AATAACTAAT	ACTTTTTTCAT	240
TCGGTCTAGT	TGCTAAATAA	TCTTTAGCTA	ATTGAATTGC	TGGTGTTGCA	GCATAACAAG	300
CTTCTTTCAT	TTCAAAGCAG	CGTGCAAAG	GTTGGnATAC	CTAATAAGTT	GTGGAATTTG	360
nACAGCGGCT	GCTTTACGAA	TTCCAACGTC	TGATTCCAGT			400

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(2) INFORMATION FOR SEQ ID NO: 3915:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:

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TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120  
 GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180  
 5 TCGAAATTGA ACGAnAATTC AAAAACATTA TATCGTGA CT TAGTTGAAGA AAAATAATA 240  
 CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300  
 AGTCATTTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360  
 10 ATTAGAAACA G 371

## (2) INFORMATION FOR SEQ ID NO: 3916:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATTCCAAAT AGGTTTCATCT ATAAAATAGC 60  
 25 TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120  
 TATCGTTTTA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180  
 GACTAATAGT AAAAAAGTTA ATCACAAAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240  
 30 AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCCTTGAA 300  
 AGAGCTTGAT TTAAATTGA GAAAACAACT TATTGAAAAA CAGATCTTTA CGGTAACATG 360  
 35 GGTTTCAGGAC AATCGTATTA AATGAAAACG GGGGAATATA 400

## (2) INFORMATION FOR SEQ ID NO: 3917:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGCCnTGAAG GAATAACAaC CTTTAGACCT 60  
 GGAGATTGAG CTAAAATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120  
 50 CCACCAAATG GGCTACGAAT TGTTACAGGT GCAGTTTTAG TACCGCCTGA ACGGAAACGA 180  
 GTACGTGCAA TTTGTCCAGC AATCGCATCA AATACTTCGA ATACGAAACC TAAGAATTGT 240

GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTGT TAGTCCTTCA 360  
 GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

(2) INFORMATION FOR SEQ ID NO: 3918:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAn TCGCATATGC AGGCCCAATA CCCATAATTT 60  
 TCGGGTCAAC GCCTACTGCC TTAAAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120  
 CTTTCACTTT ATCTCCAGAC ATTAAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180  
 ATGTTCTGCT AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240  
 CCATCGTGGT GTCAGGGCGT ATnAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300  
 GGTCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTC ATCTTTGGAA 360  
 CCGACCATCA CGGTGTGCGT TCATAGGCAC GTTGATGnAC 400

(2) INFORMATION FOR SEQ ID NO: 3919:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60  
 AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAACTG 120  
 CTGAAGTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTG 180  
 GTAAACTGC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240  
 CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTTCATC ATTAGAAGCT GGAACGCAAT 300  
 ATCGTGGTGC TTTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnC TTCACAAATG 360  
 CCGTACTATC TTTGATGAAAn CCATCAATTA TCGGTTTCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

10 CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAACT GGTACACCAG 60  
 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC 120  
 ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 180  
 15 ATGGGCGAAC AGCCAAGnCC TTGGGACCGA CTACAGCCCC AGGATGCGAT GAGCCGACAT 240  
 CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG 300  
 GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA 360  
 20 GTCCGTCTTT TCGAACCTGG CTCGGACTTG TAGGTCTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3921:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACTTTGAA CAACATTTGT 60  
 35 TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAATT GCTAGTTGGT GATGAGTTTA 120  
 AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTGCAT 180  
 CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA 240  
 40 ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG 300  
 GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG 360  
 45 TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3922:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GTGCGCTCTA ACCAGCTGAG CTATAGGCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60  
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120  
 5 TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180  
 CAATCATTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT 240  
 10 GTTACAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT 300  
 AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360  
 AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTGn 400

(2) INFORMATION FOR SEQ ID NO: 3923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60  
 TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120  
 30 TCCTGTAGGA TGGAAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGGCACT 180  
 AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240  
 GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTCATGTTA TCGATATGTG 300  
 35 AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360  
 AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60  
 CTTCAAATA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACCG 120  
 CCACCGCCAA TAATCAATAA CATCATTCGG ATTGGATAAA TCGCATTCGT CACTGATTCC 180

GCTATTAGCA TGGCTGTCCC TGCTGTTCCCT ATCATATAAA TGATAGATTC AAATAGATTT 300  
 GTAGGGTTGT CATGCCAGT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360  
 5 TGGTAATGTT GCTGTTAATA AACTCATACC AAnTCCGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTCTG AACCAACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60  
 20 TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120  
 AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTCGCTACC CCTCCAGCTT ATTCATATAA 180  
 TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG 240  
 25 CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300  
 GTGTTACCGC CGTGaAAGGG CGTgtgCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360  
 GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420  
 30 TGTGGATTAA TATTATGCCT GGCAACGTTT TGAnnCTAGC GGAAnTGAAT TCGGACTGAC 480  
 CATCGACGCh AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

(2) INFORMATION FOR SEQ ID NO: 3926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGTT GCTTATTATG AAGCGATGCA 60  
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120  
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180  
 50 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240  
 TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG

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(2) INFORMATION FOR SEQ ID NO: 3927:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT 60  
 GGTTGCATTT AGCGCAACAT GACCATAGTT TTAATAAGC ACAGCGCGCA AGTGATTAAA 120  
 GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATTT TTCAATAGAT 180  
 CAGGAAGACT ACCAAGCTTA TGTGGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT 240  
 ATGTTGTATT ACCGTTTACA ACAGCATCAC TTTGGAACAA CATTTGTTAA CGGATTATTT 300  
 GGCAATTTCGG TTAGTTGTG AACAATTGCT AGTTGGTGA TGAGTTTAAG TCCATCGCTA 360  
 AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAAC 400

(2) INFORMATION FOR SEQ ID NO: 3928:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTTTGTGC 60  
 AnTTTGTAA ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATA 120  
 GTAATACATC TCCAACATTT GCCTTTAATT CTTTGTGCGAT GACTACCGGT CCTGGATGTG 180  
 GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTTAACA 240  
 CTGAAACATT TGCGCGTTTT GCTACTGTAA ATACTAATGG AATCAGTAAG ACTAAACCTA 300  
 CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTCG CCCATTGGTA 360  
 CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3929:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

	CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTTAAA CGCTGTTATC TTTATGCCAG	60
10	TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTTCTT TGGAAATAGT AACGTTGAAG	120
	TTGTACTCAC TGGTGATACA TTTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG	180
	AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTTCT GGACAAGGTA	240
15	CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA	300
	TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAACCT	360
	ATTCACCTAC CACGnAAATT ATAGGTGTTG AACCCnAGT	400

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(2) INFORMATION FOR SEQ ID NO: 3930:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

30	ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGGTTCT AAACATGACG CCCTTATGCT	60
	CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCCAATGA TACATCGAAT	120
35	GGCACATATC ATTCGTCGCA ATATGATTAC TATGATGCAT TTATTAAGCA GCAAGAAAAT	180
	GTAACATATA TTTCAACCGA TCGTGCAGAT GCTAATACAG TGTTATGTCA CTAATTTATA	240
	AAAAATAAAT GAATAAGTAA GGTTCACACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT	300
40	TGTCGTTGTG CCAAATTTGA ACGnTTTAGA TGGCAATAAG CATGACCATA CAGATTGTGT	360
	ATTATTTCCA TGnA	374

(2) INFORMATION FOR SEQ ID NO: 3931:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

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TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120  
 TTTTCGCTTTT AAGTCAATTT CATCAAATC TTTCCACCT GTTAACGGTG CACCACTATG 180  
 5 TCGTTTCCGA CCAAATGTAG CCTCTTGTTT TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240  
 GTGTATTTGA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCCATC CGTCATCAAT 300  
 AAACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTAAAAATGC 360  
 10 CATTnAAATT CTAGGTGTTT CCnTAnC 387

(2) INFORMATION FOR SEQ ID NO: 3932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAAATGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG 60  
 25 AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120  
 TGACCGATAG TGAACAGTA CCGTGAGGAG AAGGTGAAAA GCACCCCGGA AGGTAGnTGA 180  
 AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240  
 30 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 300  
 GCCGTAGCnG AAGnAnGTTT TGAATAGGGC GTTTAGTATT TGGTCGTAGC CGATAACCAG 360  
 GTGATTCTAC CCTTTGGTCA GGTGAAGTT CAAGTAACAT 400

(2) INFORMATION FOR SEQ ID NO: 3933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

GCGATGGTTG AAACATTGAC TTATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60  
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120  
 50 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180  
 CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360  
 nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 3934:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60  
 CTTTTGCGCT GGCAACGTC TACTCTAGCG GAAnTAATCG AACTACCATC GACGCTAAGG 120  
 AGCTTAACCTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180  
 ATATGAATGT AAATTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240  
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300  
 GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360  
 AAnCTCATCT GAAGGGGGCT CAGCTAGATG CTTCAAnACTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 393 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTTAT TTCGTTCGnT 60  
 CCCACCCCAA CTTGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCTG TGTGGGGGCC 120  
 CCGCCAACTT GCCATTGTCT GTAGAAATG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180  
 CCCCAACTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCTGTGTTG GGGCCCCGCC 240  
 AACTTGCACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTGGGGCC CCGACTATTT 300  
 TTGAAAGAG CGTGTTACAC GGGCATTGTT TTACAGTCAA CTACTGCTAA AATAAAATTA 360  
 ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

10 AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG 60  
 TTGTATTTTA AAAATAGTTC TTTAAATTAT ATACCCACCA CATTGGGTGG AGAACCTAAA 120  
 AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT 180  
 15 GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC 240  
 TAGCTGGATT CGAACCAACG AGTGACGGAn TCAAAAGTCC GTTGCCCTTAC CGCTTGCGTA 300  
 TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT 360  
 20 TTACAGTCCG CCGCGTTTAG CACTTCGCTA CCCTCCAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3937:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGTT CGATTCCCTG TCGAGACCGC 60  
 35 CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA 120  
 TGTGTCGGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAgT 180  
 40 GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCCTC AGCCGCCCCA 240  
 TAATCGTTTA CATTAGCGGG TGTAGTTTAA TGGCAAAACC TCAGCCTTCC AAGCTGATGT 300  
 TGTGGGTTCG ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG 360  
 45 GTAGAGCTAT CGGCTGTAA CCGATCGGTC GTAGGTTCCA GTCCTACCTG TGGAGCCATG 420  
 GCTCyTTGGt CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC 480  
 CGTAGaGTyC ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA 540  
 50 TkGTTGgAGG aAGtTGtCG AgCyGGGCCG AAGGaGCACG CCTGGAAATG TGTAAGCGTT 600  
 CACAAGCTT 609

(2) INFORMATION FOR SEQ ID NO: 3938:

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- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

10 TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGGAAATCGCT 60  
 AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTACA CACCGCCCCGT 120  
 CACACCACGA GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT 180  
 15 CGAAGTGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG 240  
 CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC 300  
 GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA 360  
 20 GnGGTTAnAG CGCACCCTGA TnAACGTGAA GTCGGTGGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3939:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

AGTTTTGAAT GTATAAATTA CATTCATATG TCTGGTGAAT ATAGCAAGGA GGTCCACCTG 60  
 35 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC 120  
 CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA 180  
 40 TCGGCTGTTA ACCGATCGGT CGTAGGTTTCG AGTCCTACCT GTGGAGCCAT GGCTCTTGGT 240  
 CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACACG GGTTTCGAGTC CCGTAGAGTT 300  
 CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC 360  
 45 GGTTTCGAAC CCTnCATTTT CCACCATTTG GTTATTAAAn 400

## (2) INFORMATION FOR SEQ ID NO: 3940:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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ACACAACAGC TGTTTCAAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60  
 ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120  
 5 AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180  
 ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240  
 CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300  
 10 AAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360  
 TAGATAAGGT GCCnTGCAGG TATCGTCCAA CTATTATTAG 400

(2) INFORMATION FOR SEQ ID NO: 3941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

ATACAAITTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60  
 AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120  
 25 TGCAACGAAA GCATTTGAAA CAGAAGATGC AATTCAAAAT GGTGCAGATG AAATTGACAT 180  
 GGTCATCAAC ATCGGCGCAT TAAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240  
 AGCAGTGGTT AAAGCTGCGA AAGGTCACAC AGTAAAAGTG ATTATTGAGA CGGTATTGTT 300  
 35 GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGA CTTCGTT 360  
 AAAA ACTTCA GCAGGTTTTG CCAGTGGCnG TGCGACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60  
 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120  
 CATTTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAAA TCTATATTTT ACTTACTnAT 300  
 CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360  
 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

## (2) INFORMATION FOR SEQ ID NO: 3943:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60  
 TTAAGCCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120  
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180  
 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240  
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300  
 CGCCTTATAT AGTTTGTAAA TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360  
 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

## (2) INFORMATION FOR SEQ ID NO: 3944:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCTGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60  
 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTC TGTAACAAG 120  
 GCAACCCGTT GACCATTGCC CACACCATTG GATAGGAGCA TGTGCGCAAT GGCATCCACA 180  
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGACTAGCGC AACATGATTA 240  
 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300  
 GCATTCGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGTA 360  
 TATCACAAAT TTGTAGTGTA wCtTGaTGCT TCmAAATAtC AATCAn 406

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTCTGAAT 60  
 AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT 120  
 TTAAAGGAAA TTCAAGAAGA TGTTTCGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT 180  
 GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT 240  
 CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGACCA 300  
 GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAn GCCAGGACAA 360  
 ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3946:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGtnt TAATAGGnTC TGAAACGATA 60  
 CGTGTTGCCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT 120  
 GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC 180  
 CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTCGCA GCATCGCCGG 240  
 CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC 300  
 GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC 360  
 CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT 400

## (2) INFORMATION FOR SEQ ID NO: 3947:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

5 GCCGGCCAGA GGACTTGGA CCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60  
 GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC 120  
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180  
 10 GGCAACGTTT TACTCTAGCG GAAntAATTC GnACTACCAT CGACGCTAAG GAGCTTAACT 240  
 TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300  
 TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGChTTTCG CAAAACATTT 360  
 15 A 361

## (2) INFORMATION FOR SEQ ID NO: 3948:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 382 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60  
 30 ACTACGTGCT TTGGGCAGAC TTCGCAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120  
 ATAAAGCGGA TTTCGAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACGG CAAGATATAT 180  
 ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240  
 35 ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT 300  
 TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTGChGA ATAGGCCACC 360  
 GATACATCAC CAACAATTGG nA 382

40 (2) INFORMATION FOR SEQ ID NO: 3949:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA 60  
 GACCTTGCGG TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120

TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240  
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG 300  
 5 TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGn CTCAATGnGG 360  
 GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

(2) INFORMATION FOR SEQ ID NO: 3950:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

20 ACTCGTTTT GCTTGAAAA TCTATATTTA CTACTTATC TAGTTTTCAA TGTACAATTT 60  
 CTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTAAACCAAA 120  
 AAATATTTGA ATGTTAAATA AACATTCAA ACTGAATACA ATATGTCACG TTATTCCGCA 180  
 25 TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240  
 CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC 300  
 TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAACT CTCGTGGTGT GACGGGCGGT 360  
 30 GTGTACAAGA CCCGGAACG nATTACCCG 389

(2) INFORMATION FOR SEQ ID NO: 3951:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

45 AAAGCTCGAC TTGTTTACGA TGTTGAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60  
 TTACCAATTT TAAATGAATT TAATAAGAC TTAGTGATA ACCTTGATAC CATATTCAAT 120  
 GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTC TATTACTCTG 180  
 50 CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240  
 GGTTCAACTG GAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300  
 AAACAnTGAT GGGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360

## (2) INFORMATION FOR SEQ ID NO: 3952:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCATA AAGTTGTTCT CAGTTCGGAT 60  
 TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT 120  
 ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCCCTC ACACCACGAG AGTTTGTAAC 180  
 ACCCGAAGCC GGTGGAGTAA CCTTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG 240  
 GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA 300  
 AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA 360  
 GntTTTGAAT GTTTnnTTAA CATTnCAAAA AAATGGGGCC 400

## (2) INFORMATION FOR SEQ ID NO: 3953:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG 60  
 CATCCATTTT TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG 120  
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT TCCTCTTCTT CGGCTCTCGC 180  
 TTAICTATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 240  
 TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT 300  
 AAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360  
 CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3954:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

	AAACTACATA ATGAAAATGC CGTTTTAATC GGTAAATTAA ATATGGATGA GTTTGCAATG	60
5	GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTGTA CCATAAAGCA	120
	GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATT	180
	AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC	240
10	GGTATGAAAC CAACATACGG TCGTGTATCT CGATTGGAT TAGTGCTTTG CATCTTCATA	300
	GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG	360
15	TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG	400

(2) INFORMATION FOR SEQ ID NO: 3955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

	TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTCAACG TAATCGGTTTC	60
	GGTCCTCCAT TCAGTGTTAC CTGAACCTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG	120
30	GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA	180
	CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTTCATT CTACAAAAGG CACGCCATCA	240
35	CCCATTAAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT	300
	TCCGGGGGTG CTTTTCACCTT TTCnCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG	360
	TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA	400

(2) INFORMATION FOR SEQ ID NO: 3956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

	GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT	60
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ATAAAAATGG AGCAGAAGAC GGGATTGCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180  
 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240  
 5 CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT 300  
 AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360  
 10 AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAA 400

(2) INFORMATION FOR SEQ ID NO: 3957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60  
 TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT 120  
 25 AAGACGCCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT 180  
 CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240  
 TTTTGGGGTG CATATTTTTG ATATGGGTTC TGATGAACAA GGTATTGTTC ACATGGTAGG 300  
 30 ACCTGAGACA GGAATTACAC AGCCTGGCnA GACCATCCGT nTGTGGGTGA CTCTCACACA 360  
 GCCACACATG GnGCCTTTT 379

(2) INFORMATION FOR SEQ ID NO: 3958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAAATAA 60  
 ATATATTCAA GGTCAGAnAC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT 120  
 AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAACAG CAGTAAGATA 180  
 50 ATTTTCAATT AGAAAATATC TTAAGTCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240  
 GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300

AATAAGACAT TTGnCCAACT TGACACTACC ATTAAAACT

400

(2) INFORMATION FOR SEQ ID NO: 3959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

15 GAGCCGCGAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAAC 60  
 CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTTAA GAGGAGTGGT 120  
 20 TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAAC TATAACGGTC 180  
 CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT 240  
 GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 300  
 25 CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA 360  
 CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG 400

(2) INFORMATION FOR SEQ ID NO: 3960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

40 TGGTCCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 60  
 TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120  
 GGCGCATATG TTTTATATGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC 180  
 45 ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA 240  
 ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC 300  
 CGCTGGAAC TTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCA CGCCGTAGGC 360  
 50 TTAAGATTCC TGAAGTCTAG TGCGTCTGGC CAATTTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

	TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
10	AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120
	GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
	GGTGATGGCG TGCCTTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAAGC	240
15	AGTAAATGTG GAGCCGTAGC GAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA	300
	GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG	360
	GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

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(2) INFORMATION FOR SEQ ID NO: 3962:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC	60
	AAGTGCTCTA CCAAGCTGAG CTA CTCTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC	120
35	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
40	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG	300
	ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTT	360
	C	361

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(2) INFORMATION FOR SEQ ID NO: 3963:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

	AAGTGTCTTA TTTTTTAAA GTATTTCAAA GTAAAATTAC ATGTTAATAC GTAGATTAAT	120
	GGCGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA	180
5	AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA	240
	ATTGAAAATT ATCTTACTGC TGTTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT	300
10	ATATTCAC TAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC	360
	TTGGAATATA TTTAT	375

## (2) INFORMATION FOR SEQ ID NO: 3964:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

25	AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACTTACA	60
	ATTTTAAATA GATTTTAAAG ACCTTGTTGG TTTGTACAA TTAATGTGAC ATGACTAGGT	120
	CTTGACGTT TATATGCATC TTCATTACTG AGTTTTTTGT TGATTTGTT ATGATTTAAT	180
30	ACGCCTAATT CTTTCATTTG TTGAACCATT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA	240
	TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC	300
	AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAAG TATCGATAAC	360
35	ACCATTCGTT GGATGGTCCA AACC CAAGAC GTTCATATCC	400

## (2) INFORMATION FOR SEQ ID NO: 3965:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

	ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAAA GTAAATTGCT	60
50	TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAAC TAC CATGCTTGT	120
	TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT	180
55	TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTTGTT TTCCAATTCA	240



TCAGCACCTG CTTTAGGTTCTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAnGAA 360  
 TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

(2) INFORMATION FOR SEQ ID NO: 3966:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA 60  
 TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120  
 GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180  
 AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTA 240  
 AAAGTATTTT AAAGTAAAAT TACATGTTAA TACGTATaTa ATGGcGAGAC TCCTGAGGGA 300  
 GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCCtAGG AAAGCGAcnC ATTcAATACG 360  
 AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

(2) INFORMATION FOR SEQ ID NO: 3967:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60  
 TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120  
 AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180  
 TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAAC TGTATCGGCG 240  
 AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300  
 GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTThTTCTT 360  
 TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

10 ACCCCGGCAC TATAAAATG GAGCAGAAGA CGGGATTGCG ACCCGCGACC CCAACCTTGG 60  
 CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC 120  
 CACGCCGTAA nCTGAGGATC CTAAGTCTAG TGCGTCTGCC AATTCCGCCA CACCCGCAAA 180  
 15 TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC 240  
 AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT 300  
 GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT 360  
 20 GGTGGAGAAT GACGGGTTTC GAAncGCCGA CCCTCTGCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3969:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG 60  
 35 CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT 120  
 TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG 180  
 40 GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG 240  
 ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT 300  
 CATGTATTCC TATTTTAAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA 360  
 45 ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC 400

## (2) INFORMATION FOR SEQ ID NO: 3970:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 419 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

GATAAGATCA GCCGAAAATG GATGGTGTGA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60  
 TTTTAAATGG CATTGTGTAC GACACCATTA CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120  
 5 CTATTTGGTG GTGTTGTTGA TGCATCAAGT GCGTTTGCGA GTGCAGAGGC GCCACTGAKA 180  
 GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240  
 10 TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300  
 TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAAATg ATTGAAACGA CACATATGCC 360  
 AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTnCA ATGTCTAAT 419

(2) INFORMATION FOR SEQ ID NO: 3971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACTTGGGA GACTTCAATA ACAGATTTAG GTTTATCTAA AAATCAGGCA TATAATTTCT 60  
 TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120  
 30 GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG 180  
 AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240  
 TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300  
 35 CACCAACACT AAAAAATCCA TTAAGTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360  
 GGGTTTCCAn AGTCCGTTAT G 381

(2) INFORMATION FOR SEQ ID NO: 3972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60  
 AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTCTG 120  
 TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

GAnGTTAATA GGTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300  
 TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360  
 5 GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3973:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACGTAATGGC TTACCAGTTT TTAACATATG TGCAATCCTT TCATATGATT 60  
 20 TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120  
 TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA 180  
 25 TATGATAATC ATGGTCGCTA ATAAAATGAC CCCGTCCTTG CGCATCTAAT TGTCCTTGGA 240  
 TCAATGCTTT GAAGCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATAGT 300  
 TTGTTTCTGC TTCATATTTT GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360  
 30 nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

(2) INFORMATION FOR SEQ ID NO: 3974:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTT ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG 60  
 45 GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAAGTCTAA ATCAAAGTTG ATTAATAAAT 120  
 CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180  
 TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240  
 50 ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAAACT 300  
 TCACCTTGTC AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TTCGCTGAAA 360  
 55 CACTTGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

```

10 CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GCGACCGCC CCAGTCAAAC TCCCCGCCTG      60
   ACACTGTCTC CCACCACGAT AAGnCGGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA      120
15 TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT      180
   ACAAGCTGTG CCGAATTTCA ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC      240
   TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC ACCGAGTCTC TCGTTGAGAC      300
20 AGTGCCCAA TCGTTAACGC CTTTCGTGCG GGTGCGAACT TACCCGACAA GGAnTTTCGC      360
   TAACTTAGGA CC                                                              372

```

(2) INFORMATION FOR SEQ ID NO: 3976:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

```

35 AGGGAATCGA ATTTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT      60
   GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC      120
   CCCATTTCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA      180
40 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA      240
   ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT      300
   TTAAAGCTCA TTTACATAAG TAAACTCTGC TTAAATGAT TTAACCTATT GTCTGCTAAA      360
45 ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTn                                     395

```

(2) INFORMATION FOR SEQ ID NO: 3977:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

5 TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG 60  
 ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120  
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180  
 10 CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 240  
 GGAGCAGAAG ACGGGATTG AAGCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC 300  
 TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360  
 15 CTTAAGTCTA AGTGCGTCTG GCCAATTTCC GCCAnACCCG 400

## (2) INFORMATION FOR SEQ ID NO: 3978:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGGTTAA ATATTATAGA AAACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60  
 30 CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120  
 CTTTTGGTTA CAGAAATTC AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180  
 ACAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240  
 35 AGCTCTAAAA GTTGATTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTGGTG 300  
 GAGGAACCTA AAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360  
 GGATTCCGAA CCTCGGACCC TCnGAnT 387  
 40

## (2) INFORMATION FOR SEQ ID NO: 3979:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

50 TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCAACCTT GGCAAGGTTG TATTCTACCG 60  
 CTGAAGTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120  
 55

CGAACCTCTG GACCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240  
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300  
 5 ACCAATTGAG CTAGGCCGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360  
 ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

(2) INFORMATION FOR SEQ ID NO: 3980:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

20 TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTGT CCCTATTGTC ACAGCATTTG 60  
 CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTGGCC AAGCATACAA GCCGGCATTT 120  
 ATCATGTTGG TGGATTTGTA ACGAAAACAG GTGCCATCGG TACTTTTGTT TATGGCTTCA 180  
 25 TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG TTTTGGCAGA 240  
 CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCACCTAGT TCAAGGTACG CAGAACATCT 300  
 TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360  
 30 nGTCAGCCGT TTTAATACGA GGATGTTCGG CTAnGTGGTG 400

(2) INFORMATION FOR SEQ ID NO: 3981:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

45 CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 60  
 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120  
 CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC 180  
 50 AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240  
 GGATTTTACA GTTGTGCGAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT 300  
 GGnCATATTG ATATCACGCC TAATGAnTCC ATTCAGGACA TTTAATTAAT CCAACTCAAG 360

## (2) INFORMATION FOR SEQ ID NO: 3982:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

```

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA      60
TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAAGCAAA    120
GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTTC    180
AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC      240
TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT      300
AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGGCGATA TTACATTGGA      360
AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn                               400

```

## (2) INFORMATION FOR SEQ ID NO: 3983:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

```

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA      60
AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT      120
TCGAAAGAcG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG      180
CAGACAATGA GTTAAATTAT TTAAAGCAG AGTTTACTTA TGTAATGAG CATTTAAAT      240
AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AAACATAGAT      300
TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC      360
GTTACTAACG ACGATATGCC TTGGGGGAGC                                         390

```

## (2) INFORMATION FOR SEQ ID NO: 3984:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

5 GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT 60  
 GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120  
 10 CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC 180  
 TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GGC GTTCTAA 240  
 ATCTTCATAT AATGAATAGT GATCACCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA 300  
 15 TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360  
 GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

## (2) INFORMATION FOR SEQ ID NO: 3985:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

30 GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAAC TAAAGAAATT 60  
 ATTTCTGATA TTGAAAGTAA AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT 120  
 AAAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT 180  
 35 ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC 240  
 GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAC ATGTnAATTT 300  
 TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360  
 40 AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCCTnCTA 400

## (2) INFORMATION FOR SEQ ID NO: 3986:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

55 TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTGGGA TTCTTAGTGC TGTTCTTATT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATT 180  
 GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCCGT GCGGGAACGA 240  
 5 TTTTGTATAA TATGGATTTT ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300  
 CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG 360  
 AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400  
 10

(2) INFORMATION FOR SEQ ID NO: 3987:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTCGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC 60  
 CGGACTTGGG TATTCCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA 120  
 25 CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180  
 TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC 240  
 30 TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAA TAATATGGTG GGGACTAnCG 300  
 GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA 360  
 GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT 400

35 (2) INFORMATION FOR SEQ ID NO: 3988:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTGGGT AAACGGTTGA TTAATGnAAA 60  
 ATGTTCCGCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120  
 50 CGCCTATTTA TCAATCTGAA ACAAATTATC ATTCGAAAGA TCGCGGTAAG TCTAAAAATG 180  
 GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240  
 TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGA CTCTAG GCGGTGAACG ACCATCCAAA 300  
 55

CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT

400

(2) INFORMATION FOR SEQ ID NO: 3989:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

15	CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA	60
	ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA	120
	GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG	180
20	CTTGCTTnGn GGTnTGTAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC	240
	ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG	300
25	AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCCGTC GGAATCTGGG AGGACCATCT	360
	CCT	363

(2) INFORMATION FOR SEQ ID NO: 3990:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

40	TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG	60
	GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTCTACTT TTACTTTCTA GGATCGACCA	120
	ATTCCCATTA AATTTTTCTG TTGGCTTAAA GAAATTCAAT CCAAATTTTC CCATATTTAT	180
45	ATCCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAATGC	240
	CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTCACA AACATAAAAT ATTAGGGAAT	300
	CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT	360
50	CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT	400

(2) INFORMATION FOR SEQ ID NO: 3991:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

	AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTAA GAAATACAAT TTATTACCCA	60
10	GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAAATTAAT CAAGTGAATT	120
	TCTTTTGGTT ACAGAAATTT CAACAACCTT AAAGCAnGTA TAATGATGAT TTTCAGCTTG	180
	TACAAAGGAG AAAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn	240
15	GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTTGGT	300
	GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
	ATTCGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT	400

20

(2) INFORMATION FOR SEQ ID NO: 3992:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

	AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCAATTATT ATTACCGTTA TTGTATTAGT	60
	CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGTnGACA	120
35	TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT	180
	AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA	240
	CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA	300
40	AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT	360
	TAAAGCCTTn AAATGGATGG TGATATTGAT AATGAATGCC	400

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(2) INFORMATION FOR SEQ ID NO: 3993:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

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TTATCAGAAG AACAAATTCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120  
 AATAGTTTAA TTGAAAATGT CATCGCGCAA GGNGCATTAC CCGTTGGATT ATTACCGAAT 180  
 ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGGAAGAGCC TTCAGTTGTC 240  
 GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300  
 TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAAnTnT 360  
 CCGCCGGCAT TGAGAGCCTT AGA 383

## (2) INFORMATION FOR SEQ ID NO: 3994:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60  
 GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120  
 GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA 180  
 GCACCGGGCA GCGGTCACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240  
 GATAAACAGT CGCTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTTAACC CTGAAAGAGC 300  
 ACCCCTTCTC CCGAATTACG GGGTCATTTG CCGATTCCTT AACGAGATTC GCTCGCTCAC 360  
 CTTAGA 366

## (2) INFORMATION FOR SEQ ID NO: 3995:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60  
 TTCATTAAAA GCAACGTTAT GnTGAATCGG ATAGAGGCAT CTAAGGGAA ACGATTACAA 120  
 ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180  
 CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTA TGTGCTGAGC 240

GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCAnTGCG ACAAGCATG 359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

15	CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA	60
	ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTAA	120
	TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC	180
20	TGCTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA	240
	AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTT	300
	GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTGCCTG .GGCAACGTTT TACTCTAGGC	360
25	GGAAnGTAAG TGGGACTTAC CATCGACGn TAAGGGGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3997:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

	GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT	60
40	GTCAnGCGGG CAGTTTGACT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG	120
	TTCCCTCAGA TGGTTGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCG	180
	AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA	240
45	GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG	300
	TTACACGAC GGGGAGGTTT GGCACCTCGA TGTCGnCTCA TCGCATCCTG GGGCTGTA	358

(2) INFORMATION FOR SEQ ID NO: 3998:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

5 TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAAAACATTA TTTCTGAAG 60  
 ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTTA CAACAAGTAG 120  
 ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG 180  
 10 TACCCGAGGA CTATTTTAAA GATCTGGGAG A<sub>r</sub>TTAAATTA TTTTAACA<sub>r</sub>T CCATTACTTT 240  
 ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCA<sub>n</sub>CTATT TCAGTTTTTC ATGTCTTACC 300  
 TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTACCAA GGTTAGGGCA 360  
 15 TAACACTTTC TATTTCCGAG GTAGCAAAGA CAAATTGCGA 400

## (2) INFORMATION FOR SEQ ID NO: 3999:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCCTTAG TGCTGCA<sub>c</sub>TA ACGCATTAAG CACTCCG<sub>s</sub>CT GGGGAGTACG ACCGCAAGT<sub>g</sub> 60  
 30 AAAC<sub>t</sub>CAAAG GAATTGACGG GGACCCGCAC AAG<sub>n</sub>GTGGAG CATGTGGTTT AATTCGAGGC 120  
 AACGG<sub>t</sub>AGAA CCTTACCAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC 180  
 CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT 240  
 35 GGGTTAAGTC CCGCAACGAG CGCAACCC<sub>t</sub>T AAGCTTAGTT GCCATCATT<sub>a</sub> AGTTGGGCAC 300  
 TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTGGGG ATGACGTCAA ATCATCATGC 360  
 40 CCCTTATGG<sub>n</sub> TTTGGGTTAC ACAAGTGGTT ACAATGGG 398

## (2) INFORMATION FOR SEQ ID NO: 4000:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

TGTTCTTGCA ACGCTATT<sub>t</sub>a GTATCAGGTT TAACAACAGG TGCGACAAA GGTTAGTTTG 60

GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180  
 CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240  
 5 ATTTGCAAAG CAGCGaGTGC GGCAGAAGCA TACCGAACTG ACAATGsCAA aGtTTATGAT 300  
 GATTACmAAG CaTTGTtAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360  
 TGGACCCCGC ATTGTGG 377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTTGTCA 60  
 CTTAACTTCT TGTTTTTCCG ATGACAGCTT CTATTTAGAG AATGTCATGA TTATTTTATA 120  
 25 TTCACTTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180  
 AATTTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTTT TCATTTTAAT AACAAATTTA 240  
 CCTGAACCAA CGTTACCGTA CAGATTATTT TTTTCAATAA GTGTTTTCTC AATTTAAAAT 300  
 30 CAAGTTCTTT CAAGGAAATC TGTTCTTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360  
 TTGTACCGTA TnATCTTnCC TAGTAAT 387

(2) INFORMATION FOR SEQ ID NO: 4002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60  
 GACGTTTAAA CGTTTTAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120  
 TTATGCATAC AGATCCAATG AAATCTTAC CTGAAGATGG TAGCTTGCAG TTAAGTGCTG 180  
 50 GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240  
 CAATGCAGCG TATTGCACTG GCTAACAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG 300



TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT

400

## (2) INFORMATION FOR SEQ ID NO: 4003:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

AGAAATATAT GCATTTTCGGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG 60  
 ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA 120  
 CGACAGGTGA TGGGGTTGAA AGTGTAACGn GCTACACTGG TCATGATGCT GCTAAACTAC 180  
 GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG 240  
 TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT 300  
 GGTTCCTCGG GTACCATTCC CGGTGCACTT TTAAATTAG GAAAAACAC ATGATTTAAC 360  
 AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTCAGCATT 400

## (2) INFORMATION FOR SEQ ID NO: 4004:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC 60  
 GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT 120  
 GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC 180  
 AGGTGATCTA CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA 240  
 CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG 300  
 AGGATAnTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA 360  
 nACTGTTTGA CGAGGGGCCC TCTCGGGTAC CGAATTCAGG 400

## (2) INFORMATION FOR SEQ ID NO: 4005:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

	ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
10	GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
	ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTTTTA	180
	TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
15	GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG	300
	ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTAAATTT GGTGTTGGAT GACGTTGnAA	360
20	TGTTGCCTAA TTTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC	415

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 444 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

	CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
35	ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
	GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
	AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACCT CGGGAGAAGG GGtGCTCTTT	240
40	AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC	300
	AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT	360
	TAA nGAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
45	CGTAACTATA ACnGTCCTAA GGTA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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TTTGAAGTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60  
 CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120  
 5 TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAAT 180  
 AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT 240  
 CGTGCCGAAC TGGAAGTTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT 300  
 10 TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360  
 GCTTCGnTTC ATAAATTTAA AACATGTTAA ATTAGACGTG 400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAAACATTA GTTTAAACCA ATGCTTAGAG 60  
 CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120  
 30 TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTGGTG 180  
 CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240  
 TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAACTTC ATTAGGTGAT AGCTTTAATT 300  
 35 TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360  
 TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60  
 AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120  
 55 AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300  
 ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCCAAAAG 360  
 5 GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

(2) INFORMATION FOR SEQ ID NO: 4010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTAATAATG GTATTTATTC ATCGAGTTAC 60  
 20 ATCTATAGTT TATTAAAATC AGAATACGAC CAAAATGAC AAATTAGACT TACAAAAGAG 120  
 TGATGACATT TAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTTGTTGA 180  
 CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA 240  
 25 TGGGAGGATG CTTTAAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300  
 GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360  
 30 ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

(2) INFORMATION FOR SEQ ID NO: 4011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60  
 45 CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGCACTGG CACTGCTCCC TCAGGAGTCT 120  
 CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180  
 CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTTA GAATTCCTCA AAATGATATT 240  
 50 TCGCGACATG TTAATGAAAT TGTTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300  
 CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360  
 TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG

494

## (2) INFORMATION FOR SEQ ID NO: 4012:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

15	TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA	60
	AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTTT TACTCTAGCG GAAGTAATTG	120
	GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTC	180
20	CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT TCTCGTTTCG	240
	TCAGATTCAA ACGTTTTTAC TTCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG	300
25	ACGTTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT	360
	TTTTGGCCTG GGCAACGTTT TnATnCCAGC GGAAnTnAAT	400

## (2) INFORMATION FOR SEQ ID NO: 4013:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

40	CGAACTGCCG AACCCGAAGA GCGGATTTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC	60
	TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC	120
	GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT	180
45	CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA	240
	AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG	300
	CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG	360
50	AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC	400

## (2) INFORMATION FOR SEQ ID NO: 4014:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

	ATTAGGACCT CAAGACGATA TTAATAAATT TGAATACTTA AAAAAATCTT CTCAAAATAC	60
10	AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
	CGTGTGAAAT CATTTGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC	180
	ATTGTTAATT TAACACATAG TAAGAAAAAC AGTCATAAAT TGATTCTCTAA TTGAAATCAT	240
15	CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTT	300
	ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTGTAG ACATAAAAAA	360
20	nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT	400

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

	GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
	ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC	120
35	ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT	180
	AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC	240
40	GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCGAAC	300
	TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GnTACCCCTG	360
	CCAGnTTATT CATATGA	377

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(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

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ATGACGCACC TGACATCCTC TCGGTTTCATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120  
 5 GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180  
 TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240  
 CTCTGTACAT TTTTCCCAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATGTA 300  
 10 AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTATAT CCTCCTACGG 360  
 GTGAAAATA CGGTGTGTAG AnGTCGTGGT TTTnAAATA 400

## (2) INFORMATION FOR SEQ ID NO: 4017:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

25 CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAACCTG CCCGnCTGAC 60  
 ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120  
 CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA 180  
 30 AGCTGTGCCG AATTTCAATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCCTGT 240  
 CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTTCAAC GAGTCTCTCG TTGAGACAGT 300  
 GCCCAATCG TTACGTCTTT CGTTGCGGGT CGGAACTTAC CCGACAAGGA ATTTGTTAC 360  
 35 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

## (2) INFORMATION FOR SEQ ID NO: 4018:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

45 TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAG ATCGAGCGGC 60  
 50 ATATGAGGCA CGCCAAGCGA TTCCAAACAT TAATGAAAC AGTCCGCCAA TATTAATTGT 120  
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180  
 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240

CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360  
 TGTGGTACTT ACATGCCGTTG GAATTAGGGG TCCGGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60  
 TTGGGCTGTT CGCCCATTAAG AGCGGTACCA AGCTGGGTTT AGAACGTCGT GAGACAGTTC 120  
 GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCCTTAGT ACGAGAGGAC 180  
 CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240  
 TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGGAG 300  
 ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360  
 GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60  
 AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120  
 GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180  
 ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240  
 TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300  
 TTTGTTAATA ACTTGCCGGG CTTCACACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG 360  
 TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTTCAGG 400

(2) INFORMATION FOR SEQ ID NO: 4021:



- (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

10 CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCCACACAG 60  
 CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTGTGAT GTCAGAGCAG 120  
 TTTGCAAGTn TAAAAGATCG TCCATTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAGA 180  
 15 GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTTCTTTT AATGGTTGCA 240  
 GCAGTTAAAA AGACACATAT GATTTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT 300  
 TTGACAGTAC CTATAAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTTATCAnT 360  
 20 AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT 396

## (2) INFORMATION FOR SEQ ID NO: 4022:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 376 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTTGA 60  
 35 TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT 120  
 AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT 180  
 ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GTCGTTAAT TTTATTTTAG 240  
 40 CAGTAGTTGA CTGTAAACA ATGCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC 300  
 CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA 360  
 45 ACACAGAGGC TGGCGG 376

## (2) INFORMATION FOR SEQ ID NO: 4023:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CAAATGGTGG AGCCATAGGA GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60  
 CTACCAACTG AGCTAATGGC TCTTCCATGG nGcNggCCAG AGGACTTGAA CCCCCAACCT 120  
 5 ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180  
 GGTGGAGAGT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG 240  
 10 CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC TACTCTAGCG GAANTAAATTC 300  
 GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTC CGGCATGGGA ACAGGTGTGA 360  
 CTCCTTGCTA TATCACCAGA C 381

(2) INFORMATION FOR SEQ ID NO: 4024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60  
 GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120  
 30 TACATGAAGC TGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCT 180  
 GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240  
 GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300  
 35 AACAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360  
 ATTTCCGnAA CATcTTCTT CCAGAAGATG CCGGTAATAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60  
 50 TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCCT AAGCTGAGGC 120  
 CGACAnGTAn GGCATGGAT AACAGGTTGA TATTCCTGTA CCACCTATAA TCGTTTTAAT 180

GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300  
 GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

(2) INFORMATION FOR SEQ ID NO: 4026:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60  
 CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120  
 TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCTG GAAATCTCTG GATCAAAGCT 180  
 TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTTCATCGGC TTCTAGTGCC 240  
 AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300  
 AnGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGGTTATTA ATCTTGTGnG 360  
 TGTTCTTTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

TCAIGTTTTG CTTGGTTTAA TGCTGTAAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60  
 ATTTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTAGTT 120  
 TCTGCTTCCG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180  
 ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTATAA CGTTACTAAT TGGCTATTAT 240  
 CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT 300  
 AGTTAGTGCG TGCAGAAACT TGTTGTGGTG TTGCACGCTC ATThATGAAG CACTGTTGGT 360  
 GCCTCCGTTT TCGCATAnTG GATTGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

10 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC 60  
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120  
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA 180  
 15 TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTTA TTTTGACGTT 240  
 TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300  
 CTGGGCAACG TTCTACTCTA GCGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC 360  
 20 TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

## (2) INFORMATION FOR SEQ ID NO: 4029:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60  
 35 GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG 120  
 TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTTC 180  
 TACTCTAGCG GAAnTAATTC GGACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240  
 40 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTTGATA 300  
 CATTCAAAAC TAGATAGTnA AGTGAAAAGT GATTTTGGnT TCGCAAACC ATTTGATTTT 360  
 GATTGAAGTC CTTGATCGA TTGAGTGATT CGTGCAGCTn 400

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## (2) INFORMATION FOR SEQ ID NO: 4030:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60  
 GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTACC TGTTGTTTCT 120  
 5 TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTTG GTGTAGCTAA TAACCCTGAT 180  
 TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240  
 10 TTTGAACGCC ATATAAATAA TGATTTTGGA TGATTCTTTT CAAATCAGGA TCTTCTATTG 300  
 CAAATTGTGG TTTGTnTTGG ATTTACnTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360  
 TGAATCTATA CCCTGCATCT TGTAGCnTCC 390

(2) INFORMATION FOR SEQ ID NO: 4031:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

25 TGGTTCGAAT CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGAAGG CAGAGGTCTG 60  
 CAAAACCTTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120  
 30 CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTCCGCT 180  
 CCATAATTTA ATAATAATGC GGGAGTATTT CAACTCTTAG AATACATTCC TTCCTGGAAT 240  
 GAGGTATAGG TGTAATCCT ATCTCCGCT CCATAATTTA ATATTTGCGG GGAGTAGTTC 300  
 35 CAACTTTTAG AACACGTTCC TTCCCGGGAA GGAGGTATAn GTGTATCCTA TCTCCGCnC 360  
 CATAATGCCT TCCAAAGGGG AATTTTTTGG TTTnACCATT 400

(2) INFORMATION FOR SEQ ID NO: 4032:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

50 GTATCGATGA GTTTCTTCGG TCGTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC 60  
 ACATCGGGAT GACCATTAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG 120  
 TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCACATG 180

TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300  
 AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360  
 5 CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnaATGGTAT 400

(2) INFORMATION FOR SEQ ID NO: 4033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTTT TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG 60  
 20 ACCGACTACA GCCCCcAGGA TGCGATGAGC CGACATCGAG GTGCCAAAct CCCCGTCGAT 120  
 GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCggGGTA GCTTTTATCC GTTGAGCGAT 180  
 GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 240  
 25 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATTCTG 300  
 AGGGAACCTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCAGTC AAACTGGCCG 360  
 30 CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA 400

(2) INFORMATION FOR SEQ ID NO: 4034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAGTG nCGAAGCGAC 60  
 45 TTTCTGGTCT GTAAGTACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120  
 CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTTAG GGGGTTTCCG CCCCTTAGTG 180  
 CTGCAGCTAA CGCATTAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAA 240  
 50 GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTCGAA CAACGCAGAG 300  
 AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360  
 CAAATGACAG TGGTGCAngT TGTCTCACT CGTGTCGTGA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

TTGCTTTGTC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG 60  
 GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTTGTTGTA AGCTGACTAT 120  
 ATGTCACCTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC 180  
 CATTAATACT ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT 240  
 CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG 300  
 CCTGTTTTTG GATTTATGAA GGCTATTTGG GGTTCACCTG AATGTCAGTT CGAGGAATAA 360  
 TAAAGTAAAC GAGAGCCAGG TTTGTAATTA TGGCACTTAT 400

(2) INFORMATION FOR SEQ ID NO: 4036:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA 60  
 TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA 120  
 AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA 180  
 CATTCTTCTA TCGATTTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC 240  
 CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC 300  
 TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAAATG GCTATTGCAC GTACAAAGGC 360  
 TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4037:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGA CT TGTGA CAATCGCTTG CTCTTTCTCT CTCCTTCGGC 60  
 5 TCTCGCTTAC TCATTTAGCT CTA CTAAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT 120  
 CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTATT TTGACGTTTT 180  
 AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTTGCCT 240  
 10 GGCAACGTTT TACTCTAGCG GAAnTAAATT GGGCTACCAT CGACGCTAAG AACCTTTCTT 300  
 GACTTGTGAC AATCGCTTGC TTCTTTCTCT TTCTTCGGCT CTCGCTTACn CATTTAGCTC 360  
 15 TACnAAACTC GTTGCCTCT T 381

## (2) INFORMATION FOR SEQ ID NO: 4038:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA 60  
 30 TACACAACGG CTGTTTTATG TTTAGCATCG ATTGTTTTAC TGTCATCGTA AAATGCAGCT 120  
 AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180  
 AATTGATAAT CTTTAGGAAT AACTTTAACG ACGACATCTT CAATGCGATC AAAATGTTTT 240  
 35 AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTTGCTTA 300  
 ATGAATGCTT TTnCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

## (2) INFORMATION FOR SEQ ID NO: 4039:

## 40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60  
 50 GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120  
 CACCGCAGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG 180



GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GCTnAGGATC 300  
 CTAAGTCTAG TCGTCTGCC AATTCCGCCA CACCCGCAA TGGTGAGCCA TAGAGGATTC 360  
 5 GAACCTCTGG ACCCTCTGGA TTAAAAAGTC AGATGCTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTCTTGAC TTGTACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 60  
 20 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120  
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTGA CGTTTTAGAC ATAAAAAAG 180  
 AGACCTCAG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240  
 25 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300  
 GGCTCTCGCn TACTCATTTA GCTCnACTAA ACTCGTTGCG CTCTTGTTCT CGTTTCGGGC 360  
 30 AGATTCAAAC GnTTGTCA 378

(2) INFORMATION FOR SEQ ID NO: 4041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60  
 GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAAC 120  
 45 GATCATTCGG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180  
 TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240  
 50 CTATCGATT ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300  
 CTGTATCACC ATCCATCATA CGATTAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360  
 TATTGGCACC CnAACCTTTG GACTTCnAAT CTAACGGCCA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AAAGTGGTAA CACACCAGAC GGACGTAAAG 60  
 CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT 120  
 TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA 180  
 ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT 240  
 TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT 300  
 TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA 360  
 ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA 400

(2) INFORMATION FOR SEQ ID NO: 4043:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACCTCT GTGACATATA 60  
 AAGCAGGTCT TACAAACCAA GAAATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA 120  
 AATTATTTAA AGCAGATAAT ACACCAITTA ATGTACACAAA TATTACTCAT GGTAGCGGTT 180  
 TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAAATCTT 240  
 CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG 300  
 TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA 360  
 TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4044:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

5 AAAATGGCTT GATTTGAAAA ACGACCAGCA TCGCTACTG G<sub>n</sub>ATAATAGC GAGGCTACCA 60  
 TGTGTTTCA TCGTAG<sub>n</sub>CGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120  
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180  
 10 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240  
 TCTTTTGTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300  
 ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360  
 15 CnTTTCCATT GCAAT 375

## (2) INFORMATION FOR SEQ ID NO: 4045:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60  
 30 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120  
 CATTTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAAATGAT TAATTGCACA 180  
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240  
 35 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGT<sub>n</sub>G 300  
 ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTG<sub>n</sub>AAGT 360  
 GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGG<sub>n</sub>Cn 400

## (2) INFORMATION FOR SEQ ID NO: 4046:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC 60  
 TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240  
 CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300  
 AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACThACn GGATTCTGAG 360  
 TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60  
 TTACGTTTCA GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT 120  
 GGATCATTAT ATTTAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA 180  
 ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TGCGACATTA 240  
 GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300  
 ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG 360  
 GAATTTGACG GnGGACCAAG ATGCnTGTTT CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

CAAACCATCT GACATAATAT ACACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT 60  
 CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGA CTCAGAT 120  
 GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC 180  
 GTACTAGTTG CCCC GCCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240  
 ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTA ACTGT 300  
 TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360

## (2) INFORMATION FOR SEQ ID NO: 4049:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60  
 GACACTACCT TCCCACTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120  
 CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTC CAACATTTGA 180  
 ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240  
 GCTATATGAT TAAATATTAAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA 300  
 ATACCTTTTC ATTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360  
 CCCATACCGG GGTCATCGTC CAATACACGT TCCAACTnC 400

## (2) INFORMATION FOR SEQ ID NO: 4050:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATTCG 60  
 GTAACCCGAG AGGGGCCCTT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120  
 GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC 180  
 CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAAGTC GGTTCGGTCC TCCATTCAGT 240  
 GTTACCTGAA CTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300  
 CTAAACGCCT ATTCAGCTCG ATTTCGTACGG CTCCACATTT ACTGCTAAAnC TTGCATCAAT 360  
 CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAnTA 400

## (2) INFORMATION FOR SEQ ID NO: 4051:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

5 AGTGAAAATG ACTTTATCGG GCTGTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60  
 AACAAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120  
 10 CCATTCGTTC ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCCTAATC 180  
 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240  
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300  
 15 CCAACATGTG GGnTCCGGTT CATTGTGGTA ACGTGTGGT AAAGAACGCA AGTGTATCGT 360  
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

## (2) INFORMATION FOR SEQ ID NO: 4052:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

30 TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60  
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120  
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180  
 35 TTCCCATTTC GGAAATCTCT GGATCAAAGC TTAATTACAG CTCCCCAAAG CATATCGTCG 240  
 TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300  
 TTAATChATG TTTTCCACCA TTTTTTATAA GTnCAAAGGC TTCACATACG GCTTCGGTTT 360  
 40 TTCATTAAATT TTAAATGGCh CAATTTAACA 390

## (2) INFORMATION FOR SEQ ID NO: 4053:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

55 AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAAA GGCGGAGGAA 60

GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCGGTA ATTACATTTT 180  
 AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240  
 5 GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300  
 AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTCAAGT 360  
 CGATGATCGT GAAATTGAA CGCAGGATTT CCGATATAGA 400

(2) INFORMATION FOR SEQ ID NO: 4054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT 60  
 ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120  
 25 CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTTCTACAG 180  
 AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA 240  
 TACCTGCAAA TGCATATCCG CAAAATATCG TTTACTAATAT TTGGGnCATA CTCATCATAC 300  
 30 CACCCTGTTT TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360  
 AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

(2) INFORMATION FOR SEQ ID NO: 4055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAAATTC AAGTCTTCCA TAATTGGTTT AACAACTACT TCTACTTGTT 60  
 CTGTAATTTT ACTCATACAG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC 120  
 50 ACTCTTCTGC CTGAGTTCAC TAATTTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180  
 GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAG AGTTTGTTCC TTTATTTTAC 240  
 CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG

400

(2) INFORMATION FOR SEQ ID NO: 4056:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

15	ATTTTGGTTT ACTTCATGTT GAGTTTTAGA CATTTTAACC ATCTCCAATA TAAAAATAAA	60
	TTAAATTAAA TTCTCAGGGA CTTCATGAC GCCACCTGTA TTGCGCTAG TTACTAGGGC	120
	AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG	180
20	GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTTG TTAAATCAAT	240
	AGTAATCTCA TCACCATCTT CAATTAAgGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA	300
25	AATATGaCCA ACTGcAATAC CTCTTGTGGc ACCGGtAAAA ACGCCCATCA GTkAATTAAT	360
	GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG	420
	nCATACCTGG GTCCACCTTT TAGGTGCCTT TCAnTATCTn ATGGACAACG ACGTGGGCCT	480
30	G	481

(2) INFORMATION FOR SEQ ID NO: 4057:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

	TTTTTGCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG	60
45	ACCTTTCTTG ACTTGTGACA ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC	120
	ATTTAGCTCT ACTAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTC	180
	CTTCGCCAAG CCATTTTCTT TTGTGTTTAC TTTTATTTT GGACGTTTTC GACATAAAAA	240
50	AAAGAGACCT TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT	300
	ACTCTAGCGG AAGTAAATTG GGCTACCAnc GACGCTAAGA ACCTTTCTTG GACTGTGACA	360
55	ATCGGCTGCh TCTGTnCCT	379



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60  
 AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120  
 TTAAAGGCT AAAC TACCAA TGTTTTCAAT GGATTTCCTAA AATGAATCAT CTGGGATGAC 180  
 TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240  
 AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTCAAT AAATGTTGAT ACACCATTG 300  
 AATACCATT TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360  
 GGCGCATTTG ATTTAATGAT ACGTGGATTT GGACCCTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 4059:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGTnGAnCTA CCATCGACGC 60  
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120  
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180  
 TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTGTCGA GCTCCACATG 240  
 TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCTTATAAAC 300  
 CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360  
 ATCCCGT 367

## (2) INFORMATION FOR SEQ ID NO: 4060:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTCAG ACACCGCATT 60  
 5 CAGATTCAGC ATAGCGATTG AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG 120  
 GATTCAGATA GCGATTGAGA TTCCGACAGT GACTCAGATT CCGACAGTGA CTCAGACTCA 180  
 10 GACAGTGATT CGGATTGAGC GAGTGATTG GATTCAGATA GTGATTCCGA CTCCGACAGT 240  
 GACTCGGATT CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTGAGA TAGCGATTG 300  
 GACTCAGATA GCGATTGAGA ATCAGACAGC GATTCAGATT CAGACAGCGA CTCAGACAGT 360  
 15 GACTCAGATT CAGA 374

## (2) INFORMATION FOR SEQ ID NO: 4061:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 432 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

AAAATCATAA TATTTGGCAA TTTTTCAAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60  
 30 AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCACGAT ATTCATCTAA 120  
 CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180  
 TTAAATAGA TTTTAAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240  
 35 TGCACGTTTA TATGCATCTT CATTACTGAG TTTTtkGtG ATTTCGTTAT GATTTAATAC 300  
 GCCTAAwTCy TTCATTTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360  
 ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTtagCCA AGAAATTCAA 420  
 40 ACCATGTTTA CC 432

## (2) INFORMATION FOR SEQ ID NO: 4062:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

TATCTTCGTT CTCAATAGAA TGATTTAAAC CTTCGATTTC TTTATCTAAA TGACTIONACAA 60  
 55

TTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATT TTCGTTCAAT TTCGATTCGT 180  
 GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240  
 5 TACCATCAAT AAGATTTTGC TTTAAACATT GACTATGAAA CTGGGATAAA TAAAGAnTCA 300  
 ATTAACGCAT CAGTATTAGG GAnTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG 360  
 nTTGGATTTG GAGCTAACCA CATCCA 386

10 (2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60  
 GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120  
 25 GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCCTAAGC TGAGGCCGAC ACGTAGGGCG 180  
 ATGGATAACA GGTTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGGACG 240  
 CATAGGTATA GGCGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT 300  
 30 AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360  
 CGAGTTCGTT GgnTTTCACA ATGGCC 386

35 (2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC 60  
 TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120  
 50 CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT 180  
 ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240  
 AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

AGGGGGGGCT TCATGCCTTT AGAATG

386

(2) INFORMATION FOR SEQ ID NO: 4065:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

15	AATTCTTTTCG CTACTTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA	60
	GCAGGTGTAT ATTTTGATTC TGCATCGTCG TATCCTTTTG ATTCTAATT ATGATCAAAA	120
	CGACGCACGC CATATTGACT TGCCATTAAG TCAAAAATTG TAGCAATACG GACTTTGTCA	180
20	CCATTTGCTA AAGTGACTTG TCGAGTTGGA ATTGACGAT TGAATATCCC ATCTCCATCA	240
	CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT	300
	GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTAA AGTTCCACTT CTTACCTTCT	360
25	TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC	400

(2) INFORMATION FOR SEQ ID NO: 4066:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

40	ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA	60
	GGAACAATCG TTATTAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA	120
	CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA	180
45	ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA	240
	GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG	300
	nATATTCATT TGTTTGTAAG AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT	360
50	GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTTAAC	400

(2) INFORMATION FOR SEQ ID NO: 4067:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

	CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATTA TTATTAAATT	60
10	ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG GGAAGGAACG TGTTCTAAAA	120
	GTTGAACTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT	180
	TTTGACAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTCTG	240
15	AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAATA	300
	ATAAGGGCGG CTGAAGGGGA TCGAACCTC GAATGTCCGA ACCACAATCC GATGTGTTAA	360
	CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC	400

20

(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

	TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAG TGCTGCCAGT TGAGCGCCCA	60
	TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT CCAATTTAGT	120
35	TGAGGATAAG ATAACCATTA AGATAATTGG AATAACGTTG CTATTTTATA AAATTAATTA	180
	AGTATCTTTG ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG CTTAAATATA	240
	GTCTTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA	300
40	ATCTCCAGTC AAAGCGCGTC CANTACTAAG GCATTAATTT CATGTGTACC TCGTACGTGT	360
	AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA	400

45

(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

55

AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT 120  
 ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180  
 5 TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240  
 TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300  
 10 GTTTAAACGT TTTTAACGCA TGThCTTAGA AAAAACCGTA CGAAATGATG ATTTCh 356

(2) INFORMATION FOR SEQ ID NO: 4070:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTAG GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60  
 GCGATTGTCT TTCAAGCATC GTGTTTAAAC GAGTTTGTTG TTAAGGGGCG TTTAAGTAAT 120  
 25 ATTATTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG 180  
 GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240  
 30 GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300  
 ATGGCTGTTG CTAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360  
 AATGGATTAC CCAAGGATGC CATTTAnTTA AGCCnGCCAn 400

35 (2) INFORMATION FOR SEQ ID NO: 4071:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAG CCTTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTTCG CTA CTCACAC 60  
 CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120  
 50 ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG 180  
 TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240  
 CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGnAACGCCA CATCCTTTTC CACTTAACAT 300

T

361

## (2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

15	ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCCGGCAC AGGCGTTTGT GGTGCTGCTG	60
	CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG	120
	GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT	180
20	TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA	240
	CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT	300
	AAACTTGGTA GGAGTATTCT TACTGGATTC CCATTAACCA TCGTACTTAA TTTTAAATAT	360
25	GCGGTnCCG TnCATCAGG AnTCATCTAG GCAAGGGGTC	400

## (2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

	GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGGA TGAGGCCAAAA	60
40	TGTTCAATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT	120
	GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT	180
	TATGAAGGTA ATGAAGTGGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT	240
45	GTAAATGATA CTGAACCACT TGTGAACCGG AACAAAGCAAT GGTAGTTACC AnAATTCTTG	300
	AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA	360
50	CCGTAAGGG GGCnCATCCT GGACCAAATT TAAAAGTTGG	400

## (2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA 60  
 10 TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG 120  
 TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACAC 180  
 CATCCATTTT CGGCTGATCT TATCACCTAG CTTCCCCCAT ATCGGCGGAG TTATGCATCG 240  
 15 TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACAn CTGTATTCTT ACGGACTGAT 300  
 AGGATTTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAGT ACTGTTTCAGT 360  
 CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATnAAATG 400

20

(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

GGTTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTTGAGAG 60  
 GAGCTGTCCT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG 120  
 35 CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGATAAGT GCTGAAACTC TAAGCATGAA 180  
 GCCCCCTCA AGATGAGATT TCCCAACTTC GGTATAAGA TCCCTCAAAG ATGATGAGGT 240  
 TAATAGGTTT CGAGGTGGAA GCATGGTGAC ATnTGGAGCT GACGAATACT AATCGATCGA 300  
 40 AGACTTAATC AAAATAAATG TTTTGGCACA AATCCACTTT TACTTACTAT CTAGTTTGAA 360  
 TGATAAATTA CATCCATATG 380

45

(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

55



TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120  
 CTA CTGCGTC CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180  
 5 TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240  
 TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300  
 10 AnCGGCATTTC TCACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360  
 AAGGTTCTTA CCATGGTCAA 380

## (2) INFORMATION FOR SEQ ID NO: 4077:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATTT AAATCGAAGA AACCAGCAAC 60  
 25 AGATTCTCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGCACCT GCAGCTGGTA 120  
 ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180  
 30 TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240  
 CAAGGCGGGA AnAAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300  
 GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360  
 35 ACGGGCTCTT 370

## (2) INFORMATION FOR SEQ ID NO: 4078:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60  
 50 TGA CTTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120  
 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180  
 CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

TAAGAGGGGC CAACCATTTGT TAGAnATAAC AACGGTTGGC TCTTTAAntG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

15	TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA	60
	TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAACTTGAT TCTTCTGACG	120
	CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT	180
20	TTTGACCAAA TGTGTTGGATT TTACTTTGAG GTTGTCCACC AGAAATTTGT AATGGTGACC	240
	AGAATGGACC AGGCGCTACA CAGTTCACCT TAATTCCTTT TGGTCCTAAT TCTTCTGAAA	300
	AACTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATAnG	360
25	GCCAGGGAnT AAAACCCTGG ACnAAAGAAG CCGTGGAAT	400

(2) INFORMATION FOR SEQ ID NO: 4080:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

	TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT	60
40	AGTAAAATTA AATAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA	120
	TATATAGATC AACTTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC	180
	GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTAAATAT	240
45	GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTG CCGTAATAGG ATTCCCATA	300
	GGTGCGTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC	360
50	AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAAAA	400

(2) INFORMATION FOR SEQ ID NO: 4081:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

	CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
10	TGTCTGGGCA ACGCACATCC TTTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT	120
	CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTCTGACT CCCAAGTTAA	180
	ATTAATTGGC ATTCCGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA	240
15	ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA	300
	GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA	359

(2) INFORMATION FOR SEQ ID NO: 4082:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

30	TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGTT GTTTTGAAT TAAATGCATT	60
	TCACATTAGT ATTCATATTA TTTTtaggag GAATTTATAT GACATTTGAA AAAGAAACGG	120
	TCTTAAAAAC ATTATTTCTT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG	180
35	AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
	TAATCAACAT TGGATAGACG CTA CTGTACC CGAGGACTAT TTTAAAGATC TGGGGAGAAT	300
	TAAATTATTT TAACAATCCA TTA CTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT	360
40	CCAAC TATTT nCAGTTTTT	379

(2) INFORMATION FOR SEQ ID NO: 4083:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

	TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
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TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180  
 CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240  
 5 CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300  
 TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360  
 TGTnCAAT ATTACCCnGG GTAGCGGTT TTAGTTCCGG 400

10 (2) INFORMATION FOR SEQ ID NO: 4084:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60  
 CCCTTAATAA CTTAATCTAT GTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120  
 25 GTTCTTTTGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180  
 ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAT 240  
 TTCTTTTTAG TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 300  
 30 TAAATAAACA TTCAAACTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360  
 ATGTTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

35 (2) INFORMATION FOR SEQ ID NO: 4085:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

45 TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60  
 CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120  
 TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180  
 50 GAACCAGCTG GAGCTATAGG CCCATTAATT TGGAATGAAC AAACATTCAA AACTGGAATA 240  
 CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

AAGCATTTGT TCCCACCTTC GACGGCTGAG CTCCTAAAAG

400

## (2) INFORMATION FOR SEQ ID NO: 4086:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

15	GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAAATTCCA TGTGTAGCGG	60
	TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAACTG	120
	ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT	180
20	AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCCTTA GTGCTGCAGC TAACGCATTA	240
	AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAACTC CAAAGGAATT GACGGGCGCA	300
	CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA	360
25	C	361

## (2) INFORMATION FOR SEQ ID NO: 4087:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

	GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG	60
40	AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA	120
	CCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT	180
	AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCCTGCAAA	240
45	GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC	300
	AGGATTTCGAA CCTGCGACCC CTTTCCCAAA CCAAGTGCTT TTACCAAGTT GGTACTTCCn	360
	GTATAATTTA ACGGGCCCCG TAGGAGTTCG GAACCCTTAA	400

## (2) INFORMATION FOR SEQ ID NO: 4088:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA	60
TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAGGA CCTGATTATA CAATTTTAA	120
GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAACC ATATTTAGTA AATACAGATG	180
GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA	240
AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA	300
AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA	360
GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAATAT	400

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(2) INFORMATION FOR SEQ ID NO: 4089:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG	60
GTGACAATCA AACGCTACAA CTA CTGCTGAAAA AGATTCTGAA CACCCATTGG	120
CAGAAGCCAT TGTC AATTAT GCAAAAGAAA AGCAATTAAT ATTA ACTGAG ACAACAACAT	180
TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT	240
TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA	300
TGGATTTAAC ACATTATGAA CGAGATGGTA AA ACTGCTAG CTCATTGCTG TTGAATTATT	360
nCATAACGGT ATCA	374

(2) INFORMATION FOR SEQ ID NO: 4090:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

55

TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA 120  
 ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTCCGT TGTGACAGTA AGTGACGCGT 180  
 5 TACCAAATGG CGGAGTTAAA GCAAAATCTT CAATTTCAAT GAACAATGTG ACGTATACGA 240  
 CGCAAGACGA ACATGGTCAA GTTGTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300  
 10 ACAGTGCACC AGTAACAGTG ACACCACANT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360  
 TTAAGTT 367

## (2) INFORMATION FOR SEQ ID NO: 4091:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAAATGCGC TTGCAACAAG CTTTTTTTCAA 60  
 25 CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120  
 TGGGGTGTGG GCCCAACAC AGAGAATTTT GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180  
 GGGTGTGGGC CCCAACACAG AGAATTTTGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240  
 30 GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG 300  
 GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360  
 35 CGGGGGCCCA ACACAGAAGn TGACGAAAAT nCTnGAACCA 400

## (2) INFORMATION FOR SEQ ID NO: 4092:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60  
 AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120  
 50 ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA 180  
 CCTGTGTCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360  
 CATTGACCT TCATTGGTT GCAATGGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60  
 TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120  
 AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180  
 AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA 240  
 CATCATCGAA AAAGCAAAAG AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300  
 AGCGTATTTT AGTCTCATTG ATTAAnATGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTATAAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60  
 TGTTCTTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTTAA AACTCTTTAT 120  
 TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATChAGTTT TCAATGTACA 180  
 AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCCTGCAAA GCAGGCGCTC 240  
 TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG 300  
 AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

5 ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAAG 60  
 TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG 120  
 AAGTGAAGGA TGTTATAATT TATCCTTCGC TTCTTTTAT TAATTTAGTA ATGAATAGTA 180  
 10 GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240  
 ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300  
 TGGTTCTTTG TCATTAGCCA CAGCTATTTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA 360  
 15 CTCCTTGAGA GGAAATACTn ATTT 384

## (2) INFORMATION FOR SEQ ID NO: 4096:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTCAACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60  
 30 TTACGCCTTT CGTGCGGGTC GGAACCTTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120  
 TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCTAG CTTCGCAGAA AGAGCCGACT 180  
 CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAT 240  
 35 CAGAGACCTG TGTTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300  
 GTTAACCCTn AAAGAGCACC CTTCTCCCG AAATnACGG GGTCATTTTG GCCGAGTTCC 360  
 TTAACGAGnA TTCGCTCGGT GCAACTT 387

## (2) INFORMATION FOR SEQ ID NO: 4097:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

50 CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTCAG 60

TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTCAGAT 180  
 AGCGATTTCGG ACTCAGACAG TGATTCAGAT TCAGACTCAG ATAGCGACTC AGATTCTGAC 240  
 5 AGCGATTTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300  
 TCAGATTTCAG ATnGCCACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTTCGGAC 360  
 TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTTCAG 400

(2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60  
 CTGGATTTCGA TGTAATTTTG TTTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120  
 25 GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180  
 AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240  
 TATCGCTTAT AATTGTAAAT TTAATGTTAA GATTAGGTAA AATTATTTAA CAATATATGT 300  
 30 TATTTGTATA TGACTTGTA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGAAT 360  
 GGCCAGTTTG CCAAGCACTG GTTTGACCA n ATGGnGGCAn 400

(2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTTCC ACTTAACATA TATTTTGGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60  
 CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTTCGG 120  
 AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA 180  
 50 TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTTCCGAGA GAACCAGCTA TCTCCAGGTT 240  
 CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTTCGG 300

## (2) INFORMATION FOR SEQ ID NO: 4100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT TGCCAAACAG CATGCTTAAT TTCAATATCT TCTTTGACTG CTTCGATATA 60  
 TAAATCAGCA TCATCATTTA CCAAGTCATC ATCAAAATTA CCATATGTTA AATGACTCGC 120  
 TAGATTTAAG TCGAATAGTA GCGGCCGTTT CTTATCTGTA ATTTTATCGT AAGATTTTTT 180  
 CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT AATAGTTTTA CTTTAAGTCC 240  
 AGCATTCAACA AAAAGTGCTG CCAGTTGGAG CGCCCATTGT GCCTGCGCCA AGAACGGnTA 300  
 CTTTATTAAT TGGTCATAGT GAnTCCnCCC ATTTAGTTGA GGGATAAGAT AACCATT 357

## (2) INFORMATION FOR SEQ ID NO: 4101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC TGGGGACATA AATCAATATT CTATGCTCTA CGAATTATAT TGGCAGTAGT 60  
 TGACTGGnCG AAAATGCGCT TGTAACAAGC TTTTTTCAAT TCTAGTCAGG GGCCCCAACA 120  
 CAGAGAATTT CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGAGGG CCCCACACA 180  
 GAAGCTGACG AAAAGTCAGC TTACAATAAT GTGCAAGTTG GGGATGGGCC CCAACAAAGA 240  
 GAAATTGGAT TCCCAATTTT TACAGACAAT GCAAGTnGGG GTGGGACGAC GnGATAAATT 300  
 TTGCGAAAT ATCATTTCTG TCCCACTCCC ATCAAAAGAA TGACAT 346

## (2) INFORMATION FOR SEQ ID NO: 4102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60  
 GCGATTACACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120  
 5 CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180  
 GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240  
 AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300  
 10 ATGAAAATGT ACGTGAGGAA ATThTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360  
 CAT 363

(2) INFORMATION FOR SEQ ID NO: 4103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

25 GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTTA TGITCAGGTT TAGCTGTGTG 60  
 ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120  
 AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGa TCACCAAGTT GAGCAAAGAA 180  
 30 GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240  
 CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300  
 GAAGCCATAA rCAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtK 360  
 35 AaTGCCGGTT TGTATGGTTG GCCCAAnTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

50 AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60  
 ATTTTTTTAA AGTATTTAAA AGTAAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120  
 TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300  
 ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

(2) INFORMATION FOR SEQ ID NO: 4105:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60  
 TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120  
 TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180  
 GTATTTATTA AAGGTGGCGA CGGTTTTGAT TTCGGACACG TGGAAAGATT TATTCAAAAC 240  
 CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300  
 CGGTAACACT TCATAAAACT GCGGTTTGTh ACCATTACCT AATnGTCAAG GGTACGGCGT 360  
 TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTn 60  
 TGCCAGGCAG TTTTtTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG 120  
 TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180  
 TTGAAACTG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAACTA TAAGTTACAA 240  
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTCATGGGA GAGTTTGGAT 300  
 CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360  
 GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGCh 400

(2) INFORMATION FOR SEQ ID NO: 4107:

(A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

10 GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA 60  
 AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA 120  
 TTGGTTTTAA ATGCATTTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180  
 15 GTCCTATTAC CTTGTCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240  
 CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT 300  
 AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA Gnt 343

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(2) INFORMATION FOR SEQ ID NO: 4108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

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ATACAAAACA CCAGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60  
 ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120  
 35 TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180  
 AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTTGGT 240  
 CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGAnTGGTCA AGTAGTAGAA 300  
 40 AATCCTACTA CTATGGAAGA CGATnAAGAC GAAACTGTTG TGGGTTGGCA G 351

(2) INFORMATION FOR SEQ ID NO: 4109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

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CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180  
 GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240  
 5 AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300  
 TTGCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCTG 360  
 CACTGTA 367

10 (2) INFORMATION FOR SEQ ID NO: 4110:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT TGAAGGATGG AGTACTGTCG CATTTGCGAA AGACTGGCAA GGACCACCAC 60  
 GTTTGCAAAA CGGAACAAGT TGGTTCATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120  
 25 CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAACAGA GGAGTTAAAG CATCAACATC 180  
 CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240  
 ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300  
 30 CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAAACCA AACACCATTG GCCATAnGAA 360  
 AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

35 (2) INFORMATION FOR SEQ ID NO: 4111:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

45 TCAGATGAAG CTAAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60  
 GTTGCTTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTTATGCC AGTCACTACA 120  
 CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180  
 50 ACTGGTGATA CATTTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240  
 ATGAACTTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

AATTGGTGGT GCGGTTTAA TTCCAGTAT TAGTACTAAC

400

(2) INFORMATION FOR SEQ ID NO: 4112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60  
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120  
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180  
 GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT 240  
 TATTCACCTG GntTTGCTTG GGAAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT 300  
 ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC 360  
 GG 362

(2) INFORMATION FOR SEQ ID NO: 4113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TGCGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG 60  
 AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA 120  
 AAGCTGTAGG TGACATTGAA GATTTTTCATC TCGTTTCATC GATGGTCGGT GCCACAAACA 180  
 ATCATACGCC GATTGAAGAA AATGTCACCTG TTTACCAAGA GATCGTATCC ATTTTATCA 240  
 ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTTCAACG CCACATATCG 300  
 CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC 360  
 TAC 363

(2) INFORMATION FOR SEQ ID NO: 4114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 394 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

	GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
10	GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCCC TGGAGTTGGG TCTTTCGGAT	120
	TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATAACG TACAACATTC TCATTATTCC	180
	AACCGAAAAT ACTGTAGTCT CTATTTGTTA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
15	TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300
	TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG	360
20	nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn	394

(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

	GGCGATTATA TTAAAAAGCC AATTACAGAA TGTAGTGGTA ATGAAATATG CCAAGAATGG	60
	CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT	120
35	ACGATTCCTG TTTATATGCC ATATATCACA TCTTATTTCa TGACGCGTGC TATCGGCGAC	180
	AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA	240
	AACAGAGCGA GACACTGTAT TTACAACAGA ATATTCGGTT CGTACTGCCA GGAAGCTGT	300
40	TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC	360
	TThCGCGTnc TTAATGGGAT GGCCATATAC GAACTGGATG	400

(2) INFORMATION FOR SEQ ID NO: 4116:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

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TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120  
 GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180  
 5 ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240  
 GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300  
 TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGGTTTG 360  
 10 GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

## (2) INFORMATION FOR SEQ ID NO: 4117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60  
 25 TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120  
 ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TCGCCCCCGG 180  
 30 GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GGCGGGGCCCC 240  
 CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300  
 AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGGCCCC 360  
 35 CCACCACAGG GAATTTGAA AGAAATnCT 389

## (2) INFORMATION FOR SEQ ID NO: 4118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60  
 50 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAAnTAAGTT GACTACCATC 120  
 GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA 180  
 GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT 240

ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360  
TATnAACCGA A 371

(2) INFORMATION FOR SEQ ID NO: 4119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60  
TGAAACAGTG GTGCTAATTG CGGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120  
AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180  
TGAAGCTACA CTGCTATTTT CAGCCCATn AAGCACGCTT TGAGACGCTT CTTCCATTCC 240  
TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300  
ACCATTTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC 60  
GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120  
CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTGCGGG GTAACCTGCA TCTTCACAGG 180  
TACTATGATT TCACCGAGTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC 240  
GGGTCGGAAC TTACCCGACA AGGAATTTTCG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300  
CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360  
CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

AATAAATCTT GCTTTATTCT TTTTACCAGT AATATCTAAA TGAGTTGGAT ATTTAACTTT	60
CGCATTAAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATACATAAT	120
AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC	180
ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC	240
ATTTGGCCAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATTG CGCCACCAAA	300
CCCTAACATT ACCAGGCCAT ACCAGCATAC CCAGGGCCAC CCGnGGAAGG AAATTAAGTA	360
GCGGTGGTAC TACCAAnGAC CAGTGAAGG TnCCAATTAA	400

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(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT	60
AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn	120
ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA	180
TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA	240
CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT	300
ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT	360
TT	362

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(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

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CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120  
 TCTGGGGTGG TGTCTCAGAT ATTGATTAA TGTATGAAGA ACGTGTTCGAT TTAAGAGGCA 180  
 5 TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240  
 GCGATTCCAA ACATTAAATGA nAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAG 300  
 10 ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352

(2) INFORMATION FOR SEQ ID NO: 4124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTTGA AGTTCAGGTA ACACTGAATG GAGGACCGAA 60  
 CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA 120  
 25 ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180  
 TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCTCTTC GGGTTTACCA ATTTTCAGACA 240  
 AACTTCCGAA TGCCAATTAA TTTGAACTTn GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300  
 30 GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG 360  
 GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAAATT TATAAAGAAT ATGTAGAAAA CTTTATTTA CATCGAGGCT 60  
 ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTTCAA 120  
 TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA 180  
 50 CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240  
 GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

TTGTCACTAA AACATTAAAT ACCGGGATAC AGCCGAGTAA

400

(2) INFORMATION FOR SEQ ID NO: 4126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

AATCTATATT TTA CTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTTA GTCAAGCGCT 60  
 CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAAACT 120  
 GAATACAATA TGTACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA 180  
 GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCCAA 240  
 TCATTGTGCC CACCTTCGAC GGCTAGCTCC TAAAGGGTT ACTCCACCGG CTTCGGGTGT 300  
 TACAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGnATTC 360  
 AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnCGGGAT 400

(2) INFORMATION FOR SEQ ID NO: 4127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

CGAAATTTGT AGTAAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG 60  
 GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA 120  
 CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 180  
 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 240  
 CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT 300  
 CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAAGT AAGTGATTGA GCCACCGTAA 360  
 TGGTTGGnTT CCCAGTTTG TCGGCAnCCA CAACCGGAAC 400

(2) INFORMATION FOR SEQ ID NO: 4128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

	GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC	60
10	AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTCG	120
	AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA	180
	AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
15	GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
	TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA	360
	AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC	400

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(2) INFORMATION FOR SEQ ID NO: 4129:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

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	AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG	60
	ATTGGAAGTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
35	CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC	180
	GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CCAAATAAT	240
	GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTT TTGAACCGCT	300
40	TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCGG	360
	TThAACAGCC GGAT	374

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(2) INFORMATION FOR SEQ ID NO: 4130:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 431 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

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ATTAAATTTT AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120  
 GTGCTTCAGA AACATTTTCGT GAATGATAAC CGATACGTTT AAGAACrCsA ATCATATCGA 180  
 5 TATATAGTAA TCCGCCTTTT GTTGTACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240  
 TCGGTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT 300  
 TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360  
 10 TGAATAA<sub>n</sub>T TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTTCATCATG 420  
 TTGGCGGTTT T 431

(2) INFORMATION FOR SEQ ID NO: 4131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GCGGGTGTG TCGCATTTGC TGTTTGTGTC GGTGCTTCTA CTTTAGTTGA 60  
 GGGCGGTGTT GTCGCGTTTG GTTTGATTG CGGTGCTTCT ATTTTAGTTG AGGGCGGTGT 120  
 TGATGTGGTG CTTCCACTTT AGG<sub>n</sub>AA<sub>n</sub>TGA GTGTTGTCGC GTTGTCTGCT TGC GTTGTGCG 180  
 30 TTGTGATTAC ACCTGTTGTT AAAAGGCCCTA GTGCTAAACT TGTTTTAGCA ATCGTTGTTA 240  
 TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTG TTCGATACAT TCATTGAATC 300  
 ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AAACCTGT<sub>n</sub>T AACCAGATTG 360  
 35 GAAGCAGCGT TGAAT<sub>n</sub>AAAT GAAGAAAGCC AGAAGTTCGT 400

(2) INFORMATION FOR SEQ ID NO: 4132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCAGTG TATGTCTTTG GCCACCACCT TGACGTTGTT GTTGTGTTG TTGATTTTGA 60  
 50 TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120  
 TGATCATTAT CAGATTCATC TTTAGTCGCT TTGTCTTGAT CCTCTTTTGA TTTATCACTG 180



TCAGCATTAT TTTTATTTGT ATTCGCGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300  
 TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360  
 5 ATGGTAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTh 400

(2) INFORMATION FOR SEQ ID NO: 4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTGTACC 60  
 20 ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AAACATTGAC TATGGAAGTG 120  
 AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAAC GATTAATAGT 180  
 TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240  
 25 TTTCTCTATT CTTCGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTAA 300  
 CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCGC 360  
 TAnCGGGTAC CGTTCACCA ATTCCATTAA CATATCGCGG AATATCATTT TGAGGAA 417

(2) INFORMATION FOR SEQ ID NO: 4134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGThTTTATG TTCAATATTA AATGGATTCT CTACTACGTT 60  
 CTACAATTTT ATCTTTTTTC GTTTTGTGAT AAACATCTAA CATGTCGATG GCTTTATCAA 120  
 45 ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180  
 CGnAATATCT TCATCATGTT GGTCGTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240  
 CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300  
 50 TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTTTCG AATGCTATCA TTGT 354

(2) INFORMATION FOR SEQ ID NO: 4135:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

10 CTGGGATCGC CACCTTTAAG TCTAACAACC TTGTTATATC GACGCGCTGC TTCCACGATA 60  
 CAGTCATTTA TTTTTTCTTG CTGAATATGT TTTGCATACG GCTTTTTTACC AACATCGATA 120  
 ATTTTCAGTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA 180  
 15 ATGACATCCG CTTACAGTAT TAAACGCTCA GCCTTTTTTCG TCAAATAATT CGGATTACCT 240  
 GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC 300  
 CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT 360  
 20 GnATTAAACA ATTTTGTATC GTGGGGGGGC AAATACATAT 400

(2) INFORMATION FOR SEQ ID NO: 4136:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

35 ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTTCG CACTGTATGG 60  
 TGGGTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC 120  
 ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC 180  
 40 TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT 240  
 ACCAACACGT AACAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT 300  
 TTATChTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG 348

45 (2) INFORMATION FOR SEQ ID NO: 4137:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTCTCTCA 120  
 GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA 180  
 5 TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT CACACCACGA 240  
 GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300  
 GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TGCGGCTGGG 360  
 10 AT 362

## (2) INFORMATION FOR SEQ ID NO: 4138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCCGAAAT CTCTGGATCA 60  
 25 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120  
 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA 180  
 30 AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATTT ACATAAGTAA 240  
 ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT 300  
 TTAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC CAGCGATTAn TTCnTGAGGA 360  
 35 ATTCAAGCCT AnTTAAAACC CTTA 384

## (2) INFORMATION FOR SEQ ID NO: 4139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC 60  
 50 AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120  
 ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180  
 TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTTG AACCACCCCG GAAGCAATAC 360  
 TTAAAAATAA ATTTAnTATC ACACCGGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60  
 GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGaCTCG 120  
 AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT 180  
 ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC 240  
 CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300  
 AAGCCTGTCTG GGCTCAGCTT AAGGACCCGA CTAACCCAG AACCgGAAGA GCCTTCCTCT 360  
 GGAAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA 60  
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120  
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTCACACC ATTTTTATAA 180  
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240  
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 300  
 AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360  
 TnCAAGCnTA TTTAAACTC TTAATCACnC GGTTTTGcNT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

10 GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTTC 60  
 TTTGTGTTTA CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120  
 CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 180  
 15 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 240  
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAA CGTTTCACTC 300  
 GCCAAGCCAT TTTCCTTGGG TTACTTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360  
 20 TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCh 400

## (2) INFORMATION FOR SEQ ID NO: 4143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAAATTG ACATTATTAC TGACCAAACA AGTGCACATG ATCCGCTAAA TGGATATGTG 60  
 35 CCACAAGGAA GCGAAAGTAT TGCCTGAAAA AGATCCGAAA AAATATGTTG AACTGTCCAA 120  
 AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGAATT CCAAAAACGT GCGCTGTAG 180  
 40 CATTTGATTA TGGTAACAAT ATTCGTCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT 240  
 TTGGACTTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG 300  
 GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG 360  
 45 GAGGAAATG 369

## (2) INFORMATION FOR SEQ ID NO: 4144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 370 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60  
 ATGTTTTAGT TGCCTAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120  
 5 TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TGCGCTCGAC ATAGTGCCAC 180  
 ACGTTGTTTC ATACCCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCCTGT CTTCTAAATC 240  
 AACTAATTTA AGCTGTGcNT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300  
 10 AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAAACAAh 360  
 CGGGAGnGGC 370

(2) INFORMATION FOR SEQ ID NO: 4145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

CGAGGTAGCA AAGAACAAAT TGCGAAATAT GTACCTAAAT TACAGTCACA TGAAGTGGT 60  
 ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCCGACG TTGCnGGAGG TCTTGAAACA 120  
 30 GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180  
 GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA 240  
 TTGCTTTGTA GTCAGACCAG AACAAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300  
 35 ATCGCACTTC GGCATTGTTC CTAACGCCCT AATTTnAATT AAnTAATGTT CAAAGTAGGA 360  
 TTGAAGCGGG 370

(2) INFORMATION FOR SEQ ID NO: 4146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

TGGGGTGTTT TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC 60  
 50 CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120  
 CAATTGAGCA AACAACCGAA TCAAATTAAT GATTGGGGAA CATTGATCA TACTAAATTT 180

GAATGTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTTnTTTT ATCAGGAGGA 300  
 GGATGGCGGT ATCCAATTTA TTTCCATTG GAAATATATG GnGCCCCGTT TTGGGAACnC 360  
 5 ATTTTTTGA AAGCCAAGCT 380

(2) INFORMATION FOR SEQ ID NO: 4147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC 60  
 20 ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AAACGAATA CAATATGTCA 120  
 CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC 180  
 AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCCAATCATT TGTCCCACCT 240  
 25 TCGACGGCTA GCTCCTAAAA GGTTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT 300  
 GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTGn CTGGGTTTAC 360  
 nT 362

(2) INFORMATION FOR SEQ ID NO: 4148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTGAA AATGATGAAC GATTCAGTGG 60  
 TTACGGCAAG CTTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120  
 45 TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCCGTGG 180  
 TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240  
 GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300  
 50 AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360  
 AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGCnCTA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

10	CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTACAG TTGGAGGATA	60
	CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC	120
15	AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCCAGGTG GTGGTCAGGT	180
	TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAGGTA TTGTAAGTGG	240
	CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TACACTGAAG TAATCTGATT	300
20	GAATAGTGGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA	360
	AACCATCATC ATATTnCnCAT CTGGTTAGGA CTGAAATGGC	400

(2) INFORMATION FOR SEQ ID NO: 4150:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

35	AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT	60
	CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATTCCGTCG	120
	GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT	180
40	ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAAACCGTG	240
	TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG	300
	GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG	360
45	AATAGGCGTT A	371

(2) INFORMATION FOR SEQ ID NO: 4151:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT 60  
 5 TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA 120  
 TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTCT 180  
 TTGACTATAG ATGTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTAAA 240  
 10 GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTCGAATT TGGTTTCATG 300  
 CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC 360  
 15 TCGTTT 366

## (2) INFORMATION FOR SEQ ID NO: 4152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60  
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120  
 30 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180  
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA 240  
 35 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300  
 CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA 360  
 TCGCnTGCTT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG 400

## (2) INFORMATION FOR SEQ ID NO: 4153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGnATAGGCG 60  
 ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC 120

CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240  
 AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300  
 5 CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360  
 TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

(2) INFORMATION FOR SEQ ID NO: 4154:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

20 TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60  
 nCAGATTTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120  
 CATACCTCCA TCTACCAAA ACGTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT 180  
 25 TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240  
 GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300  
 CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360  
 30 CCATACATCG TCATCGTTTG CACCGTCAA TACTGGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

45 GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG AATTAAGAAT 60  
 CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120  
 AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCG AGAAAGAACG TAAATTTAAT 180  
 50 CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA 240  
 ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300  
 AAAGAAGAAA TCACAnAAGT CCAAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360

## (2) INFORMATION FOR SEQ ID NO: 4156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATT AATTGGGCAC TCTAAGTTGA 120  
 CTGCCGGTGA CAAACCnGGG GnAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180  
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG 240  
 CAAATCCCAT AAAGTTGTTC TCAGTTCGGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300  
 GGGAAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGAnTACGT TTCCCGGGGT 360  
 CCTTGTTACA CACCGCCCCGT 380

## (2) INFORMATION FOR SEQ ID NO: 4157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACTTA 60  
 TGGATGATGG ATTCTGCCAA GTTAAAATAA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120  
 AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180  
 GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTC TAAAGGGCAA 240  
 TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TCGTCAGGA 300  
 GTTTCAGTGG ACCAGCTGGG GTGGAnTTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA 360  
 ACTTnACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

## (2) INFORMATION FOR SEQ ID NO: 4158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

5 AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60  
 CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120  
 TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180  
 10 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT 240  
 CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300  
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

15 (2) INFORMATION FOR SEQ ID NO: 4159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

25 AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTCT 60  
 TCTCTTGTtTA CTTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTTACG TTCTTTCTTG 120  
 30 AATGGAATyT CTTCTTTTTC TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTTACG 180  
 CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCtGGAT TCTTAATTCC TGGTTTACCT 240  
 GGAACTTcYT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATTCTCTCTG ATGACCTGGT 300  
 35 GTTATCGTTT CTGGTCCGTA TTCTGTtAAT TCATTAAATCG GATCTTTTGT GATTTCCTTCT 360  
 TTTGGTTTcAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCTG 420

(2) INFORMATION FOR SEQ ID NO: 4160:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

50 ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60  
 CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

55

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240  
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300  
 5 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC 359

(2) INFORMATION FOR SEQ ID NO: 4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60  
 20 GGCCCGnAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120  
 TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180  
 CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240  
 25 AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA GAAAAGCCTC TAGATAGAAA 300  
 ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAAnTC T 351

(2) INFORMATION FOR SEQ ID NO: 4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTTCGATCC CGCTAGTCTC CACCATTAT 60  
 TTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120  
 GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180  
 45 ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC 240  
 GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300  
 GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360  
 50 AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 4163:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

10 ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTTT 60  
 AAAATAATAC CAATCTCATT TTAAATTCT AACTTGGTT TCGTATAATA CGCTCTTAAA 120  
 TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG 180  
 15 TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTG ATGGAGGTGT TGTCACITTA 240  
 GTTGnAAGGC GGTGTTGTCG CATTGCTGT TTGTGCGGT GCTTCTACTT TnATTGCAGG 300  
 20 CGGTGTTGTC GCGTTTGGTT TTGnATGCGG TGCTTCTATT TT 342

## (2) INFORMATION FOR SEQ ID NO: 4164:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC 60  
 TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTTGGTAA GGTTCTTCGC GTTGCTTCGA 120  
 35 ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCTTTGA GTTCAACCT 180  
 TGGGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA 240  
 40 AACCCCCTAA AACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GSTATCTAATC 300  
 CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGCCCA 360  
 nGGGGGTnCC nCCAAACTT TGGGGATTTA ACGGTAAAAA 400

## (2) INFORMATION FOR SEQ ID NO: 4165:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120  
 GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180  
 5 ACTGTCTCAC GCAAACGTAA GGCATTTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240  
 TATTCACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300  
 10 TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTAATAATnG GTTGCCGAAT 360  
 GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

## (2) INFORMATION FOR SEQ ID NO: 4166:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60  
 25 TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120  
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 180  
 30 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 240  
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300  
 CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAAATAAT CCnGGTnGTC 360  
 35 CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG 400

## (2) INFORMATION FOR SEQ ID NO: 4167:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAAT AAGCCGATAA 60  
 50 AGATACACAC CTTTACCGAC TATTTAAAAT ACACTTCACC AATTCATTTT AATTAAATGG 120  
 ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180  
 ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA 240

GTTTTTTGTA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT 358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

15	TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA	60
	TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTCT AAATATGCAT	120
	ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT	180
20	GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTTACCA GCATCTTCTT	240
	CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTCGACTTC GATATCGATA	300
	TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAAnTTG AGAGCTTnTG GnTTAGCTGG	360
25	ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

	ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT	60
40	TCGTTAAATA AAAGTATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGATAA	120
	ATTCAGGTCT CTTCCACGTC ATATTTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG	180
	AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACTTC TTGTTTTTCC	240
45	GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCACCTCA ATGTTATCAA	300
	TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC	360
50	GTGTACnTCC ACGGTTTTCA TTTAAAnAACA ATTTACCGGA	400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 395 base pairs



(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60  
 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGCGC ACTGTCTCAA 120  
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA 180  
 AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA 240  
 TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGnAGGCGCT GGGTGGGGAT 300  
 ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAnt TATCGTGGTG GGGAGACCAT 360  
 GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG 395

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(2) INFORMATION FOR SEQ ID NO: 4171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG 60  
 GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA 120  
 GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTTGGCTT ATTACCGAGT GGCGGTGGCC 180  
 TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT 240  
 CCATGACAAA AGTACTGACG AATATCGCAT TCGGAAnGCT CTACAAATGC CTTTGAGGCA 300  
 CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT 360  
 CGAAGTGGCG C 371

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(2) INFORMATION FOR SEQ ID NO: 4172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

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GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA 120  
 CCCCTTGCTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG 180  
 5 CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240  
 CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CnGAATGAA CCGGTACGTG 300  
 ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCG GACTATAAAA 360  
 10 T 361

## (2) INFORMATION FOR SEQ ID NO: 4173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60  
 25 TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120  
 GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180  
 AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTTATC 240  
 30 TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300  
 TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360  
 35 AGnAATCCCA CCGTTGTAnG 380

## (2) INFORMATION FOR SEQ ID NO: 4174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG 60  
 CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTGGAAGTC GTTGATTCA CACTGCCGAG 120  
 50 AAAAGCCTCT AGATAGAAAA TAGGTGCCCC TACCGCAAAC CGACACAGGT AGTCAAGATG 180  
 AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG 360  
 CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT 400

(2) INFORMATION FOR SEQ ID NO: 4175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGA CTCTGAAC CTACGACCGA TCGGTTAACA GCCGATAGCT 60  
 CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG 120  
 TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCCGGCAT GGGAACAGGT 180  
 GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240  
 AGTAAGTAAA AGTGATTTTG CTTTCGAAAA CATTATTTTT GGATTAAGTC TTCGATCGAT 300  
 TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTA AAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC 60  
 GCTCTTAAAT CTTTAAATT AGGATTTATT TCTGTTGGTA CTTGTTTTGT GGTGGCGAT 120  
 TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTTGTGGCG TGTTTGTTGA TGGAGGTGTT 180  
 GTCACCTTAG TTGAAGGCGG TGTGTGCGCA TTTGCTGTTT GTTGCGGTGC TTCTACTTTA 240  
 GTTGAGGGCG GTGTTGTCGC GTTTGGTTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC 300  
 GGTGTTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

5 CAGAACCTTG NAATGAATCG CGATGGAATA TCTCTATCTG nAAACAGATT TCTTTTTGTC 60  
 CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTTGCG CTTCTTTATC AATGTCATAA 120  
 CCTAATGCTT TTAACCTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180  
 10 CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTC ATATGTTTCA CGATGTTTTA 240  
 ATACGCCATC TTGGTGAATA CCTGATTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300  
 ATTTCTAGGC ACTCGAATAC CTGCATATCT TGA<sub>n</sub>ATTAAA TCCGAGGTTT TAGTTCCTCG 360  
 15 AG 362

## (2) INFORMATION FOR SEQ ID NO: 4178:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

GGAGCTAATA CCGGATAATA TTTTGAACCG CATGGTAAAG nTGGAAAGAC GGTCTTGCTG 60  
 30 TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC 120  
 AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGA<sub>n</sub>ACTGAGA CACGGTCCAG 180  
 ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAACTT<sub>n</sub> ACGGAGCAAC 240  
 35 GCCGCGTGAG TGATGAAGGT CTTCGGATCG TAA<sub>n</sub>ACTCTG TTATTAGGGG AGGACATATG 300  
 TGTAAGTAAC TGTGCACATT TTTGACGGTA CCT<sub>n</sub>ATCAGG AAGCCACGGT TTACTAGGGG 360  
 CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT 400

## 40 (2) INFORMATION FOR SEQ ID NO: 4179:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

GTTGTTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

55

GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180  
CACAGAGGTC GTGTTGAACA TGTTGAATCT AATGAAATTC TTGTTTCGTCG TCTAGTTGGA 240  
5 AGAGAACGGC GGTGGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300  
ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360  
10 GTTGGnnnTA C 371

## (2) INFORMATION FOR SEQ ID NO: 4180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT 60  
GTGCCTTCTG ATATGCTATG TATTACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120  
25 TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT 180  
TAGTAACGTC CTTTCATCGGC TTCTAATGCC AAnGCATCCA CCGTGCGCCC TTAATAACTT 240  
30 AATCTATGTT TCCACCATT TTTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300  
nTnAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAAT AATT 344

## (2) INFORMATION FOR SEQ ID NO: 4181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCG GAACATCTTC 60  
TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTGAGTT TTGAATGTTT GTTCATTCAA 120  
ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG 180  
50 TTCGAGTCCA CTTAGGCCCA CCATTAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240  
GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTGATC CCGCTAGTCT CCACCATTAT 300  
TTGTACATTG AAAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

```

10 CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC      60
    TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA      120
15 GTCGATCTGC TAATTTTGCA AGTGTCCTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC      180
    CTTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT      240
    TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATTG CCTCTTCATA      300
20 TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTnCTTTTCA      360
    TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA      400
  
```

(2) INFORMATION FOR SEQ ID NO: 4183:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

```

35 AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATT      60
    ACACAGCTGC AGGTGGTTCA TGGATTTCAT TCCATCACGG TGGCGGTGTT GGCATGGGAT      120
    ATTCACTTCA TCGGGGTATG GTTGTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT      180
40 TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGTCG CGACATGTTG nATGCTGGCT      240
    ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA      300
45 GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT      360
    CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT      400
  
```

(2) INFORMATION FOR SEQ ID NO: 4184:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60  
 5 CATTGCAGTT ATCATTGGTT TCGTCATATG TCGGATAGGT AATGGTTT TAG TCGCAACACC 120  
 TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTT TAG CTACAGGATT 180  
 ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GCACTAAGTA CTACAGTTTT 240  
 10 CAGTATGTTA CAACTAAACT ATGCACCAAG TG TAGCTGCA ACCGTAACAT TTATAGTCAG 300  
 CATTGTATTG ATGnTCCTTG GGTnCATTTGT CTGCATACAT GA 342

## (2) INFORMATION FOR SEQ ID NO: 4185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTA CTTGAAT 60  
 TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120  
 30 GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTCAGC GGAACACATG AAACGTTAGC 180  
 ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA 240  
 CGTTATGAAG TACAAGTTGA TGGAAGCAAC AAAGTAAGTG CGATThAACA AGTTGCTTCT 300  
 35 GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

## (2) INFORMATION FOR SEQ ID NO: 4186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60  
 50 GAATCTTCAA CTGTAAATTC ATCTGGATTC CATGAACCCC AAGCGTTTGC CGCATGATGC 120  
 TGTTTATTTA ATTTATGGAA TGTTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180  
 ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360  
 GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG 400

(2) INFORMATION FOR SEQ ID NO: 4187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACnCCC CCAAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60  
 TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120  
 ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG 180  
 TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240  
 AGAGCCCGTT AATGGGTGAT GCGGTGCCTT TTGTAGAATG AACC GGCGAG TTACGATTTG 300  
 ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60  
 AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCAGTAC CGTGAGGGAA AGGTGAAAAG 120  
 CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180  
 GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240  
 GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACAGTCTGA ATAGGGCGTT TAGTATTTGG 300  
 TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA 336

(2) INFORMATION FOR SEQ ID NO: 4189:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60  
 ATTAATAATA AGATAAAATT AATCAAGTGA ATTTCTTTTG GTTACAGAAA TTTCAACAAC 120  
 TTTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180  
 AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240  
 AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAA GCACTTCCCC 300  
 AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCCTCTn nCCCCCTCT 358

## (2) INFORMATION FOR SEQ ID NO: 4190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT 60  
 AAnGTACCAC CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120  
 GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT 180  
 ACAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240  
 ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300  
 AAACCTAAAT ACGGTGGTAA TACCATTGTG GnTATTTGTT GTGAAGTATT GCGGTCATAA 360  
 TA 362

## (2) INFORMATION FOR SEQ ID NO: 4191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

TGATCACCCA TGTTCTGGAC TCCCAATTGA AATTGAATTG GGCATTCGGA GTTTGTCTGG 60  
 nATTTCGGTAA CCCGnGCAGG GTCCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCCTC 240  
 CATTCAAGTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300  
 5 ACCAAATACT AAACGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTAGTGCTTA 360  
 AC 362

(2) INFORMATION FOR SEQ ID NO: 4192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

20 CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAAACCTTA TTATCAGGGT GCTGAACGTC 60  
 AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTTGGGGTGG CAGTGGTATC TGTTCACTCT 120  
 TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG 180  
 25 TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240  
 ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300  
 GTTGTCAATTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG 360  
 30 CCAATCGGAA ATTGTAGCAT CnTTAATTTC CTAAAAGGTG 400

(2) INFORMATION FOR SEQ ID NO: 4193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

45 AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60  
 TGTGATTAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120  
 ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180  
 50 CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC 240  
 GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300  
 TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATThTCATA TAATCCGGnA 360

## (2) INFORMATION FOR SEQ ID NO: 4194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT 60  
 CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT 120  
 CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG 180  
 TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT 240  
 TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGCG 300  
 AGTTtACGAT TTGgAttgCA AGGTTAAGCA GTAAATGTGG GAGCCGTA 348

## (2) INFORMATION FOR SEQ ID NO: 4195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACGCCTG GCAACGTTCT 60  
 ACTCTAGCGG AAnTAAGTnG GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120  
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180  
 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240  
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT 300  
 TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG 340

## (2) INFORMATION FOR SEQ ID NO: 4196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60  
 GATGTAGAAG TAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAATGGTT 120  
 5 GAAGCAGGTG CGACACGTAT TGGTGCAGC GCnGTGTTCA AATTATGCAA GGTTTAGAAG 180  
 CAGATTCAGA TTAATAATAT ATATnAATnT TGGGAGTGAT AGCTATGACA AGACCATTTA 240  
 10 ATCGTGTA TTTAATCGTA ATGGATTCAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300  
 ATTTTTAAAG ATGGAGGTTT ACATACTTTT A 331

## (2) INFORMATION FOR SEQ ID NO: 4197:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTG GCATGGGTGC 60  
 25 AGCTGCTATA TTTGAATATG TCGGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120  
 TGTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180  
 30 TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTAA 240  
 TGGGATGGTG GTTATTTCCG TTTTAGAATT TAACATTAC ACGTCTAATT TTAAATCATT 300  
 GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATn TATTGCTAAT GCnAGTAACT 360  
 35 nATCTGATTG T 371

## (2) INFORMATION FOR SEQ ID NO: 4198:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGThATTC TACCGCTGAA CTAATTCTGC ATATGCGGGT 60  
 50 GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT 120  
 TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTCGAA CCTCTGACCC TCTGATTAAA 180  
 AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

TAAGAATAAA TGGTGGAGAA TGACGGGTTT G<sub>n</sub>ACCGTCGA CCCTGTGCTT GTTAAGGCAG 360  
 ATGGTTTTCC CACTGGGGTA AATTTTCCGA TTTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGCGCCTT GTGGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60  
 AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120  
 CCATCCTAGT ACGCCAATAC CATTTATCAT TGTTGTATGT GAATCAGTAC CAACTAATGT 180  
 ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCACGAACA TGTACAACAC TTGCTAAATA 240  
 TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300  
 ATGCTTTTCGG TTGGCCCAAT TTAATAAACT GGATAACGTT CATnGTTACG TTCCAATTCC 360  
 TAATTTCCnA ATTACGGTTC CAnGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACCTTAC GCCTACGCAT CGCTTGTACA 60  
 CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120  
 ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180  
 TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240  
 CACACCATGG TTCAATGCnT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300  
 ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

	ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT	60
10	CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC	120
	AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC	180
	AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG	240
15	TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG	300
	TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA	360
	GCGGTTGGAC	370

20

(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

	CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCATTCCA GCTTTGTnGG AATGAGtCGG	60
	gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
35	CAGAAATCAT AAACGTCTTC AGTGTAAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
	GGaTTAgTGC AATAACCATC GCAACTGnGC CAnACCTTGT GTTGGCTCGC CGCCTGAATT	240
	CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTG GTCTAGTTGC	300
40	TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTCAGCA TAACAAGCTT CTTTCATTTC	360
	AAAGCAGCGT GCAAAAGGTT	380

45

(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

55

GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTGTAGAT 120  
 CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TATTATCTG AAGCTGAATT CAGAGATTAT 180  
 5 TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240  
 CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG 300  
 CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360  
 10 CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCTTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60  
 25 AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120  
 AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnGA 180  
 AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240  
 30 TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300  
 TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

## (2) INFORMATION FOR SEQ ID NO: 4205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AAACCTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60  
 ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCGCAA ATATTAAATT 120  
 50 ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA 180  
 GTTGAAATAC TCCCGCATT TATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240  
 CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

## (2) INFORMATION FOR SEQ ID NO: 4206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACTAATA GTGTGAATAT TACATTCCCA 60  
 AATCCAAATC AATATAAAGT AGAGTTTAAAT ACGCCTGATG ATCAAATTAC AACACCGTAT 120  
 ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA 180  
 ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG 240  
 CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300  
 TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360  
 CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

## (2) INFORMATION FOR SEQ ID NO: 4207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT 60  
 CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120  
 ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG 180  
 GCTTGGTCCA TACACCTTTC CAAAATTTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG 240  
 CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA 300  
 TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360  
 AATGTAACAC GCCGGTGA CT CATCCAGCT GAATAGACGC GT 402

## (2) INFORMATION FOR SEQ ID NO: 4208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

5 GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60  
 CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA 120  
 AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180  
 10 AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240  
 GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300  
 AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360  
 15 CAGCATCTGG TACnGGTAAG 380

## (2) INFORMATION FOR SEQ ID NO: 4209:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60  
 30 GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120  
 CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT 180  
 TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240  
 35 GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC 300  
 CnAAATACGC CAGAGCAGTA TTAAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT 360  
 ATTGGCCCGA TGCCAACnTT TATATTGAAC CAAGCACCTG 400

## (2) INFORMATION FOR SEQ ID NO: 4210:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

50 GCCCACAACC ACAAAGGCTG TAGGCTACAA ATATGGAGAC GGCGGGATTT GAACCCGCGT 60

AAAAGTGATA AACAAACCAAC ATGATGCTAG TTTGATTAAAG TTTCTTCTAA ACAGACTTCA 180  
 AACGGCATnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240  
 5 TGTTAGGCCGA TGCAGAGTGC GATTAGGCAG CTA CTGCGAA ATTATTGTnT GATTTGCCAG 300  
 TTATTATnAA CTGTGTGGTG TTGATGACGA 330

(2) INFORMATION FOR SEQ ID NO: 4211:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

20 AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC 60  
 GTTTTCACTT CGCCAAGCCA TCTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120  
 AAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180  
 25 TTCTACTCTA GCGGAACGTA AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240  
 TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300  
 ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTTGC 339

30 (2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AAACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60  
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120  
 45 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180  
 CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240  
 TTTTAGCACA TAAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300  
 50 GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

(2) INFORMATION FOR SEQ ID NO: 4213:

- (A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

10 CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAA TCGTTACGCC TTTCGTGCGG 60  
 GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120  
 TGGGGCTTCG ATTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG 180  
 15 GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240  
 GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300  
 TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

20

(2) INFORMATION FOR SEQ ID NO: 4214:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

30

CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAAGACCT 60  
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 120  
 35 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180  
 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA 240  
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300  
 40 TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGA nTG TGGACAACGn 360  
 TGG 363

45

(2) INFORMATION FOR SEQ ID NO: 4215:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

55

TTATTTGTAT TGTATAGAGA GAAATAAAAA GAnACCTTGT TTTACAAGGT TTCTAATACG 120  
 TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCGG GGTCGAACCG AACTCCACA 180  
 5 AGTGGAACGG GGATTTTGAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240  
 AAACAAAAAA CTTCCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300  
 CTCGTTCGGG GAAGGACGTG TTCTAAAAGT TGACTACC 338  
 10

(2) INFORMATION FOR SEQ ID NO: 4216:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60  
 ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTCAGT 120  
 25 TGTTTCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC 180  
 TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTTAA 240  
 GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTTA CCAGATCCAG AAATGCTTTT 300  
 30 AATGnTAACA CcTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360  
 CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

(2) INFORMATION FOR SEQ ID NO: 4217:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60  
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120  
 50 CCCATTTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180  
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240  
 TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGnCT TTCGAACATA 300

## (2) INFORMATION FOR SEQ ID NO: 4218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

```

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA      60
AGCTATTTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA      120
GTTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCCTC CAnTCAGTGT TACCTGAACT      180
TCAACCTGGA CCAAGGGTAG ATCACCTGGn TTCGGGTCTA CGACCAAATA CTAAACGCCC      240
TATTCAGACT CGCTTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT      300
AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTA                        345

```

## (2) INFORMATION FOR SEQ ID NO: 4219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

```

TCTTATGACT GCTTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTG AAACGTTTTTC      60
ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA      120
AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC      180
TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG      240
GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA      300
CATTCAAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACnTTAT TTTGGTTAGT      360
CTTCGTC                                           367

```

## (2) INFORMATION FOR SEQ ID NO: 4220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

AAGAGCCTTT CTTGACTTGT GACAAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60  
 5 ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120  
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTGCTTTTTA TTTTGACGTT TTAGACATAA 180  
 10 nAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 240  
 TCACTCTAGC GGAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300  
 CGGCATGGGA ACAGGTGTGA CCCCnTGGC TATAGTCACC AG 342

## (2) INFORMATION FOR SEQ ID NO: 4221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

ACCGGATGAC AGCCCCAGGA TGCATGAGC CGACATCGAG GTGCCAAACC TCCCCGTGCA 60  
 25 TGTGAACTCT TGGGGGAGAT AAGCtGTTAT CCCCggggTA GCTTTTATCC gTTGAGCGAT 120  
 GGCCCTTCCA TCGGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180  
 30 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACTCTAT GAATGATTTC CAACCATTCT 240  
 GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAACCTGC 300  
 35 CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

## (2) INFORMATION FOR SEQ ID NO: 4222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT 60  
 50 TTACCAAGCA AAACCGAGTG AATAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA 120  
 TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180  
 GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

ACATAGATTA AGTTATTAAG GGCGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360  
G 361

(2) INFORMATION FOR SEQ ID NO: 4223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60  
TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAATCCT GCGGTGAGAG 120  
ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180  
ATAGAGCGTT TGAATACGGA TCAAGAGGTT ATGGGTTCTGA CTCCTATCGG GCGCGCCATT 240  
TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300  
CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATT AnGGGGGCTA 360  
GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

(2) INFORMATION FOR SEQ ID NO: 4224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60  
GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120  
TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180  
TAGTGTCATT TCCAGCAATT TGTTCCGGCA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240  
GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300  
CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360  
TTCGATCCAG TTGATAATT GAACTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

- (A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

10 GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60  
 TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTCACCA TTCAACCAAA ATTGATCCTG 120  
 TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA 180  
 15 TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG 240  
 TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300  
 TCTCAATCCA AGTATGTGCT GCACCAGC 328

20

## (2) INFORMATION FOR SEQ ID NO: 4226:

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

30

TGACGGGTTT GAACCGCOGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA 60  
 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAnGTAAG TTCGnACTAC 120  
 35 CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180  
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 240  
 GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTGTCAGC 300  
 40 TCCACATGTC ACCATGCTTC CACCT 325

## (2) INFORMATION FOR SEQ ID NO: 4227:

## (i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TTnTTCAACA 60

55



AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180  
 AATTCAAGnA ACTGCTGAAG TTTTAAGTAG ACGAACTAAA AACAATCCTA TATTAGTTGG 240  
 5 AGAAGCTGGT GTTGGTAAAA CTGCGATTGT TGGAAGGTTT AGCACAGGCA ATCGTTGGAA 300  
 GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

## (2) INFORMATION FOR SEQ ID NO: 4228:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

20 AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60  
 TCGAACCTC GAATGTCGGA ACCACAATCC GATGTGTTAA CnCTTCACCA CAGCCGCCAT 120  
 GGCAGGGGCA GTAGGAATCG AACCACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG 180  
 25 AACTATGCCC CTATTAAAAA TAATAAATGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 240  
 AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300  
 GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

## (2) INFORMATION FOR SEQ ID NO: 4229:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

40 CTCTTACTTT GTAAACCAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60  
 TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120  
 45 ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180  
 CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAAATTAG AGGTGATGTT 240  
 ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300  
 50 TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TThATGGTAA GGAGTTTCAC 360  
 CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTC ACTCCCCTTC 60  
 CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCAC TCGGTCAC T AGAGAGTATT 120  
 TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTACTCA 180  
 GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTCATC 240  
 TTTcCAGATG ATTTCGTCTAA TGTCGTCCTT TGTAAGTCCG TATAGAGTGT CCTAsAACCC 300  
 CAACAAGCAA GCTTGTTGGT TTGGGnTCTT GCCGTTTCG 339

## (2) INFORMATION FOR SEQ ID NO: 4231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

GAAGTCATAT GCATACACTT GGTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG 60  
 AATTTTCGTTA CCTGCGCCTT CTTTTGCGT TTTTAAATAA TCGAAAATTT CAGGCGTTAA 120  
 TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTTCAAC 180  
 AAACTTTTTC ACTTCAGACT GACGTCCGn TTTAGTTAAT GGGTCAATAA TTCCATAACG 240  
 ATGAGTATCT GCTTCCGGAA CTTCTTGAC ACCTATAACT GAGTGCCCTG TnTCTTCATA 300  
 AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG 349

## (2) INFORMATION FOR SEQ ID NO: 4232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

CCAGGATGCG ATGACCGACA TCGAkGTGCC AACCTCCCC GTCGATGTGA ACTCTTGGGG 120  
 GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCG 180  
 5 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAkTCA 240  
 AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTTC AAC CATTCTGAGG GAACTTTGaG 300  
 10 CGCCTCCGTT ACCTTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG AACTGTCTC 360  
 CCACCACGAT AAGGTCG 377

## (2) INFORMATION FOR SEQ ID NO: 4233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCCTCTC 60  
 25 GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTAACTTGG GAGTCAGAAC 120  
 ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180  
 AATATATGTT AAGTGGA AAA GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240  
 30 AAGCAGCCGT CATTTAnAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300  
 GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTn 355

## (2) INFORMATION FOR SEQ ID NO: 4234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CCTGCCTGTC 60  
 ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120  
 TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG 180  
 50 TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT 240  
 AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTTATGG AGGGGTAACG AnTGGGCTAA 300

TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA

400

(2) INFORMATION FOR SEQ ID NO: 4235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTGT CACGATAATA 60  
 GCGGTAATAT CACTCTTTGC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA 120  
 TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAT 180  
 TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTCTAAAC CACTATCTGA TACAAGACCA 240  
 ATTGCATGnT TTGTTGGGAA AATCAITTTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA 300  
 CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T 341

(2) INFORMATION FOR SEQ ID NO: 4236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCTTAAAT ATAATTTTAC 60  
 AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCCGA CCTCACGGGT ATGAACCGTA 120  
 CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA 180  
 GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAG 240  
 CCCCATAAT AATTACAGTA TATCGGAAG ACAGGATTCTG AACCTGCGAC CCCTTGGTCC 300  
 CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT 360  
 TGAACCCATG AACCTnTTGA TCCnTAGTnC AAACGGTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

nAnTTCTTGA CCTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC 60  
 5 TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG 120  
 AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTCGCACC ATAGAATGAG 180  
 10 ACGTTACCAG CAATAATTTT ATTTTGTCTG TCTTCAAAAG GTGCTTTGAC AATGACCGTA 240  
 CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAAG 300  
 CCTTTCGGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTCGTATA AACATTAAAT 360  
 15 GTATTTTCAG GAAGTC 376

## (2) INFORMATION FOR SEQ ID NO: 4238:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

CGATTTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT 60  
 GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA 120  
 30 TTTTCTGGGA AAAGTTTGGC CATTTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA 180  
 CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT 240  
 35 GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTCACTCCG TATTGAAGGC TACTTGACGA 300  
 TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG 335

## (2) INFORMATION FOR SEQ ID NO: 4239:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGGTTTTGAT 60  
 50 TTCGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT 120

TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240  
 AATGCAAAGG CGCCATCACG TGATGTGAAA GGTCAAAATT TGCTGTTGGA CGGATGCGAT 300  
 5 GAACTACATT ACATTTGTCC AATACAACAC AGATnGTATC ACTGCAGC 348

(2) INFORMATION FOR SEQ ID NO: 4240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60  
 20 AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120  
 TTATGAATGG CATACTGCT GTTGTTTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180  
 CAAGTGC GCA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240  
 25 TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300  
 ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360  
 ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

(2) INFORMATION FOR SEQ ID NO: 4241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60  
 ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120  
 45 CTTTATGTTG GGGCCCCGCC AACTTGCATT GTTTGTAGAA TTTCTTTTCG AAATTCTTTA 180  
 TGTGTTGGGCC CCGCCAACTT GCATTGTTT TAGAATTTCT TTTCGAAATT CTTTATGTTG 240  
 GGGCCCCGCC AACTAATTCC AATATATCAT TGTAGAGCTT AGGTCAITGA TTTTGGCTC 300  
 50 GGACTTTTAT GGCGATATGA ACCATGTAAA T 331

(2) INFORMATION FOR SEQ ID NO: 4242:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

10 TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA 60  
 TCATCTAAAT GATTTTTAGC TGTGATTAAAC TCACGTTTAT CCGCTTTTGT GAAAATGGAC 120  
 TCTTGACTT CTTCAGTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG 180  
 15 CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA 240  
 TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTTGAACC ATAATCTTTC 300  
 20 ACAATTnCAG TTGTGTTGAC AGATGAGnGG CGGTGACGTA AGGACTGGAT ACACTACGAG 360  
 TGACCGGACT GCTTCGGGnA ATGTGATGA 389

## (2) INFORMATION FOR SEQ ID NO: 4243:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

35 ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT 60  
 TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT 120  
 GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT 180  
 40 GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTh TTTTGAAAT GATTGCGGCG 240  
 ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTTCCGAAT 300  
 AAACGACAAG GTGCAATTTT GG 322

45

## (2) INFORMATION FOR SEQ ID NO: 4244:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120  
 ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180  
 AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240  
 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGTT AACATGAAGT 300  
 TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC 339

## (2) INFORMATION FOR SEQ ID NO: 4245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCTATTT CACTCCCCTT 60  
 CCGGGGTGCT TTTCACCTTT CCCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120  
 TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTACTC 180  
 AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTG 240  
 ATCTTTCCAG ATGATTCGTC TAATGTCGTC CTTTGTAACT CCGTATAGAG TGTCTACAA 300  
 CCCCACAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCGG TTTCGGTTCG GCCGnAA 358

## (2) INFORMATION FOR SEQ ID NO: 4246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA 60  
 CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120  
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180  
 TTCAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240  
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300  
 TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CGGATCACTA 60  
 AGTCCGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT 120  
 ACACTCTATG AATGATTTCC AACCATTCTG AGGGAACCTT GAGCGCCTCC GTTACCTTTT 180  
 AGGAGGCGAC CGCCAGTCA AACTGCCCCG CTGACACTGT CTCCCACCAC GATAAnGGCG 240  
 GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC 300  
 TCACGTTTCA AAGnTCTACC TATCCTGTAC A 331

## (2) INFORMATION FOR SEQ ID NO: 4248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG 60  
 ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTTCAG 120  
 GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTTCG TCATTCTTCA AATAAACCAG 180  
 AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG 240  
 GCACCGGCAG ATnCTTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA 300  
 ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC 360  
 TAATGCCCAA T 371

## (2) INFORMATION FOR SEQ ID NO: 4249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60  
 ATTGAAGCAG TGGTGAAAGC TCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120  
 TGTGGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180  
 TCGTTAAAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240  
 GAAAGATACA GTAGGTGCTG ATATAGAAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300  
 GTTTCAATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

## (2) INFORMATION FOR SEQ ID NO: 4250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

GAGCCCAAAC CAACAAGCTT GCTTGTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60  
 AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120  
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG 180  
 GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240  
 ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300  
 GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GGCCTGCCTT TT 352

## (2) INFORMATION FOR SEQ ID NO: 4251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

CATTTACTGC TTAACCTTGC ATCAAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60  
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTAC 120  
 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180  
 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 240  
 CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTTCTGACT ACAGGATTAT TACCTTCTTT 300

## (2) INFORMATION FOR SEQ ID NO: 4252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT 60  
 AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC 120  
 CTTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC 180  
 ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCa ATATATTTCT TTCCGGTTGT 240  
 ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT 300  
 TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCCAA CCTGTAAAT 360  
 CCGATGGTTA TCCAnATGAT GATCACCATG TCATCAnACC 400

## (2) INFORMATION FOR SEQ ID NO: 4253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA 60  
 ACTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA 120  
 GTTATTTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA 180  
 TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACACTT 240  
 GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC 300  
 AGnCAGCGAC TCAGACTTCA GACAGCG 327

## (2) INFORMATION FOR SEQ ID NO: 4254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

5 AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTAT 60  
 TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120  
 TAGGATTGTn CTnTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180  
 10 CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240  
 GGTGACCTTC ATGCCAAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300  
 AGTACCGATC CCTAATTCCA ACGCATGTnG 330

## (2) INFORMATION FOR SEQ ID NO: 4255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

25 ATTAGTGATT GTAAAAAGT AAAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60  
 CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTTC 120  
 30 TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTAAATACA 180  
 CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240  
 AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA TATAATTCAA AAAAGGGTCG 300  
 35 AAGATATGAn ATCACATCTT CGACCCTTnn TTGTACTAAT TTAA 344

## (2) INFORMATION FOR SEQ ID NO: 4256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

50 CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTCGCAT TAATTTCAAT ATTAAATTGC 60  
 GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120  
 AAGCTAAATT CTGCGACAAA GCCGCCATT GCAGCACCGA CAGCCACACC AATATTTTGC 180  
 55 GCTAAGTATA TCGCATTAAA CGTTTGTCTT CCGCCATTG GCCACACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGAn AGA

323

## (2) INFORMATION FOR SEQ ID NO: 4257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

15 GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCGACTAT TTTGAAAAG AGCGTGTTAC 60  
 ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT 120  
 TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT 180  
 20 AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT 240  
 TTCGGTTTTG AGACAATTCTG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC 300  
 25 TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT 360  
 GCGGAGTGA 369

## (2) INFORMATION FOR SEQ ID NO: 4258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

40 CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60  
 TTTTAAATA CTAAAATACA TGTTGGAATA CTTGTCCCAT AGAAAATATT GGCTGGTAAC 120  
 CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT 180  
 45 GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA 240  
 ATGTACCAGT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GGCGCAACTT GCCGTAACCA 300  
 CTGAATCGTT CATCATTTCA AATTTGAACT GCTGT 335

## (2) INFORMATION FOR SEQ ID NO: 4259:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

5 ATTTGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTGTA 60  
 GCTTCGCAGC nACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCTATAC 120  
 ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180  
 10 CTGCGGnTCT TCTGGGCGTT AACCTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA 240  
 TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC 300  
 CTGTGTCGGT TTGCGGTACG GGCA 324

## (2) INFORMATION FOR SEQ ID NO: 4260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

25 AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAATGAG 60  
 CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT 120  
 30 GAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAGAG 180  
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA 240  
 TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAntT 300  
 35 ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT 360  
 ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

## (2) INFORMATION FOR SEQ ID NO: 4261:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

50 AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTTCTA TAGAAATTAG 60  
 TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG 120

CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240  
 TTGTCTTGTT TATATTATGT GATTCAAACA TTAGTAGTCT TGGTAAATCT AATTCGTAAA 300  
 5 ATGCTAAATC TAACCATCTA TTAAATTTAA AACC 334

(2) INFORMATION FOR SEQ ID NO: 4262:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT APTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT 60  
 20 ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGCG TCTCAATGCG GCTCATCGCA 120  
 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT 180  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCnTCTTTC CTCTCCTTCG GCTCTCGCTT 240  
 25 ACTCATThAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300  
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT 330

(2) INFORMATION FOR SEQ ID NO: 4263:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCTAC GnAATGTCCG AACCACAATC 60  
 CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120  
 45 CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACATATGC CCCTATTAAA AATAATAAAT 180  
 GGAGGGGGGC AGATTGGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240  
 AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300  
 50 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

(2) INFORMATION FOR SEQ ID NO: 4264:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

	GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC	60
10	AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
	TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTAGTCTGT	180
	TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA	240
15	ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC	300
	TTTTTGAAA ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T	351

20

(2) INFORMATION FOR SEQ ID NO: 4265:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

30	ATTTTCACTT TAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT	60
	GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA	120
	AGTAACGCAA TCATTTCTTC TAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA	180
35	TGAGGCCCTA GGAAAGTATG TTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC	240
	ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA	300
40	CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT	346

(2) INFORMATION FOR SEQ ID NO: 4266:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

	TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG	60
55	GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTAAAGTCCT GTGCGTCTGC	120



CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240  
 GTCGAACCCC CACGCCGTAA GgntGAGATC CTAAGTCTAG TCGTCTGCC AATTCCGCCA 300  
 5 CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

(2) INFORMATION FOR SEQ ID NO: 4267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTTCT CTGGACCTA TATCATGTTT TTTATTTTCT AATGCAGGAT CTTTAATTGC 60  
 20 ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTCGCA GTGTTTGCTG GTTGCCTGAG 120  
 GTnTGTGTTT GATTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATTT 180  
 25 TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240  
 ATTA AAAATA GTGTACTGAC AATGACCGAT GCAACGCCA GAGTTGATTT TCTAATAGAA 300  
 TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA 337

(2) INFORMATION FOR SEQ ID NO: 4268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60  
 AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120  
 45 AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180  
 TGTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TTAACCACTG 240  
 GAATCGTTCA TCATTTTTC nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300  
 50 GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360  
 TTTTCCAATG GGGGTCATCA TTAAnGGGAT CnTCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 4269:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

10 GGCTCATCGC ATCCTGGGGC TGTAAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 60  
 CGGTACGGAG CTGGGTTTCAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT 120  
 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180  
 15 TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240  
 nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT 300  
 CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345  
 20

(2) INFORMATION FOR SEQ ID NO: 4270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

30 AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTTAT CTTGTCCATT 60  
 TTATTTTTTTA ACCAAAATTT GATTAAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120  
 35 TAAGTCGaCT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 180  
 TGACCTCctT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAGTAGATA 240  
 40 GTAAGTAAAA GTGGATTTTG CTTCGCAAAc ATTTATTTTG ATTAAGTCTT CGATCGATTA 300  
 GTATTCTGTC GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360  
 CGCAGGGAnC 370

(2) INFORMATION FOR SEQ ID NO: 4271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

55

ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTAA CACAATTATG ATTGGCGTAA 120  
 AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACTTG TGGCACAATG 180  
 5 GaTTAATTTA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGtA ATGGAATAA 240  
 AGCGACACAA ACCGTCACGT CAGTGTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300  
 GTAGGGCTTA TCATGGCCAA TCTGTTA 327

(2) INFORMATION FOR SEQ ID NO: 4272:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCITTA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60  
 GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAAACCTT 120  
 25 TCAAACCTTAT CGATGATTTT ACCGTTATGA ACTTTACAG CTGCAAnTCG ATGATTTTAT 180  
 CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240  
 ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACCTTCC 300  
 30 ATACCGGnAT ATCATTTTAA nGCCA 325

(2) INFORMATION FOR SEQ ID NO: 4273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGCTT GTCGTTAAGA TGA CTCTAGTA CTCTTATGTT 60  
 45 TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120  
 TATAGAATGG TGTACATACCT GAACCATAAT CCTTAACTGG GAAAACATCA ACAGTCTTCT 180  
 50 TATTAATAGG ATTTGCAATA ATACCCGCTT GCTTTTTCAA ATCATTTCTTA AGTGTGTCGA 240  
 TnAATTTGTC GACTGCATCA TCTnTGCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300  
 CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

```

ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA      60
GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA      120
GTTGCTTCTG GGCCTTTTGG TGTAAGTAGT GATTATTTAC AACATGCCAA AGAAATTCAA      180
ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA      240
TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG      300
CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG      360
GAAAAATGGC GAATTAAGGT TGCnGATTTT CCCCGGGTAA      400
  
```

(2) INFORMATION FOR SEQ ID NO: 4275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

```

AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC      60
TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT      120
TAATTCCTAT TAAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA      180
TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG      240
GGAGAAATAG TCACTTTCAT AGGGGAAAAG TGGTTGCGGA AAGTCTACTT TACTCAATAT      300
TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n      341
  
```

(2) INFORMATION FOR SEQ ID NO: 4276:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAAGTT 60  
 ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTTC TTTATTTTAA ACATGAACAA 120  
 5 TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180  
 TTAAACAAT GATTAAAATT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC 240  
 CATTCCATTA AACCACTTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300  
 10 GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA 360  
 ACGGTCCG 368

(2) INFORMATION FOR SEQ ID NO: 4277:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

25 ATGGAAGTAC GTGACGTTCA CTA CTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60  
 GAGGGACCAA ACATTGGATT GATTAACTCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120  
 30 GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180  
 ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AACTCTAAA 240  
 TTAGATGAnA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA 300  
 35 TACAGTnATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

45 CACTTGTA CT TTCTGATGTT GAGCCAGACT CTGATGTACT TACCGATGTA GATAAACTTG 60  
 CAATGGTCGA CATGCGGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120  
 50 TGCTTTGTGA ATCGGATTCG CTCGTGCTTG TACTTGTTGA GTTTGAGGCA CTTTGGCTTG 180  
 CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

TACTTATGCT CATTGGATGT TGAATCGGAT TTACTTTCAC TTGAATGATG TTGAGTCGGA 360  
 TTCACCTTCA CTTGTAGAAC CACTTAATGA TGTGGGATGT 400

(2) INFORMATION FOR SEQ ID NO: 4279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATTTAAAAG ATATTAGACA TAAATCTAA AAnCAGCAGT AAGATGATTT 60  
 ATGATTAAAA ACTATCTTAC TGCTGTTTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT 120  
 ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAAATA TCAATTTTAC 180  
 ACTCAATGCG GCTCATCGCA TTCAATTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240  
 AGTTAGCTAC CATCCTCGCT AAGAACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC 300  
 CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60  
 GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120  
 AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180  
 AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240  
 GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300  
 CCTATAATCG TTTAATCGAT GGGGGG 326

(2) INFORMATION FOR SEQ ID NO: 4281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

5 TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTCG 60  
 GTTTTGCTTG GTAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120  
 GTGGGCCTAA GTGGAATCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180  
 10 CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240  
 GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCGAAT ATATCCTTAG AAAGGnAGGT 300  
 15 GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTTGAC GACTTGCACC CCAAGCATT 360  
 GTGCCCCAnCn 370

## (2) INFORMATION FOR SEQ ID NO: 4282:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

30 GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60  
 CTTACAGATT GnAATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120  
 AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180  
 35 TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTAC CAACTAAAAT ATCTCCATCT 240  
 TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCCTAAG TGCACTTTCA 300  
 GAAACATTAG GnATATCTCT TGTGATTTC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360  
 40 GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGn 400

## (2) INFORMATION FOR SEQ ID NO: 4283:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

55 AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60

TCTGTCCCAC TCCCGATTAT CTCGTCGCAA TATTTTTTTC AAAGCGATT T AAATCATTAT 180  
 CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTTGGA TTTGGTGAAA 240  
 5 TGATGGACTC TTTGCCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT 300  
 CThAATCCAT GATAGACTGn CCCG 324

(2) INFORMATION FOR SEQ ID NO: 4284:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

20 AAATCGTAAC GAGTGAAC TT TCTTATTTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60  
 AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120  
 GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTTGGC 180  
 25 AAGATGCGTT ATAAGCATT A GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240  
 AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300  
 TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTAAAGCCA GATTTACGTG 360  
 30 ATGTCTAACA AGTTTTnTnC GCTAAATCn GGGTGGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 4285:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 560 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

45 CATTTTTCTT TGTGTTTACT TTTTATTTTG ACGTTTTAGA CATAAAAAAA GAGACTCACG 60  
 GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120  
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180  
 50 TACTCATT TA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 240  
 TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 300  
 AAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360



TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480  
 ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT 540  
 5 TTCTTTGTG TTTACTTTTT 560

(2) INFORMATION FOR SEQ ID NO: 4286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GnATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60  
 20 CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAGA CGGTCTTGCT GTCACCTATA 120  
 GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180  
 TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGA ACACGGTCCA GACTCCTACG 240  
 25 GGAGGCAGCA GTAGGGAATC TTCCGCAATG GGCAGAACTG GACGGAGCAA CGCCGCGTGA 300  
 TGnATGGAAG GTCTTCGGAT CGTAAAACTC TGTATT 337

(2) INFORMATION FOR SEQ ID NO: 4287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60  
 CATCTTTAAT GACAACTGTA CCATTTTTCA CAACATTTAA TTCATCTAAT TCCTTACCCT 120  
 TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA 180  
 45 TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240  
 GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300  
 50 GTCGTCAATA CACGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

(2) INFORMATION FOR SEQ ID NO: 4288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

	CTATTCAC	TG	CGGCTCT	TCT	GGGCGTT	AAC	CCTAAAG	AGC	ACCCCTT	CTC	CGAAGTT	AC	60
10	GGGGTC	ATTT	TGCCG	AGTTC	CTTAAC	GAGA	GTTGCT	CGC	TCACCT	TAGA	ATTCT	CATCT	120
	TGACTA	CTG	TGTCG	GTG	CGGTAC	GGGC	ACCTAT	TTTC	TATCTA	GAGG	CTTTT	CTCGG	180
	CAGTGT	GAAA	TCAAC	GA	CTC	GAAGAC	ACAA	TGTCT	TCTCC	CCATCA	CAGC	TCAGC	240
15	CGAGTA	CCGG	ATTTG	CCTAA	TACTCA	GCCT	TACTG	CTTAG	GACGT	GCAAT	CCAAT	CGCAC	300
	GGTTTn	GCCT	ATCCTA										316

(2) INFORMATION FOR SEQ ID NO: 4289:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

30	TThTTT	TATGT	CTAAA	ACGTC	AAAATA	AAAAG	CAAACA	CAAAA	GAAAG	ATGGC	TTGGC	GAAGT	60
	GAAAAC	GnTT	GAATC	TGACG	AAACG	AGAAA	TGTAA	AGTAT	AATAAAA	AAGC	AGTCAT	AAGA	120
	TGATTT	CAAT	TAGAA	ATCAA	TTTAT	GACTG	TTTTT	CTTAC	TATGT	GTTAA	ATTAAC	AATG	180
35	AATATA	ACAT	CTTAT	TTTTCA	TTAATA	TATAA	TATTG	GAAAG	ATCGAn	ATGA	TTTAC	ACGTT	240
	GTTTG	AGTTG	TATTAA	ATCA	TCATG	ATCTT	TAAGT	TGAAT	ACCAATA	AATG	ACAGT	ACCTG	300
40	TATTTT	GAGA	GATTTT	TTTAA	GT								322

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

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	TCATTT	AGCT	CTACTA	AACT	CGTTG	CGCTC	TTTTCT	CGTT	TCGTC	AAGT	CAAAC	GTTTT	60
	CACTTC	GCCA	AGCCAT	TTTT	CTTTG	TGTTT	ACTTTT	TATT	TTGAC	GTTTT	AGGCAT	AAAA	120

55

CTCTAGCGGA AnTAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240  
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACTCGTTG 300  
 5 CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCA 338

(2) INFORMATION FOR SEQ ID NO: 4291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60  
 20 TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACTTCACGT 120  
 GCTTTTTTCA CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180  
 TTAAGGCGTT ACTTTACCAA CTAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240  
 25 GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGAATGATC 300  
 TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360  
 30 TTGCAAGATG GAATGAGAAG TGAnACACGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA 60  
 GGCATAAAAA AAAGAGACCT TCGGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTTGCCT 120  
 45 GGCAACGTTT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180  
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240  
 50 TACTAAACTC GTTGGCGTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 300  
 GCCATTTTTT TTTGTGTnnA CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

(A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

10 GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTTAAA 60  
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTTCGAT 120  
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AACTGAATG ACAATATGTC 180  
 15 AACGTTAATT CAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240  
 TCAAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300  
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnGnGAT GTTAGC 356

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(2) INFORMATION FOR SEQ ID NO: 4294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

30

TTATCACCCA TGTTCTGACT CCCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60  
 CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120  
 35 GGCAGCCCTA AAGCTATTTC GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC 180  
 CGCTACCCTC AGTTCATCCG CTCACTTTTTC AACGTAATCG GTTCGGTCCT CCATTCAGTG 240  
 TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300  
 40 AAACGCCCTA TTCA 314

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

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GCAATCTATC TGTGAAGAC ATTGATTGA TCGAATTGAA CGAAGCATTT GCTTCTCAAA 180  
 CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG 240  
 CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTAAACCCG CGCGTTTACC 300  
 TAATGAAATG GGGTAAACCG nCCCGATAGn CCGTAnCGCA AGGGT 345

(2) INFORMATION FOR SEQ ID NO: 4296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60  
 GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATC TTTCTTTGTG TTTGCTTTTA 120  
 TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180  
 ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAAnTAATT CgNACTACCA TCGACGCTAA 240  
 GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300  
 GACATATGAA TGTnAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTTG 360  
 C 361

(2) INFORMATION FOR SEQ ID NO: 4297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACCT GTTTTCACTT CGCCAAGCCA 60  
 TTTTCTTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120  
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300  
 TTCAC TTCG CAAGCCATTT TnCTTTGTGT nTACTnT 337

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60  
 CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAC 120  
 GGAGGAAGAG GGATTCGAAC CCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA 180  
 TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240  
 TGCGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300  
 TTTTACAAC TATAAAATAG TGG 323

(2) INFORMATION FOR SEQ ID NO: 4299:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG 60  
 AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT 120  
 ATAAATTTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG 180  
 GCTCTTTAAT TGTA AAAAGA AAACCATACG CTATGnTGTT ACAAnGAAAA AGGTTCTACC 240  
 ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAAATA 300  
 ATCAACACGA GGAGATGCTA TTT 323

(2) INFORMATION FOR SEQ ID NO: 4300:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120  
 CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGGATTA AATGAATTTG CTCCAAATAA 180  
 5 AAATACAAIT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240  
 GTTnCAATTGA AGTGTtTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTC TTGGACTGTG 300  
 CAITTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360  
 10 GCTGAATGGC TtGnTGAAT GAATT 385

(2) INFORMATION FOR SEQ ID NO: 4301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA 60  
 25 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120  
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA 180  
 GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240  
 30 GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300  
 CTTCGGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

(2) INFORMATION FOR SEQ ID NO: 4302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60  
 AGGTGTTATG AATGGCATAc ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120  
 CAGAAGCAAG TGCGCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180  
 50 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240  
 ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300

TTTTGAGCGG CAAAAACTTT GnCAG

385

## (2) INFORMATION FOR SEQ ID NO: 4303:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

15	AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTAAACGCA	60
	GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT	120
	TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGAC ACGTCATCTT TAACTTAATC	180
20	GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA	240
	GATTTATGGG CACTTAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA	300
25	TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA	360
	CCAAGCCTTG TCCC	374

## (2) INFORMATION FOR SEQ ID NO: 4304:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

40	AAAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA	60
	ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA	120
	ATTTCTTGCC GCCGCTTGCA GCAATGCTTT TTATTAAAAT TGGCTATCAC CCTATCGCTG	180
45	GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAATATA GTTGTGGTA	240
	TGCAAGATGC TTTGGTCTAT TCATTTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA	300
	TTAAACAAA CGTT	314

## (2) INFORMATION FOR SEQ ID NO: 4305:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

5 CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60  
 CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120  
 GGCCAGGTAC TGCTTTAAAT GTTGTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180  
 10 AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240  
 GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300  
 nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

## (2) INFORMATION FOR SEQ ID NO: 4306:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

25 AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60  
 TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CGGTGATTAT 120  
 30 CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180  
 AATAGCGCGG CGAACAACGA AACATCAAAT AGTGACCTG CAGCTGGTAA TGGTGTAGCA 240  
 35 TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAAT 300  
 ACCGACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnCCGGG 360  
 GAAAnAGATGG TCAAATTT 378

## (2) INFORMATION FOR SEQ ID NO: 4307:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

50 GGACTTGGGT ATTCTCCAA AATTATATGG ACCTTGCAAG ACTCGAACCT GCGACCGAAC 60  
 GGTTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG 240  
 GATCGAACCG CTGGACCTCC TGCCTGGCAA AGCAGnCGCT CTCCCAGCTG nGCTAAGCCC 300  
 5 CCATAATAAT TACAGTAT 318

(2) INFORMATION FOR SEQ ID NO: 4308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTC GGTTTTGAGA 60  
 20 CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTC ACGTAGCTTTT CATTAACTTC 120  
 TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180  
 ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTTCAG TTAAATACG 240  
 25 TGTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300  
 ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360  
 30 CAATCCTATT GGATGTCCCA AnaATTGTAC GACCAACACC 400

(2) INFORMATION FOR SEQ ID NO: 4309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60  
 45 GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120  
 GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180  
 AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCAATTG ATGACAATGG 240  
 50 TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC 300  
 TTCACACTAA TCAATGGTGG CAAAGT 326

(2) INFORMATION FOR SEQ ID NO: 4310:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

10 TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTG AGTGATAATG 60  
 TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120  
 ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180  
 15 TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTTCTCTAT 240  
 ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAc GGCATCATAA ATGGnCAATG 300  
 TCGGATCACT TTT 313

20

(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60  
 TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT 120  
 35 TTGGGAAGTG CTTTTTTTTT GGTTCCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC 180  
 TATTTTTTAAA ATACAACTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240  
 TGGTTGTCTT CnTTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300  
 40 GTGGTGAATT CTGAACCAAA GAATCACTTG ATAATTTATC TATATAATCC TCnATAGACC 360  
 ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

45

(2) INFORMATION FOR SEQ ID NO: 4312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

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ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120  
 AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 180  
 5 ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240  
 CTTTAAAATA ATTAATCAT TGTCTGChAA ACGTTTTChT TTATAAAAAG ATTAAACGCG 300  
 TTATTAAChCT GTGGAGTG 318

10 (2) INFORMATION FOR SEQ ID NO: 4313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCGG CCACCCCGGC 60  
 ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG 120  
 25 TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAnG GAGTCGAACC CCCACGCCGT 180  
 AAGGCATAGA TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC 240  
 CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCh 300  
 AATGGChTCTT CCATGG 316

(2) INFORMATION FOR SEQ ID NO: 4314:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAAC 60  
 45 AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120  
 CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180  
 50 TnCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240  
 TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300  
 GGCCATTTGA ACCGGTGGTT TCACATCGGT CATTTnCCGT AAAAGhCCAT TCCATG 356

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

```

10  TATCAGCATT TGTAACGTGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA      60
    AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT      120
    CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA      180
15  TGTAGCGGAA GGnATTTTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA      240
    TTGGTGTAC AATTATCCTT GGnGGCCTTT GCATATTCnG GGTGTAGGG AATCAGGTCC      300
20  GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT      360
    TGCCTCAGCG GAGGACACGC                                          380
  
```

(2) INFORMATION FOR SEQ ID NO: 4316:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

```

35  GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT      60
    TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT      120
    GTAATTTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT      180
40  ATTCTTTGTC CGTTCTGACG TTTAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT      240
    TAACTTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTCGT      300
    TGTGTCCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AAAC TTATAA TCCACACCCT      360
45  GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn                      400
  
```

(2) INFORMATION FOR SEQ ID NO: 4317:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60  
 5 CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAACT TATAAGCAAA 120  
 TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180  
 TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240  
 10 ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300  
 GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360  
 15 CGGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA 400

## (2) INFORMATION FOR SEQ ID NO: 4318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAACT TCCTCTTTCT 60  
 30 CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTATC GTTTCTGGTC 120  
 CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTC TTCTTTCGAT TCACCTGTAC 180  
 TAATAATTTT TCCAGTTAAT GGATTTTTTA GTGTTGGCGT CGTTATTGTC TTCTCACCTn 240  
 35 TTTGTCCTTC TCTTGTAAC TTTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT 300  
 TTCTTGAAGG AATCTCTTC 319

## (2) INFORMATION FOR SEQ ID NO: 4319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTAATAAATT 60  
 50 TGAATACTTA AAAAAATCTT CTCAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA 120  
 AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTTGA TCCTTCCAAT 180

ACAGTCATAA ATTGATTCT AATTGAAATC ATCTTATGAC TGCTTTTTAT TATACTTTAC 300  
 ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTCACTTCGC CAAGCCCATC TTTCnTTGGn 360  
 5 GTTTGCCT 368

## (2) INFORMATION FOR SEQ ID NO: 4320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 20 TCCTCTCCTT CGGCTCTCGC TTAATCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
 TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240  
 25 TCTACTCTAG CGGAAnTAAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300  
 GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA 347

## (2) INFORMATION FOR SEQ ID NO: 4321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120  
 ACTGCCGGTG ACAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180  
 45 TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGC GAGTCaAGCA 240  
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300  
 50 aATCGCTaGT aATCgTGGTC CAGCATGCTA CCGT 334

## (2) INFORMATION FOR SEQ ID NO: 4322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

	CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAATAAG CAAAAGTATT CAGATGCCTC	60
10	AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA	120
	CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG	180
	GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAAATCCG TTTGGAAnGG AGCATCGAAA	240
15	TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGACT GGGGATATGT ATTCAGAGCC	300
	CACGATCGTT TTGATGCATT TCAGTTCGGC	330

(2) INFORMATION FOR SEQ ID NO: 4323:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

30	CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTTTA GCACTGTTTT GTCGTATTTT	60
	TAAATATAAA TTTGGAATGA ATAATAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA	120
	CTTGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA	180
35	AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTCnGGG ATGGGCCCCA ACATAGAGAA	240
	ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCACAT AGAGAATTC	300
40	GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG	337

(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

	TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA	60
55	GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG	120



GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240  
 AAGAAAAATG GCTTGCGCAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300  
 5 GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

(2) INFORMATION FOR SEQ ID NO: 4325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCCTCC ATTCAGTGTT ACCTGAACCTT 60  
 20 CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120  
 TCAGACTCGC TTTGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC 180  
 TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240  
 25 AGCACACGGT TTCAGGTTTCG ATTTCACTCC CCTTCCGGGG TGGCTTTTCA nCTTCCCTC 300  
 ACGGnACTGG TTCAC 315

(2) INFORMATION FOR SEQ ID NO: 4326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60  
 CACTTTTTCG CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120  
 AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180  
 45 AGACATATGA ATGTAAATTA TACATTCAAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240  
 GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300  
 50 ACCATGCTT 309

(2) INFORMATION FOR SEQ ID NO: 4327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAAGA CGATATACTA	60
CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT	120
AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA	180
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA	240
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT	300
TTTGGTTnCA G	311

(2) INFORMATION FOR SEQ ID NO: 4328:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT	60
CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT	120
TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC	180
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA	240
CAGCTTGTAC AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG	300
TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA	340

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(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

AATCCATAGC GAAATGTATA CCATCACCCA TGCCTCCTTC TAAAGGTAAA TCTCTACCTT	60
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA	120

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TACGACGTCG AACCCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC 240  
 CGCCTGATTC TCTAGCACGT TCATAAATAG TTACTTGnTA TCCTnGTAGA TTAAGTTCTT 300  
 5 CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CAC TTCACCA CAGCCGCCAT GGCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60  
 20 GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120  
 GATTCGAACT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT 180  
 ACCCCTCCAT AAATGGTGCG GGCGnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240  
 25 TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCAGG ACAGAGTCGA 300  
 AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCCACATT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 60  
 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 120  
 ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180  
 45 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCAACAA 240  
 AGTCATCATA TGCAGGTGGA TTAAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT 300  
 GGATAGCCGG ATGGnTTAAA TTGTTAAAAT CACCATAGGG TGTCCCnGCC GTGGACTGTG 360  
 50 GTTAAAAACG TCACGGACTT TGTTTAAAAn GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

- (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

10 CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC 60  
 TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT 120  
 AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT 180  
 15 TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTTGCA GATAACTGGC TAGCACCGAA 240  
 TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTATTTTTA CAAGGAACAT 300  
 TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTTAAAA CCATTATTAC 360  
 20 CAGGAT 366

## (2) INFORMATION FOR SEQ ID NO: 4333:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTTAATATTT TTTTCAATGT 60  
 35 CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTTATT TCGTCGTCCC 120  
 ACCCCAACCTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC 180  
 40 CCCCAACTGG CACATTATTG TGAAGCTGAC TTTTCGTCAC TTGCTGTGTT GGGGCCCTCA 240  
 CCCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCCCTGGA 300  
 CTGAGAATTG GAAAAAGCT TGTTGACAAG CGCnATTTTC GTTCCATGCA ACTGACTGCC 360  
 45 AAGAGAACnT CGTGAGAGCn ATGAAGAAGA TTGGATTGTA 400

## (2) INFORMATION FOR SEQ ID NO: 4334:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60  
 GTGTTCTTTC GAACnTATGC GATTATTCT TATGAATTCA AGCTTATTTA AAACCTCTTTA 120  
 5 TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180  
 AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240  
 10 TGTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCCGCCA TCTTCTGnAA 300  
 GAAGATGTT 309

## (2) INFORMATION FOR SEQ ID NO: 4335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCACT GTGAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60  
 25 ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120  
 CGTGCAATCC AATCGCACGC TTCGCCTATC CTA CTGCGTC CCCCCATCGA TTAAAACGAT 180  
 30 TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCTG GnCTCAGCTT 240  
 AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA 300  
 CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

## (2) INFORMATION FOR SEQ ID NO: 4336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATT AATTGGGCAC TCTAAGTTGA 120  
 50 CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180  
 TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240  
 GCAAATCCCA TTAAAGTTGT TCTCAGTTCG GATTGTAGTC TGCAACTCGG ACTACATGAA 300

## (2) INFORMATION FOR SEQ ID NO: 4337:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT 60  
 TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCTAAAG 120  
 AGCACCCCTT CTCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT 180  
 CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCATTATTT 240  
 TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AntGGCTnCT 300  
 CCCATCAGAG CTCAGCCTTA ACGA 324

## (2) INFORMATION FOR SEQ ID NO: 4338:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG 60  
 ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAAATT TGATTGGGTT GTTTGCTCAA 120  
 TTGATTATAT GTTTTTCTTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA 180  
 AGATAAGTCT AACAAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT 240  
 ATTGGTAAAA ACACCCCAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC 300  
 TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTTA GCAGTAATTG CCACATCTGT 360  
 GTGACGATAA TGATATGCGC CAGTAATAnt TTGTGnTTT 399

## (2) INFORMATION FOR SEQ ID NO: 4339:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

5 TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120  
 CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TCGCTCTAA CCAGCTGAGC 180  
 10 TATAGGCCCA TTnTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240  
 GTTATCCGC ATCTTCTGAA GAAGATGTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300  
 AGCCGCACCT TCCGGATACG GCT 323

## (2) INFORMATION FOR SEQ ID NO: 4340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

25 GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTT CAGGTTGAT TGGAATTTCT 60  
 CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTGCGTC CTCCATTCAG 120  
 30 TGTTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA 180  
 TACTAAACGC CCTATTCAGA CTCGCTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG 240  
 CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTACGGG 300  
 35 CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCCAA TTTT 344

## (2) INFORMATION FOR SEQ ID NO: 4341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

45 TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60  
 50 TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120  
 TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA 180  
 AAGCCTCTAG ATAGAAAATA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

TTcNggGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C

351

(2) INFORMATION FOR SEQ ID NO: 4342:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

15	AATAATGACT CCTACGGGAC TCGAACCCGn GTTACCGCCG TGAAAGGGCG TGTACTTAAC	60
	CGTATGACCA AGGAGCCATG GCTCACCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA	120
	CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC	180
20	TCTAGCGGAA nTAAATTCGA ACTACCATCG ACGCTAAnGA GCTTAACTTC TGTGTTCCGC	240
	ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT	300
	TCAAAACTAG ATAGTAAGTA AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

35	ACCGCTTGGG CTGACATTTT TGGCTTGTTA AGCAGCTTGC CTACTTTTTT GGCAATAGCA	60
	CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTTAATT CATTCCAAAC ACACTGTTGA	120
40	AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTTCAG GATTGTCACC TTTAAAATAC	180
	GCGTCTAACC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA	240
	CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAAGT	300
45	TCCAAnCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60  
 5 CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120  
 GACGGCTAGC TCCTAAAAGG TTACTIONACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT 180  
 GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240  
 10 CTAGCGATTC CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACTT 300  
 TATGGGATTT GCT 313

## (2) INFORMATION FOR SEQ ID NO: 4345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTGTCCAC TACAATATCT 60  
 AATAGTTTTA CTTAAGTCC AGCATTACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG 120  
 CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCCTCCAAT TTAGTTGAGG 180  
 30 ATAAGATAAC CATTAAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT 240  
 CTTTGACAGT CATCTTAGCC TCTTATTAA GGnAAAAGCn TTATGCTTAA nATAAGTCTT 300  
 35 TTTTA 305

## (2) INFORMATION FOR SEQ ID NO: 4346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60  
 TTTTAAGCTT GAATTTAACA AATCATAAGC CGTATGAATA TTAAATATG CCACCATGAT 120  
 50 TGAATGGnCC CTTTCTATTA GTTAAGTTTG TCGTAAAGC TGTAGCAAGT TGCTCAAATT 180  
 CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTCGGA TGAnCAACGC CAACCAAAT 240

AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360  
 CCAACTGAGA TGCTCATTGG CTGATACGAT GntCCATACA 400

5 (2) INFORMATION FOR SEQ ID NO: 4347:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60  
 ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120  
 20 GCGGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180  
 AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC 240  
 CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300  
 25 ATGAGATTCh TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTAAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATTT 60  
 40 TTTAGGTCTC GTAGTGTAGC GATTAACACG CTGCCTGTC ACGCAGAGAT CGsGGGTTCG 120  
 ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTT TCGGTTTAAT 180  
 ATTATATTAA TAAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTCGTCCA 240  
 45 TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTn 300  
 GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

	CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC	60
5	CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA	120
	TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC	180
	CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTCT AACCTCTGAC CCTCTGATTA	240
10	AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT	300
	CGAACCAACG AGTGACGGA	319

(2) INFORMATION FOR SEQ ID NO: 4350:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

25	ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG	60
	GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC	120
	CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT	180
30	AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT	240
	TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG	300
35	TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT	346

(2) INFORMATION FOR SEQ ID NO: 4351:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

45	ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT	60
	ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG	120
50	ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG	180

ACTTACTTAT CTAGTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300  
 TGACC 305

(2) INFORMATION FOR SEQ ID NO: 4352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTCATCAAT TGCTAATTCC AGTCCGCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60  
 CTTTAAACC TGGCTTCTTT GGCTTTTTCG ATATAATGTT GCGATTGTTT TATTGTAAAT 120  
 ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180  
 GCAATCATTT CTTCTAAAAA TGCCTCATTT GAACTTGCCT CTTTAGGTAC AGCATGAGGC 240  
 CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTTCTCAG CTAAACGATT AGnCACTTTC 300  
 AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60  
 TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC CATAGAGGAT 120  
 TCGAACCTCT GACCTCTGA TAAAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT 180  
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240  
 CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC 300  
 GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CGnTTTAAAA 360  
 CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTCGAC TACCATCGAC G 411

(2) INFORMATION FOR SEQ ID NO: 4354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

	TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGGa	60
10	CGACAACCTGG TACACCAGAG GTATGTCCAT CCCGGTCCTC TCGTACTAAG GACAGCTCCT	120
	CTCAAATTTCT CTACGACCAC GACGGATAGG GACCGAACTG TCTCAGGACG TTCTGAACCC	180
	AGCTCGCGTa CCGCTTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA	240
15	GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAaC TCTTGGGGGA	300
	GATAAGnCTG TTATCCCCGG GGTAACTTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG	360
	GAAACCA	367

20

(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 313 base pairs
	(B) TYPE: nucleic acid
25	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

	GTATTTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG	60
	TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT	120
35	TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT	180
	TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAnATT	240
	AGAGGAAATA CTAATTTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAACCTT	300
40	GnCATGTGTCT GTT	313

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:

45	(A) LENGTH: 335 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

	GGGCTGGGTT CAGAACGTCG AGGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATTT	60
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55

TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180  
 GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG 240  
 5 ATGAGGTTAA TAGGTTGAG GTGnGAAGCA TGGTGACAGT GgAGCTGAC GAATACTAAT 300  
 CGATCGAGGA CTTAATCAAA ATAAATGTTT TCGGA 335

(2) INFORMATION FOR SEQ ID NO: 4357:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

20 GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTTAAATTAT ATACCCACCA CATTGgTGn 60  
 nGAACCTAAA AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120  
 TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180  
 25 ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240  
 CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCGAG ATTCGAACTG CCGAACCCGA 300  
 AGAG 304

30 (2) INFORMATION FOR SEQ ID NO: 4358:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

40 ATAATGGTGA CGTTGATGAT GCAITTAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60  
 TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120  
 45 AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTGA GCATTAGCAA 180  
 TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240  
 AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTTGAT AACATTCAnn TCGACTCAnC 300  
 50 AG 302

(2) INFORMATION FOR SEQ ID NO: 4359:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

10 GGTTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60  
 CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120  
 CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180  
 15 CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG 240  
 TCCCAAGGGT TGGGCTGTTT GCCCATTAAA GCGGTACAnG GCTGGGTTCA GAACGTCGTh 300  
 AGAAAGTTTC GTCCCTATCC GTCCTGGGGC GTAGGAAATT ThGAGAGGAG 350

20

## (2) INFORMATION FOR SEQ ID NO: 4360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

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AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60  
 GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA 120  
 TTCCAGCTTC ATGTAGTCGA GTTGCAGACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180  
 ATTTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240  
 AGCCCAAATC ATAAGGGGCA TGATGATTTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT 300  
 ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

## (2) INFORMATION FOR SEQ ID NO: 4361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

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AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA CTCTAGCGGA 60

CTnTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT 180  
TCTCGTTTCG TCAGATTCAA ACGTTTTTCAC TnCGnCAAGC CATTTTTCTT TGTGTTTACT 240  
5 TTTTATTTTG ACGTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300  
GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360  
10 TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC 420  
TCGC 424

## (2) INFORMATION FOR SEQ ID NO: 4362:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 316 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

25 CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60  
CGTGTACGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTGTTA AAGAAACGCA 120  
ATTnAnTCGT TATTTCCGGAC AAGAACGTAA CAATACTACA TACAACCTAG CACCATGAAT 180  
30 ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240  
AATCCAGCCT TTTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300  
TGGACAGCAG ATTCCA 316

## (2) INFORMATION FOR SEQ ID NO: 4363:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 318 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

45 GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTACATAT 60  
CGATAACATG ACATAACTCA TGCTGGGTTT CCCCAFTCGG AAATCTCTGG ATCAAAGCTT 120  
50 ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180  
AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240  
55 TTGATTAATC TTGTGGAGTG TTCTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC 300



## (2) INFORMATION FOR SEQ ID NO: 4364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

```

nTGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG      60
GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA      120
GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCATTACG      180
TGTACCTCAC GCGCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA      240
GAAGGGCGAC GATACATTAT CCACCTGGTG TTAAACCAAT TTAGTACGT GGTATATATC      300
GTTCCAAAAA CGT                                     313

```

## (2) INFORMATION FOR SEQ ID NO: 4365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

```

AACCATTCTGA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC      60
GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC      120
TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTn TTAATCACTG      180
CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn      240
CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTn      300
AGTCATTTTC                                     310

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## (2) INFORMATION FOR SEQ ID NO: 4366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60  
 AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120  
 5 AGTCAITTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180  
 GTTACAAATT ATTTTCAGGT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTTCAGC 240  
 ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300  
 10 ACATTAA<sub>n</sub>GG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG 360  
 CTAGTACCAT TTAGTAGCCG CTCCGTACCG <sub>n</sub>AATTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 4367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60  
 CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAACCT ATTTATCAAC GGTATATGAA 120  
 30 GGGGATTTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAACAAG 180  
 GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC 240  
 CGATGTTACT CG<sub>n</sub>ATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACG<sub>n</sub>ATG<sub>n</sub>C 300  
 35 TACAAATTTA ATCGCTAAAT CTGGTG 326

(2) INFORMATION FOR SEQ ID NO: 4368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60  
 50 CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120  
 CAATGGCAAC TTCTGTACCT GT<sub>n</sub>CAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180  
 GTGCATCATT TACACCGTCA CC<sub>n</sub>CCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

GTTTTGC

307

## (2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

15	TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG	60
	CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTTCGGAAAT	120
	CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA	180
20	TCGGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT	240
	CCTACAGGAA ACGCGTTATT AATCTTGTA GTGTTCTTTC GAACaYTAGC GATTATTTCT	300
25	TATGAATTCA AGCTTATTTA AAACCTCTTA TTCAATCGGT TTTGCTTGGG TAAAATCCTA	360
	TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA	396

## (2) INFORMATION FOR SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

40	CAGTAAGATA ATTTTCAATT AGAAATATC TTA CTGCTGT TCTCTATTTA TACAATACTT	60
	CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	120
	GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTTACATA	180
45	CTTTTAAAAA ATAAGACACT TTGCCAACT TGCACATAAA TGTTTAATTC AATAATTTGA	240
	ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAACTA AaTTArTGAA	300
	GTGCCTTATG TATAA	315

## (2) INFORMATION FOR SEQ ID NO: 4371:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

5 GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60  
 CGTGTGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC 120  
 10 CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180  
 GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240  
 CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAAATCA CCAGGGnCAC 300  
 15 CAAAATTTTT ATCGACGGCn TG 322

## (2) INFORMATION FOR SEQ ID NO: 4372:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

25 CCTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT 60  
 30 CGAACCTCTG ACCCTCTGAT TAAAnAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120  
 CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180  
 CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTTCGnA 240  
 35 ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300  
 AAAACTGCTG GGCAAGTTCT ACTCTAG 327

## (2) INFORMATION FOR SEQ ID NO: 4373:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

50 CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60  
 TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120  
 AGTCATTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA 180

TCAATTTTTA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300  
 ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360  
 5 GGnCCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

(2) INFORMATION FOR SEQ ID NO: 4374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTTCTCTTGT 60  
 20 TACTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTTA CGTTCTTCT CGAATGGAAT 120  
 CTCTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180  
 CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACCT 240  
 25 CCTCTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTTGA 300  
 nCGTTTCTGG GTCCGnAAGT CTGTnGAATT GCAG 334

(2) INFORMATION FOR SEQ ID NO: 4375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60  
 GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTCGGGAAA CCGnAGCTAA 120  
 TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACCT 180  
 45 ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240  
 GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAACT GAGACACGGT CCAGACTCCT 300  
 50 ACGGG 305

(2) INFORMATION FOR SEQ ID NO: 4376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

	GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
10	AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TGCGATTCCT GAAGTATTGT	120
	CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTGCTCT	180
	CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
15	GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA	300
	CTTAA	305

(2) INFORMATION FOR SEQ ID NO: 4377:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

30	AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC	60
	AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTGCCTAT CCTACTGCGT	120
	CCCCCATCG ATTAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
35	CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCAG AGCGGACGAG CCTTCCTCTG	240
	GAAACCTTAG TCAATCGGTG GACGGGATTG TCACCCGTCT TTCGCTACTC ACACCGGCAT	300
40	TCTCACTTCT AAGCGCTCCA CATG	324

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

50	CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
	AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT	120

55

TGGCACCAAA CTTTAATATT TTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240  
 GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300  
 5 GGAATCCCA ATTCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360  
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAntC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

20 ATAAATATA TCACTTGAAA AATTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60  
 TTGTGACTGA GATGAACCTT TATGTCTTAG AACTACAAC ACTATATTGG CAGTAGTTGA 120  
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAA TGCAAGTTGG 180  
 25 GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240  
 GTGTACTCAT GTTGCATTAA TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300  
 TCGCTACATA ATCCATCCAT TAGGTCGTTT CTTGATTCAT TCCCT 345

(2) INFORMATION FOR SEQ ID NO: 4380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60  
 45 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120  
 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180  
 CTGTGTTAAC TGGTCGTTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTAATGTAAC 240  
 50 AGATATGCTA TTATTCATGG AAGATTAGTG CTTTCATCTT TTTACCCCAA TATTTTATAA 300  
 GTGCAATATC GTAGTGCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360  
 ATn 363

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

```

ACCTGAATGA CTCAAACCTG ACTTTnCGAC AATTGACTGT nCATTnTGCA TAGTTGTATG      60
nCTCCATTnC GTAATTATTA GATTGTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT      120
ATAGTTAGCG TATTTCACCC TTTGCACATT AAACCATGTT TAATAATCAT TGAATCATT      180
TTAAGTAAAT TAAGGAATCT ATAATGTTTCG TTAAATAAAA CTGATCCCGT TGTGGCTTCA      240
CACCCGATAG ATAGGGATTT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTTGGGAC      300
CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG      360
GCCGTTGTCA CTTAACTTCT GTTTTCCGA TGACAGCTTC      400

```

(2) INFORMATION FOR SEQ ID NO: 4382:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

```

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTAC TGACGAATAC TGGCAATGAC      60
ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC      120
CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGTGT TCTGGTTCAG      180
TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTCGCAATT      240
TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG AACACCGAGT      300
AGGG      304

```

(2) INFORMATION FOR SEQ ID NO: 4383:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60  
 GGCGGTTCTGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120  
 5 GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180  
 GAATCTGCCC CCCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240  
 10 TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC 300  
 AGTTGGTA 308

## (2) INFORMATION FOR SEQ ID NO: 4384:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AAATTTGGCC AAAACACCCA TCCGCTGTAA CTTCAGAGTG TCATTGGCAT TTATTACACT 60  
 25 ATCTCCAACCT CCTAGTGGA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120  
 AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180  
 30 TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGkAGCTA CACCCTTTCC 240  
 TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTtTAT CAGTAATGGC 300  
 TTTAGAnAT 309

## (2) INFORMATION FOR SEQ ID NO: 4385:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60  
 TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG GCGAGTTACG 120  
 50 ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180  
 TTTAGTATTT GGTCGTAGCC GAnAACAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT 240  
 AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

## (2) INFORMATION FOR SEQ ID NO: 4386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

```

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA      60
ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCAnG GCAAATATCA      120
TGGCAAGGTC ATCTTCAAAA TGATTGATT CAAGTGGAAG GCATATGACG TCTCATCACT      180
ATACCCTTTT TCCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC      240
CATTGCGGGC AATCTCGGTn AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT      300
TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG      360
CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTcGnGGCAT      400

```

## (2) INFORMATION FOR SEQ ID NO: 4387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

```

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA      60
TTCACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAAA TAATTTCACA      120
GTGTTTGCAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG      180
CAACGCTATT TAGTATCAGG TTAAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTcNc      240
GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA      300
TGGATGACGA      310

```

## (2) INFORMATION FOR SEQ ID NO: 4388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTCAGGTTA 60  
 5 CTA CTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120  
 TGTTAGCGAT nCATACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180  
 10 TGA ACTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240  
 TTACTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300  
 TTTGGCGTGG 310

## (2) INFORMATION FOR SEQ ID NO: 4389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

TTTACCATAT CATCCACTAT TTATTAAACC TAATAAGAT GAATTAGAAG TGATGTTTAA 60  
 25 TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120  
 TGCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180  
 30 TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGGTTAA TACAGTTGGC TCTGGTGATA 240  
 GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC 300  
 35 CA 302

## (2) INFORMATION FOR SEQ ID NO: 4390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGC TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA 60  
 50 ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAAATGGT AGGAGAGCGT TCTAAGGGCG 120  
 TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180  
 CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC 240

TnCTTACCA CCTATAATCG nTTAATCGTG GGG

333

## (2) INFORMATION FOR SEQ ID NO: 4391:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGC GTTTG TGCAC nACT TGACTG nAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG	60
GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCAAAA	120
TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG	180
CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT	240
ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC	300
AACCAT	306

## (2) INFORMATION FOR SEQ ID NO: 4392:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTTATT AGGACATATA AATTCATCAT	60
TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATGTC ACTTTTAAAC TTTCTAGTTT	120
TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAATCA TCTATAATAG	180
CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAATAAAC	240
CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT	300
GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTTGCCnC AATTnGTAAA TGGAA	355

## (2) INFORMATION FOR SEQ ID NO: 4393:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 364 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

5 CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTTTCAGG TTTCTTCTTT GCATTTGGTG 60  
 CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120  
 TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA 180  
 10 AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240  
 CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300  
 GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTTG GATTAnTAAC GATAATGGCG 360  
 15 nnGG 364

## (2) INFORMATION FOR SEQ ID NO: 4394:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60  
 CGGCCTCAGC TTAGGACCCG ACTAACCCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120  
 30 GTCAATCGGT GGACGGGATT CTCACCCGTC TTTCGCTACT CACACCGGCA TTCTCACTTC 180  
 TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAACGCT CTCCTAnCAT 240  
 35 TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG 300  
 CATGTnCACT CGACT 315

## (2) INFORMATION FOR SEQ ID NO: 4395:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

50 AGCCCCCAA TGGGTATTGA AATTGAATGG TGGGnCTGA AnTGGACTCG AACCACCGAC 60  
 CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120  
 ACAAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300  
 ACCGGCTTCG GGTGTTACAA AC 322

(2) INFORMATION FOR SEQ ID NO: 4396:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60  
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC 120  
 GTTTTAGACA TAAAAAAGA nACCTCACGG TCCAAACTTG CCTGGCAACG TTCTACTCTA 180  
 GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTC ACAATCGCTT 240  
 GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT 300  
 CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAAGCTACAA CATTCTATA AAATTTTTC 60  
 ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120  
 GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180  
 GGCGGAGGAA TCACATGTCT ATTACTGAAA AACACGTCA GCAACAAGCT GAATTACATA 240  
 AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA 300  
 TTACATTTTA GGCTTGATTT TCCTATCGn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360  
 GCAGATGCCT GGCCAGG 377

(2) INFORMATION FOR SEQ ID NO: 4398:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 base pairs

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

	TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
10	GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG	120
	GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC	180
	AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT	240
15	AAGCAACTAA TATCATTGTC AACCATTAAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
	TCnATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

30	TGGCTATGAT CATCCAAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTCGCGAAGA	60
	TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA	120
	AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
35	TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
	AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT	300
	GCATTTTACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAAGA	360
40	ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

	CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
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55

AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC 180  
TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 240  
5 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 300  
ArATTCAAAC GeTTTCacTT CGGCCAAGGC ATTTTTCTTT GTGGTTACTT TTTAATTGG 360  
10 ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGGG 409

## (2) INFORMATION FOR SEQ ID NO: 4401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60  
ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTACT ACTGAGTCTA ACCTAGTTGA 120  
25 ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180  
TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240  
30 TGAAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300  
TCCATATTTTC C 311

## (2) INFORMATION FOR SEQ ID NO: 4402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60  
45 AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA 120  
TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180  
AAATThCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT 240  
50 TATGGCTAAT TGCCTGGGGA AATGACATAC GAATCTCAGG TTAAACAGA AAATTAAAGC 300  
AGGTCCATGT nAAGTGTGGG CGGGnCGCAT 330



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

```

10  TgntCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTTGAT TATCTGGCAC      60
    TTTGGGCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT      120
    TACTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC      180
15  AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT      240
    TTTGAGGTGG TACTTGATAT AAATTTTCTT CTCTAAAATA TTCATTTAAA ATGCGTTCGA      300
20  TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTG      340
  
```

(2) INFORMATION FOR SEQ ID NO: 4404:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

```

30  TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA      60
    CCTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTGCGAG TTTGTCTGAA      120
35  TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AACAGTGCT CTACCTCCAA TAATCATCAC      180
    TTGAGGCTAG CCCTGAAAGC TATTTGCGGA GAGAACCAGC TGATTTCCAG GTTCGATTGG      240
40  AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC      300
    TGCCATT      307
  
```

(2) INFORMATION FOR SEQ ID NO: 4405:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

AnACTTGAGT GCAGAAGAGG AAAGTGAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120  
 ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180  
 5 AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC 240  
 TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300  
 CTGGGGGAGT GACGGACCGC AAG 323

(2) INFORMATION FOR SEQ ID NO: 4406:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTA AACACAG TATGGAAGAC GAACTTGGAG 60  
 ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120  
 25 AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180  
 AACTTTCCGT AACTCATGAT GATCAACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA 240  
 TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300  
 30 ACnChAGnAT GGGTA 315

(2) INFORMATION FOR SEQ ID NO: 4407:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCCCCCATC ATAAAATAGG TGGACAGGAA TATCAACCTG 60  
 45 TTATCCATCG CCTACCCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC 120  
 CTTCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA 180  
 CACCGGCATT CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240  
 50 AGAACGCTCT CCTACCATTG TCCAAAGGAA TCnCACAGCT TCGGTAATAT GTTTAGCCCC 300  
 GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 393 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

```

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAAGG      60
TATTCGCGAA AAATTCGAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAAGC      120
ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA      180
TGTGTTAGAT ATTACAGCAG CACATTTATC TGCGCAAAGT CCCAGCTGTC GATAAAGGTT      240
GAAACTGAAA AACGGATTTT TGGATTTnGA AAATGATAAA CGTAAAGCAG TAAGTGCTTG      300
AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAAATTGG AATCCAAATC nnTTACCAGG      360
TTAAATTTGG GAAAATGGTT AATTGGTGGG ACC                                     393

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(2) INFORMATION FOR SEQ ID NO: 4409:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

```

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC      60
TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA      120
GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA GGCATAAAAA AAAGAGACCT      180
TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG      240
AAGTnAATTG GGCTACCATC GTCGCTAAAG ACCTTTCTTG ACTTGTGGAC AATCGCTTGG      300
CnTCTnTCCT CTCCTTCGG                                             319

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(2) INFORMATION FOR SEQ ID NO: 4410:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAnATACGC CTAAC TTCGT TAACTTTTAA 60  
 AATGTATTAA AATTCTAAAG TTTCTTTTGC TTTTTCnATG ATGTCATTTT TGTTTGGTAA 120  
 5 CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180  
 TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240  
 CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAAGTACGA CCAGTTTTTC AACTGAGCAC 300  
 10 AATTGTGCAC ATCGATTGGT GACAG 325

(2) INFORMATION FOR SEQ ID NO: 4411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA 60  
 25 ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120  
 TGAAATGACG ATAGAGTCAG TATTAAGTCA TTTTCAATA GATCAGGAAG ACTAnCAAGC 180  
 TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC 240  
 30 ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTTAA TTGGCCATTC GGGTAAGTTG 300  
 TCCGACCATT GCCAAGTGGG TGATGAGTTh AGGCCAGTCC GCAAAAGATT GGGAAAGTAG 360  
 TCCGGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60  
 CCCGAGCACA TTATTTTCATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120  
 50 GAATGATAAT CGAACGTCAT ATTTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180  
 TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAAATTA AACATAACCA TCACCATTTA 240

CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTGGAAT ACCCGGAGTT 360  
TTAATTCCA 369

(2) INFORMATION FOR SEQ ID NO: 4413:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60  
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 120  
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 180  
 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCnACTCTA 240  
 GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAncGC 300  
 TTGCGTCCTT ncCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCAGTA CCGTGAGGAA 60  
 AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120  
 GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT 180  
 TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240  
 TTTAGTATTT GGTGCTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCAG 300  
 GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

5 TTTATTATAC TTTACATTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60  
 TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT 120  
 CTCAAATGCG GTCATCGCA TCCACTTTT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA 180  
 10 AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACCTCTGT GTTCGGCATG GGAACAGGTG 240  
 TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTn 300

## (2) INFORMATION FOR SEQ ID NO: 4416:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

25 AGAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60  
 CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTC 120  
 GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG 180  
 30 CATATAAGAT GATTTTTTAAC ATCATCTTTG GATGATAGGA TGTGCGCCA CGATGATGTC 240  
 TGAATTCATC GAATTTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

## (2) INFORMATION FOR SEQ ID NO: 4417:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

45 TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60  
 AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAAATGT TGTTAGAAAT TAAAGATTTA 120  
 GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180  
 50 GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTC AAGCAAATA 240  
 TGTAATTTGT TTAGTCCAAC TAGTGGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

GTTTGGTGGA ACGnATTGGA nGATAACCAT GGATAATTCC

400

## (2) INFORMATION FOR SEQ ID NO: 4418:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

GTATTTACAA TCAAATAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT 60  
 CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG 120  
 GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG 180  
 CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAnCATCGA AATGGTTTAG TAACTCATAC 240  
 AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG 286

## (2) INFORMATION FOR SEQ ID NO: 4419:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTCT 60  
 CCTACCATTG TCCAAAGGnA TGChCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT 120  
 TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180  
 AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG 240  
 GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG 300

## (2) INFORMATION FOR SEQ ID NO: 4420:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAAT GACCCCGTAA CTTCGGGAGA 120  
 AGGGGTGCTC TTTAGGTTAA CGCCCAGAAG AGCCGCAGTG AATAGGCCCA AGCGACTGTT 180  
 5 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCC 240  
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAAcT ACGAATCGAA GCCCCAGTAA 300  
 10 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

(2) INFORMATION FOR SEQ ID NO: 4421:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 297 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCCCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60  
 AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTTCGATT GGAATTTCTC CGCTACCCCTC 120  
 25 AGTTCATCCG CTCACCTTTT AACGTAATCG GTTCGGTCTC CCATTTCAGTG TTACCTGAAC 180  
 TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240  
 30 TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTA CTGCTTA ACCTTGCATC AAATCGT 297

(2) INFORMATION FOR SEQ ID NO: 4422:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA 60  
 ATTCAACGAT GCCGTTGAAG CGGTTAAGGA ATTCAGGGCG GAAGAATTTT TTCATTTTCGT 120  
 45 GCATAATATC TTTTCTTCA GCGTCATTCG CATTGCCAAA GCCAGCATTT GATGTACAAA 180  
 TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT 240  
 50 CCATTACTTG TAATAACAAT GTTAAATTG TGGATTGCTT TTCGATTCAn CAATAGAATG 300  
 ACTGAGAnGG GATACGGCGA CTTTTCAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360  
 CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 291 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAAGTAT CAAGCTTTGA 60  
 AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120  
 CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180  
 AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240  
 ACAACGGTTG GCTCTTTAAT TGTA AAAAGA AAACCATACG CTATGGTAGT T 291

(2) INFORMATION FOR SEQ ID NO: 4424:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnC GTTTCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT 60  
 GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120  
 AAAGTACCAG TAGACAATGT AGGTATTGGA CTTGTCATGAG CATTTTTATn CAGTAATGGG 180  
 CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240  
 GCAACATTTT TACCTAAATC AGCCGAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC 300  
 CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATTA AATACTGATT TAGCGTTAGA 360  
 CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT 400

(2) INFORMATION FOR SEQ ID NO: 4425:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGTTTTGGCA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120  
 ATATATTTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT 180  
 5 GCGTGCTCGG ACTTAAAGCT GTAGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG 240  
 TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT 300  
 10 CCATnTTAT CATTAAAGCGT CTTAnCAGAG ATATGACAAT 340

(2) INFORMATION FOR SEQ ID NO: 4426:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 292 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACAAATTACG GATCATGATG 60  
 ATTTCACTACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120  
 25 ATAGTGA CTGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTCAG 180  
 ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTC GGACAGCGAT TCAGACTCAG 240  
 30 ATAGCGACTC AGATTCAGAT AGCGATTCAG ACTCAGACAG CGACTCAGAT TC 292

(2) INFORMATION FOR SEQ ID NO: 4427:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60  
 AACCAGCTAT TTCCAGGTTT GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120  
 45 TTTCACGTA ATCGGTTTCG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG 180  
 TAGATCACCT GGTTCGGGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT 240  
 50 CGCTACGGTT CCCACATTTA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCGnCGGGTC 300  
 ATTCTAn 307

(2) INFORMATION FOR SEQ ID NO: 4428:

(A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

10 GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60  
 TTTTtagcag CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTCAT ACGAGATGGT 120  
 ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT 180  
 15 ATCTTCTTCA GGGAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240  
 CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAa GATGATTATT ACACGTnACT 300  
 AATTGGTTTA CACCAGGTGG AnaATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

20

(2) INFORMATION FOR SEQ ID NO: 4429:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

30

GTGnACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTTGTTTAAA AGATATTAGA 60  
 CTAAAACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCACT 120  
 35 TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180  
 GTGCACATTA TTAAATATC AATTTACAC TCAATGCGGC TCATCGCATT CATTTCTTGT 240  
 CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT 300  
 40 GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTGGCTCT CGCTTACTCC ATTTAGCTCC 360  
 ACTAAACTCG TGCGGCCCTT CCCGTTCCGC AGATCCAACG 400

45

(2) INFORMATION FOR SEQ ID NO: 4430:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

55

ACCATTCACT CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120  
 ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180  
 5 ATCGATAGCG TTTTGCACAA ATTCTTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240  
 TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

20 TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GAACTCTTGG GGGAGATAAG 60  
 CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC 120  
 GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180  
 25 ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAACCTTGA GCGCCTCCGT 240  
 TACCTTTTATG GAGGCGACCG CCCAGTCAAA CTGCCCCGCCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

40 TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGGAAGA GCCTTCAGTT 60  
 GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120  
 TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180  
 45 TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCCGn TGAGGCATAT 240  
 CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300  
 50 AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

	CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT	60
10	TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC	120
	AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAnG AACTCGGCAA	180
	AATGACCCCG TAACCTCGGG AnAAAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC	240
15	AGTGAATAAG CCCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT	288

(2) INFORMATION FOR SEQ ID NO: 4434:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 336 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

	GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC	60
30	AATCGAACCT GGAGATAGCT GGTTCCTCTCn nAAATAGCTT TAGGGCTAGC CTCAAGTGAT	120
	GATTATTGGA GGTAGAGCAC TGTTTGGACG AGGGGCCCT CTCGGGTAC CAATTTCAGA	180
	CAAACTCCGA ATGCCAATTA AATTAACTT GGAATTCAG AACATGGGTG ATnAAGTCCG	240
35	TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA	300
	AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT	336

(2) INFORMATION FOR SEQ ID NO: 4435:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
45	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

50	ATTGACGCCG CATTTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG	60
	GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG	120
	GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAGGCAC	180

55

AATCATTGGC TGC GTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA 300  
ACGA 304

(2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAATAAC CGAAGAGTTT TGAATCATTG TTAAAAATGG AATTAnAGTT 60  
CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT 120  
ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTTCa TATGGTCTTC CTTCAITCTC 180  
ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATTT 240  
TTGTTCTTCA TATTTATTTT TTCTTTCGGA ATAATCATCA AATTTATnTT TGGAACTTCT 300  
TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 359 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60  
TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120  
TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180  
AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTACA AGGGGGAnAA 240  
AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGGTT 300  
GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

5 ACTTACAGTT ATTTTAACTT GGnCAGAATC CATCATCCAT AAGTTCGAAA TGTGTGAAAA 60  
 CATAAACCTT GnAAACGGCA ACATTTTGG GTCCTTCTCC ATCATTTTAT TTAAAGCGC 120  
 ATTATGATCA ATATCATGCC CAATTAACTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180  
 10 ATTGTGAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240  
 ATCTTTATTA ACAATTGCTT CATCATTAATA ATGTGAGATT AAATCG 286

## (2) INFORMATION FOR SEQ ID NO: 4439:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

20 TCGCTTGACT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60  
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTCA CTTGCGCAAG CCATTTTCT 120  
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAAcGTTCTA CTCTAGCGGA ACGTAAGTTG 240  
 30 GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTCTCn 300  
 TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAACTCGT TGCGCTCTTT TCTCGTTTCG 360  
 35 TCAGATTCAA CAGTTTTCAT TCGCCAAGCC ATTT 394

## (2) INFORMATION FOR SEQ ID NO: 4440:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 295 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

45 TAATAGGTTT GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60  
 GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTGTAA 120  
 50 TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTCCCATG 180

TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GcNtn

295

## (2) INFORMATION FOR SEQ ID NO: 4441:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTTCAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG 60  
 CGATTATTTC tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG 120  
 TAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC 180  
 GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 240  
 TAAATAAACA TTCAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA 300  
 TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT 345

## (2) INFORMATION FOR SEQ ID NO: 4442:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCAC 60  
 ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA 120  
 CGTCATTGCT CAAATCATTC ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC 180  
 ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTCGCA TCGTTAACAT 240  
 GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTTGTAGT 300  
 GTATCTTGGA TGC 313

## (2) INFORMATION FOR SEQ ID NO: 4443:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTATGTTT TAATTTTTTC 60  
 5 CAGTCTTTAA AAATAGATTG TTTATTTTTA GAATTATTTT TGAATAATTG AATTGCTTTG 120  
 TAGCCAAAAT ATGACGTTTC ATTATCATTC AAACGCATAT AAAGCGTATC TnCTGCCTCA 180  
 TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCCTTCAA 240  
 10 CTGAAACCCC ATTCCCTTTG AGCTGCCCAT ATATCTCTTT GGACAATATC GGTCCCTCTA 300  
 ATACGGnCCG TAGnCCATTC CATTTCAATT CTTTTT 336

## (2) INFORMATION FOR SEQ ID NO: 4444:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT 60  
 TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120  
 TTTCAACACC ATACGGCGTA GTGAAAGATT GGTGGAAGGG TGAAATTGAA GCGGTACCTG 180  
 30 GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240  
 ATGTCACGCT TGGGCTGTG CTTGAAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300  
 TCCGTGTCCA GTTGAACCAT TATGGAGGAn TThAAAAAGT ATGTTAAGGG ACCTGGGAGT 360  
 35 TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

## (2) INFORMATION FOR SEQ ID NO: 4445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCCCAG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60  
 50 CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATCGGATGA 120  
 GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

CACTAAGTCC GTGCTTTTCGA CCCTGACTAC GGACTTGThA GGTCTGCGGC ATTCAAGCTT 300  
 CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTTG 339

(2) INFORMATION FOR SEQ ID NO: 4446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTTGAAAAT GTCACCTTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60  
 CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120  
 CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAAT 180  
 CATTGTATAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240  
 ATAAAACAGG GTGAGAATTG GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300  
 TTTTnCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCGGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60  
 TTTTATTTCA GTCAACTACT AACAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120  
 ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180  
 TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240  
 GTAAAAAATG AACGATCAAT GGTnTAACCA TTAAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60  
 5 CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120  
 CCCC GG TACA TTTTCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTTAAAT 180  
 GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCACT 240  
 10 TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGnA TTGAACACGG 300  
 GA 302

## (2) INFORMATION FOR SEQ ID NO: 4449:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

25 CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAATGTG GACACAGTTT TTACAAGAGG 60  
 TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTGAA TGTTTAGTAA 120  
 ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180  
 30 TACAAAACAA TGA<sub>n</sub>ACGAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240  
 ACCCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300  
 35 TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

## (2) INFORMATION FOR SEQ ID NO: 4450:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

45 GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60  
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAA CAATACTTTT ATAGGGCAAC 120  
 50 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTCACAAT TAGCAGACAA 180  
 AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAAGCT 240

GCTATACGGT AGAACGACTT ATTCCC

326

## (2) INFORMATION FOR SEQ ID NO: 4451:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

GAAAAATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA	60
TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT	120
TCAACAACCTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAnAAAAAGA	180
AGACAACCAA GCCCAATAAT GGACTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT	240
TTAAAAATAG GTCTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTAACCAT	300
GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA	360
TAAAGCGGGG GGCAATTGGG G	381

## (2) INFORMATION FOR SEQ ID NO: 4452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT	60
CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC	120
TCGGTTTTGC TTGGTAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT	180
CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA	240
AATAAACATT CAAAACGAA TACAATATGT CACATn	276

## (2) INFORMATION FOR SEQ ID NO: 4453:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTAAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60  
 5 CATTGGAAAC TGGAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120  
 AAATGCGCAG AGATATGGAG GAACACCACT GAGCGAAGCG ACTTCTGGT CTGTAACGA 180  
 CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240  
 10 TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCTT AGTGGCTGCC AGCTAnACGC 300  
 ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A 341

## (2) INFORMATION FOR SEQ ID NO: 4454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60  
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 120  
 CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCAAT TACATAAGTA AACTCTGCTT 180  
 30 TAAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT 240  
 TATTAATCTT GTGAGTGTTT TTTCGAACAC TAGCGATTAT G 281

## (2) INFORMATION FOR SEQ ID NO: 4455:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60  
 TATCAATTTT AACTCAATG CGGCTCATCG CATTCAATTC TTGTCTAGCA ACGTTCTACT 120  
 50 CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180  
 GCTTGChTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGTTG 240  
 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTChGT 279

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60  
 CCATTTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 120  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 180  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240  
 nTCACTTCGC CAAGCCATTT TTCTTGTTT TACTT 275

(2) INFORMATION FOR SEQ ID NO: 4457:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60  
 ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG 120  
 TTCGGTAAGC ACATCAGCGT CATTAAGTGG TTCAGAGAGT GAATCTGATT CACAAAGTAT 180  
 CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCGTCA ACATCACTCA GTGACTCAAC 240  
 AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC 300  
 AnTGGAATCC GATTTGTCGT CAACATCTTT AAGTGGATTG AACATCTGCG TnATGCCAA 360  
 AGnnGTGAAT CCGATTCACA AAGCACATCA GCATCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4458:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120  
 TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180  
 5 GGTCTGGGGn TGGTTCCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT 240  
 GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTCGG 300  
 AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351

10 (2) INFORMATION FOR SEQ ID NO: 4459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60  
 GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120  
 25 TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTnACAATA 180  
 CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240  
 CGCTTTTAAA TAAAATGATG GAGAAGGnCC C 271

30 (2) INFORMATION FOR SEQ ID NO: 4460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 283 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120  
 45 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 180  
 GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240  
 GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283

50 (2) INFORMATION FOR SEQ ID NO: 4461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

	CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG	60
10	TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAAATC	120
	AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC	180
	TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTTAAAT CAACAAnCAT AACTTTCCnG	240
15	GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC	274

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 271 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

	GGCTGCTAAA AATCTTGGTA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA	60
30	CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA	120
	TGATGGACGT ACAGGTGAAC CATTGATAA CCGTATTTCA GTAGGTGTAA TGTACATGTT	180
	GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT	240
35	TGnTACACAA CAACCACTTG GCGGTnAAGC G	271

(2) INFORMATION FOR SEQ ID NO: 4463:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 300 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

	GCGGCTCATC GCATTCATTT CTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC	60
50	TACCATCCTC GCTAAGAACC TTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT	120
	TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC	180
	AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTAnTTTGAC	240

55



## (2) INFORMATION FOR SEQ ID NO: 4464:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60  
 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA 120  
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180  
 GAAAGACCCC GTGGGAGCTT TTA CTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240  
 GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300  
 CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG 360  
 G 361

## (2) INFORMATION FOR SEQ ID NO: 4465:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAAG TATAAATTCA 60  
 ATCATTCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120  
 AAGGTGCTAT TCCTTTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180  
 GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240  
 GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGT TTTTnTTTT TT 292

## (2) INFORMATION FOR SEQ ID NO: 4466:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60  
 AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120  
 5 AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAAACAG GTAATTTAAA ACCAAATACG 180  
 GATAGTAATG CATTAAAGA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240  
 TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCT 300  
 10 AATAnTGG 308

## (2) INFORMATION FOR SEQ ID NO: 4467:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGGAAGAC 60  
 25 AGGATTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120  
 CCCGTATAAT TAAngCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180  
 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240  
 30 GAATCGAACC GGTACGTGAT CACTCACCGC A 271

## (2) INFORMATION FOR SEQ ID NO: 4468:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TCGTCAAAG TCCAGCTGTC GATAAAGTTG 60  
 45 TAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120  
 AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180  
 AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240  
 50 AACGATTAAC TGGTATTCCA GTTCTCAAA TnGATGATAA CGnTATTGAA CGTTTAAAAA 300  
 ATATTT 306

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

GGTTTATTAA CAGCATTCCTT ATCAGCATTT GTAACGTGTA TTGTTTATAA CTTCTGTGTG 60  
 AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTT ACAAGTATTT 120  
 AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCCTT ATGCATTAGA TTTAGTCATT 180  
 CGCAACAGCT TTAAATCAAA TGTAGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT 240  
 ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTAAcNT TGGGnGCnTT TGCATTAAATC 300  
 CTGGGTTTGT AGGGTAATCC ATGGGTCCG 329

(2) INFORMATION FOR SEQ ID NO: 4470:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

AACTGGGTGA TAAGGTCTTG TTCGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 60  
 AATATATGTT AACTGGAAAA GGATGTGGCG TTGCCCAGAC AACTAGGATG TTGGCTTAGA 120  
 AGCAGCCATC ATTTAAAGAG TGCCTAATAG CTCACTAGTC GAGTGACACT GCGCCGAAAA 180  
 TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG 240  
 CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA 300  
 TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG 360  
 GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT 400

(2) INFORMATION FOR SEQ ID NO: 4471:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TCATTTTTAG AAATATTATC TTTTCCACAA ATCATTTGAT ATAAAGTGCG ATCATTTGCC 60  
 GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTTT TGGCTAGCAC TTCGGGATAC 120  
 5 TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTTGA AAATATCATT ATCTTGACCC 180  
 ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240  
 TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCCTCC GTTTTnCATG TACCGCGAGG 300  
 10 CGTAAnCTTA AAGGGCCCCAA GGnCG 325

## (2) INFORMATION FOR SEQ ID NO: 4472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA 60  
 25 TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120  
 CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT 180  
 ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240  
 30 CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

## (2) INFORMATION FOR SEQ ID NO: 4473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATTT ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60  
 45 CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAgaATA GATTGTCAAG CGCTCGCATA 120  
 AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC 180  
 AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG 240  
 50 AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCAT 300  
 TGTCCACCT TCGACGGGCT AGCTCCGAAA AGG 333

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG 60  
 AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCTTGGC GCAGGCACAA TGGGCGCTCA 120  
 ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAAnA CTATTAGATA TTGTAGTGGa 180  
 CAAAAACGAT CCnAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG 240  
 GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTTACCAT ATGGTATTTT GATGTGCTTG 300  
 GTAAATGTGT GCTGTTTGAT ATCGA 325

(2) INFORMATION FOR SEQ ID NO: 4475:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

TAACTGCGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA 60  
 CAATACATCT AGTATTATCT GGTATTTTGT ATCGTTATCC AAAGTTAAAT AATGATTATT 120  
 GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT 180  
 GACATTTnAC CACCCTGTAA GCTATACTTT AAAAATAATT TTTAATCACA CCGAGTGGCA 240  
 TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300  
 TGATATCC 308

(2) INFORMATION FOR SEQ ID NO: 4476:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 280 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120  
 GGGTCTTTCC GTTCCTGTCTG CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTCCACCGA 180  
 5 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTTCG TCGGGGTCGG AACTTACnCG 240  
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

20 GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60  
 CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120  
 25 GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180  
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240  
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

40 GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60  
 ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAATGG TCCTCCACCT TGAGCTTCTT 120  
 45 CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180  
 AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240  
 GGAnACGATT TTGATAACCT ATTGTTAATT TT 272

(2) INFORMATION FOR SEQ ID NO: 4479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA 60  
 5 GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA 120  
 ATTTCCTTTC GAAATTCTCT GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC 180  
 AAGCGCATTT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA 240  
 10 TTTATGTCCC AGCCTGAGTT AATTT 265

## (2) INFORMATION FOR SEQ ID NO: 4480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACATC ATTACGCATA 60  
 25 ATAAAAGAAG CTAAGCAACA TGTAACCGT TGTCACCTAA CTTCTTGTTT TTCCGATGAC 120  
 AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG 180  
 TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT 240  
 30 ATATTCCCAC CGTTTTTCATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT 300  
 TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCn TAG 343

## (2) INFORMATION FOR SEQ ID NO: 4481:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC 60  
 GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA 120  
 50 AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT 180  
 ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT 240

## (2) INFORMATION FOR SEQ ID NO: 4482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA 60  
 CATCAAATTA TCGGTGCTAC TGtnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120  
 CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180  
 ATGGGGATTG GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG 240  
 CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

## (2) INFORMATION FOR SEQ ID NO: 4483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACTC AATGCGGCTC ATCGCATTCA 60  
 TTTCTTGTCT AGCAACGTTC TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120  
 AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCTC TCCTTCGGCT CTCGCTTACT 180  
 CATTTAGCTC TACTAACTC GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTnc 240  
 ACTTCGCCAA GnCATTTTTT TTTG 264

## (2) INFORMATION FOR SEQ ID NO: 4484:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60



TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTCACA CTGCCGAGAA 180  
 nAAGCCTCTA GATAGAAAAA GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240  
 AATTCTAAGG TGAGCGAGCG A 261

(2) INFORMATION FOR SEQ ID NO: 4485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTAAATAGA GAACTTAATA 60  
 AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120  
 TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180  
 GATGGAnTAA ATCTTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAn GTCATGCTTT 240  
 CAAAAGACGA TATACTACGA C 261

(2) INFORMATION FOR SEQ ID NO: 4486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCATTCTC GTGTCTCACC AGATTTAGCG ACTAACTTG TAGACATACG 60  
 TAAATCTGCT TTAATAAGTA ATThATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120  
 AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGAnTTTGAG CGCCTTGCTT 180  
 TACAGCATTG ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240  
 TACCGTTGAT AAATAAGTTA 260

(2) INFORMATION FOR SEQ ID NO: 4487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

5	ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC	60
	TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG	120
	ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTTGTCTT CATATTTATT	180
10	TTTTCTTTTCG GAATAATCAT CAAATTTATT TTTGAAGTTC TTAATCTTAG TTCTTTTTTA	240
	CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTTCCCCA ATAGAATGAA TTTAAACCTT	300
	CCGATTTTCCT TTAAnC	316

(2) INFORMATION FOR SEQ ID NO: 4488:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

25	CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC	60
	TCAAAAAGTT ATAGAAGAAG CTAATAAGT TAAAACAGAG ATTGATACTG CCAGAAGATA	120
30	ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAATA AAGCGGCTAA TTCATTACGA	180
	ATTAAACCCT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTTAAA GCGTnAAAAT	240
	GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA	300
35	GACTCAA	307

(2) INFORMATION FOR SEQ ID NO: 4489:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

50	TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT	60
	GTTCCCCAAT CATTAATTTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC	120
	ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAGTGGC	180
55	ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT	240

TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA

344

## (2) INFORMATION FOR SEQ ID NO: 4490:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACC GGC ACATTGTTGT AAGCTGACTA TATGTCACTT CnTGTGTTGG GGGCCCTGTC 60  
 TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT 120  
 TTACTTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA 180  
 TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA 240  
 CAGGTACTnA GTAACTTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG 300  
 TTCATTTGAC CGG 313

## (2) INFORMATION FOR SEQ ID NO: 4491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTCTGACT CTAGAGGATC CCCGATGAGT TTAAAGAAAA ATATCAAACA CCTGAATTAT 60  
 ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTCACAA TGAGCCAGAA CGTGATGAAG 120  
 TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG 180  
 AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA 240  
 AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGChCh A 291

## (2) INFORMATION FOR SEQ ID NO: 4492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GCCGTCTCAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 60  
 ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAAA ATAAAACACT TTGCCCAACT 120  
 5 TACTACTACCA ATAGAACTG CTGTTAGAAT TCCTCAAAT GATATTTTCGC GATATGTTAA 180  
 TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTCGATGG AATTCAGACA TCATCGTGGG 240  
 10 CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300  
 ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360  
 ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGChT 400

(2) INFORMATION FOR SEQ ID NO: 4493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

25 TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60  
 GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGGAGG 120  
 30 AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180  
 ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG 240  
 ACGAATCATC TGGAAAGGTG AATCA 265

(2) INFORMATION FOR SEQ ID NO: 4494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

45 CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60  
 TAAGGAAGAG ATTTCTTGA AAGAGCTTGA TTTTAAATTG AGAAAACAAC TTATTGAAAA 120  
 50 ACATAATCTT TACGGTAACA TGGGTTGAGG AACAAATCGTT ATTAAAAATGA AAAACGGTGG 180  
 GAAATATACG TTTGAATTAC ACAAAAAACT GCAnGAGCAT CGTATGGGCA GACGTCATAG 240  
 ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60  
 ATAACTATAA TGCGAAGAAG CGTGAAGCAG AAACTGAAAT AACTGCAGCT CAACGTGTTA 120  
 TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180  
 GCATTTAACA GCATTnAAAC CAAGCGAAAC ATGAnTTTAA CTGCAGATTA CACATGCCTT 240  
 AGGAGCAAGC AGTGCA 256

## (2) INFORMATION FOR SEQ ID NO: 4496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTCA CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60  
 TTCATCATTA TCTAATTTAA AACAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120  
 ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AnATACCCAA TATACTTTTT 180  
 ATATCGTTCG GATTCTGAGT ATTTCAGACG ATTTTCTGCA TAnAAATAAA CGTGTITCAA 240  
 GGCAATATAT TGCA 254

## (2) INFORMATION FOR SEQ ID NO: 4497:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGnTATCTGA ATCCGAGTCG 60  
 CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120

GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240  
TCACTGTnGG AATCTGAATC GCTATCTGA 269

(2) INFORMATION FOR SEQ ID NO: 4498:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAAT GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG 60  
 GCAAGGTTGT ATTCTACCGC TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120  
 CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCGTCT GCCAATTCCG CCACACCCGC 180  
 AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240  
 CCAACTGAGC TAAATGGCTC TnCAGGTGC CGG 273

(2) INFORMATION FOR SEQ ID NO: 4499:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAGTAAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60  
 TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120  
 TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA 180  
 TCAACGAAGG AGACAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240  
 AGCAAGTGGA GGAATTCGAA GTTGTTCAnA CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300  
 AGCATCTTAG TCGA 314

(2) INFORMATION FOR SEQ ID NO: 4500:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG 60  
 5 GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120  
 ACTTAACTTT AATGGCGGTC GTCACATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180  
 CCATTTATGC TGTAAAAGG CGGTATAGCT GATAAAGTAT GGnCTGATTA CGGTGGCGGT 240  
 10 AATTCTATAC AAATTAGGAC CGGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG 300  
 CATT 304

## (2) INFORMATION FOR SEQ ID NO: 4501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

TTCCTTCATT CTCATAAAG TTGCATCATG ATCAGATCAG TTTAGAAAA ACTATTTCTA 60  
 25 TCTTTAAGAA TCGATTTTGG TTCTTCATAT TTATTTTTTC TTTCGGnATA ATCATCAAAT 120  
 TTCTTTTTGA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTTCT AATTTGAGCA 180  
 30 CAATCTTCGT TCTCAATAAG AATGATTTAA ATCTnCGATT TCTTTATCTA AATGGACTAC 240  
 CAATTAAATC TAT 253

## (2) INFORMATION FOR SEQ ID NO: 4502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

AGTTCGGTCC CTATCCGTCG TGGGCGTAGG AAATTTTnGA GGAGCTGTCC TTAGTACGAG 60  
 45 AGGACCGGGA TGGACATACC TCTGGTGTAC CAGTTGTCGT GCCAAnGCAT AGCTGGGTAG 120  
 CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCC CAAGATGAGA 180  
 50 TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240  
 AGCATGGTGA CATGTGG 257

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60  
 TATTGATAAC ATTGAAGTGA ATATAnAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120  
 TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180  
 GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAAAA GTGGCATTTC TATGTCTTAA 240  
 AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

## (2) INFORMATION FOR SEQ ID NO: 4504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT 60  
 ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120  
 AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180  
 AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240  
 TACCACChn T 251

## (2) INFORMATION FOR SEQ ID NO: 4505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60  
 TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120



TAGCTCAATT GGTAGAnCAC TGA<sup>CT</sup>TGTAA TCAGTAGGTT GGGGGGTCAG TCCTCTGGCC 240  
GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60  
AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120  
ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180  
TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCATTA GGTGCAACAT 240  
TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACGGGTAAAT TTAAAATCGG CTGTGGGTAT 300  
TTTGGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60  
ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTTCATCG 120  
GCTGTTAATT TACCATCAGC TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG 180  
GGAAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240  
TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

CATCGAACCA GATGTACTCG CACTTGTTGA GTCTGATGTT GAATCACTAA CACTATCAGA 60  
 5 TAATGACGTT GAATCACTCA TACTTGTTGA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120  
 ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180  
 10 TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACCTGTA CTTCTTGATG TGCTTTGTGA 240  
 ATCGGATTTT GCTCGTGCT GGTACTnG 268

## (2) INFORMATION FOR SEQ ID NO: 4509:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

CGAGAGTGCG TTAATTCGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA 60  
 25 GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCACGCTT 120  
 TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180  
 30 TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240  
 TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGGGCTT nCACATCACA CTTAnA 296

## (2) INFORMATION FOR SEQ ID NO: 4510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60  
 45 TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTG CATCTAACGT TACATAGTCA 120  
 GGCTTATTCG CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAAT TGTCTTACTA 180  
 50 TGTGCTGCA CCATTACCCA CTTnTTCAGT GTAAGCAATA TCCATTGCTT GAGTTGGGAT 240  
 TAATTAAATG GTCCTGA 257

## (2) INFORMATION FOR SEQ ID NO: 4511:

- (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

10 AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TGTAGTATCT 60  
 AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120  
 TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTAAAT CATCCATAGC AATTCTCGTT 180  
 15 TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT 240  
 TGATAAATGC 250

20 (2) INFORMATION FOR SEQ ID NO: 4512:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

30 AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA 60  
 GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT 120  
 TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTAAATAA 180  
 35 TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240  
 CTCTCCCCAG CTG 253

40 (2) INFORMATION FOR SEQ ID NO: 4513:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

50 GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA CGTTAACATG 60  
 nAAGTTACGT TCTTTTATAA AAAGATTAA ACGCGTTATT AATCTTGTGC AGTGTCTTTT 120  
 55 CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

GTGGAGACTA GC

252

## (2) INFORMATION FOR SEQ ID NO: 4514:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 244 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

15	GTCATTGAAT ATGGAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG	60
	ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC	120
	TCTTGAGAA CAGTTAAAG ACCATTTTAC TGTGTAGCC GTTGATCGTC GTGATTATGG	180
20	AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCTGACA GTGATTATCG	240
	TGTC	244

## (2) INFORMATION FOR SEQ ID NO: 4515:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

35	TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT	60
	TCGAGTCGTT GATTTCACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCGTAC	120
	CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA	180
40	AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC	240
	CCA	243

## (2) INFORMATION FOR SEQ ID NO: 4516:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120  
 ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180  
 5 CCGTCCACCG ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240  
 CCTTAAACCT GAGGCCGCAA nnGTAGG 267

(2) INFORMATION FOR SEQ ID NO: 4517:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTTAG TAGAGCTAAA TGAGTAAGCG 60  
 AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTCACAAGT CAAGAAAGGT CTTTAGCGAC 120  
 GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG 180  
 25 ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAAT 240  
 TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG 300  
 GAACGAGAAA GAGCGCACG 319

(2) INFORMATION FOR SEQ ID NO: 4518:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60  
 CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT 120  
 45 GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180  
 CATGTCAA<sub>n</sub>G TACCATTTGC AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT 240  
 ACATGAAAAA CGGGGAACA 259

(2) INFORMATION FOR SEQ ID NO: 4519:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

ATAGGGTGTT GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC	60
10 CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	120
AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG	180
TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG	240
15 TTTGGACGAG GGG	253

(2) INFORMATION FOR SEQ ID NO: 4520:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT	60
30 TTTTCTTTGT GTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT	120
CTCAACTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCnACC ATCGTCGCTA	180
AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA	240
35 CTCAT	245

(2) INFORMATION FOR SEQ ID NO: 4521:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

GGGCCTAAGT GGA CTCGAAC CACCGACCTC ACGCTTATCA GGCGTGCGCT CTAACCAGCT	60
50 GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG	120
TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG	180
CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCACCTT	240

55

## (2) INFORMATION FOR SEQ ID NO: 4522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG 60  
 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 120  
 GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCTAGAC CGAAACCTGG 180  
 TGATCTACCC TTGGTCAnGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT 240  
 ACGTTTGAA 249

## (2) INFORMATION FOR SEQ ID NO: 4523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG 60  
 GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAng CATAGCTGGG TAGCTATGTG 120  
 TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA 180  
 CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT 240  
 GACAGTGG 248

## (2) INFORMATION FOR SEQ ID NO: 4524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTAT GATGTCTTAA 60

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGAnCGGCT GTGGCTCGnA 180  
 CCAATACGGG TCGGACCTGC TThAACCATT TTATTGGAAA TCTTCTAAAT TACGGACGGC 240  
 5 ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT 300  
 CTGCAGTCGG ACCGGCAACT GCAAAA 326

(2) INFORMATION FOR SEQ ID NO: 4525:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

20 AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT 60  
 CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG TAnGGCACCT ATTTTCTATC 120  
 TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGTCTTC TCCCATCACA 180  
 25 GTCAGCCTTA ACGAGTACCG GATTTGCCTA ATACTCAGCC TACTGCCTAG nGGCATCCAT 240  
 CGCAGTTnGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300  
 C 301

30 (2) INFORMATION FOR SEQ ID NO: 4526:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT 60  
 TTTcAGTAAC TTGTnCCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA 120  
 45 CACCCATCCG CTGTAACCTC AGAGTGTcAT TGGCATTTAT TACACTATCT CCAACTCCTA 180  
 GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240  
 T 241

50 (2) INFORMATION FOR SEQ ID NO: 4527:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG	60
10 TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC	120
ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
TCGCAACCAT nCAATCATCT GGCAGTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA	240
15 GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA	300
ATACCACCCA ACACCT	316

(2) INFORMATION FOR SEQ ID NO: 4528:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

30 GTCCCAAGGG TTGGGCTGTT CGCCCATTAAG AGCGGTACCG ACGACTGGGT TCAGAACGTC	60
GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG	120
TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
35 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC	240
AAGATGAGAT T	251

(2) INFORMATION FOR SEQ ID NO: 4529:

40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

50 AGTACGTGAC GTTCACTACT CTCACTATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG	60
ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAATG AATTCGGCTT	120
TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA	180

55

ATGGTCGTTT AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300  
GTGACGCGAC AGTGTCnA 318

5 (2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60  
GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120  
20 GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180  
CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTTAA CCTTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60  
35 TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGA CTACCTG 120  
TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180  
40 AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GcncAGCCTT AACGAGTACC 240  
GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 238 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAAATA TGACGTCATC TATAACGGAC 120  
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180  
 5 CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

## (2) INFORMATION FOR SEQ ID NO: 4533:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60  
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120  
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180  
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGÄ 240  
 25 TGTGGTTGTT CCACTAGGAG TTGGAA 266

## (2) INFORMATION FOR SEQ ID NO: 4534:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTAAACGTA TTATTTCAAT 60  
 40 GAGCAGAAAG AAAATTATGG CACCAAACCTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120  
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTT GTCGTCCCAC CCCAACTTGG 180  
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240  
 45 CATTATTGTA AGCTGACTTT TCGT 264

## (2) INFORMATION FOR SEQ ID NO: 4535:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

	GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG	60
5	GACGCATAGG nATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT	120
	AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATCGGG AGAAGACATT GTGTCTTCGA	180
	GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC	240
10	AAACCGACAC	250

(2) INFORMATION FOR SEQ ID NO: 4536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

	AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT	60
25	AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACTAC	120
	CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC	180
	TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA	235

(2) INFORMATION FOR SEQ ID NO: 4537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

	TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT	60
	TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT	120
45	ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAG CTAACCACTC	180
	CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT	234

(2) INFORMATION FOR SEQ ID NO: 4538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGTnAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC 60  
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120  
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180  
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240  
 TA 242

## (2) INFORMATION FOR SEQ ID NO: 4539:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAAACCT TCCATATCTG TTCCTGTGCC AATAAAGCCA 60  
 TATTGCGTTT GGnCTGTCGT GCCAGTGCAA GATTTC AAC GATAATTTCT AGGCGTCACT 120  
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180  
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

## (2) INFORMATION FOR SEQ ID NO: 4540:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AACnGTTGAA TCTGACGAAA CGAGAAAAGA 60  
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120  
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180  
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240  
 50 AT 242

## (2) INFORMATION FOR SEQ ID NO: 4541:

55

(A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60  
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120  
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180  
 15 GnAGTGTCTTCT TTCGAACATA GGCGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT 240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA 60  
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GGCGAGGnTG ATGAATGCCT TACGTTTGCG 120  
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180  
 ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240  
 35 TG 242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60  
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120  
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180  
 55 GAnTGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG 239

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA 60  
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120  
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180  
 GTTCGAACCG nCGACCCTCT GCTTGTAAAG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

(2) INFORMATION FOR SEQ ID NO: 4545:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60  
 GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTTATTAA TCGTTTAAAT TCAGTTAGTA 120  
 AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAnATA TTATAGAAAA CATCAAAGGA 180  
 TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

(2) INFORMATION FOR SEQ ID NO: 4546:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60  
 CACTATTACT CTTCCACCT AATTGGTTCA TGGCTTGTC TAnTTTTTCA TGTGCTTCCG 120  
 CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTTGACAATG TCACTTACCG 180  
 GTTCAACTTG GnCGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

## (2) INFORMATION FOR SEQ ID NO: 4547:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60  
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120  
 GAATTAGGTT ACGAAGGTGG CCAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180  
 AAGAAGTTTA AACCAGAAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTTCG 240  
 ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

## (2) INFORMATION FOR SEQ ID NO: 4548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAACCTAGA TAGTAAGTCA 60  
 AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 120  
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180  
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240  
 GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCCGTTT 300  
 GGCACG 306

## (2) INFORMATION FOR SEQ ID NO: 4549:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:



CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120  
 ATAAAGATTG AATTAACGCA TCAGTATTAG GATTCACCTT AATACGATTA ATAGTTTAT 180  
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTGGAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAAATTTG 60  
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120  
 CGTGCCAAng CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180  
 AGCATGAAGC CCCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC CCTCAAAGAT 240  
 25 GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60  
 40 AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120  
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTn CCCTCCCTCA 180  
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240  
 45 CGTTAAAATT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300  
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360  
 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

	ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG	60
10	CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTACTTCTTA AACGATTAGA	120
	AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGG AGAACTGGG AATACCATTG	180
	AATCGTTGnA ATAGTATCTG GAAATATCAT GGAAGTGTAG CAACAGCAGT GTGTTGCACC	240
15	ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTGG GATTTCATT TTGGAATGTG	300
	CGTGCAGCTT TT	312

(2) INFORMATION FOR SEQ ID NO: 4553:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

30	AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAATA CCAATACCAA ACCATAGAAC	60
	AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTTTCGAT	120
	AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA	180
35	TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAATAATT GCTAAATGTG GnGAATTTCT	240
	CCAGTAACAA TGGA	254

(2) INFORMATION FOR SEQ ID NO: 4554:

40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

50	GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCn	60
	AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC	120
	TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC	180

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CTGGGGCTTG G

251

## (2) INFORMATION FOR SEQ ID NO: 4555:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA	60
ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCGA ATGATTTAAG	120
AGGGAACATG GATGCGAGTG AATTCCGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC	180
CTATCTGAAA AAGCCnACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC	240
AGAAGCATGG C	251

## (2) INFORMATION FOR SEQ ID NO: 4556:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTTG	60
GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT	120
TCGCCCATT AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA	180
TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC	240
ATA	243

## (2) INFORMATION FOR SEQ ID NO: 4557:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT TTAAAATAAT TTAACCTCATT 120  
 GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGT 180  
 5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60  
 20 TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120  
 ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180  
 ACGTGTTTGA TCACCCAATT TAATGATTC ACGCTTGTGC AATAATnATT TTCGAGACGA 240  
 25 GAGGATCGGA TTAAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60  
 40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120  
 GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180  
 CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60  
 TTCTACTCTA GCGGAAnTAA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120  
 5 CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT 180  
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

(2) INFORMATION FOR SEQ ID NO: 4561:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

20 TCAAAGGACG CATACCATTa CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60  
 TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120  
 CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCCAGATT CCGACGGAAT TTCACGTGCT 180  
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240  
 CTTTGATTCA TCTTGTC 257

(2) INFORMATION FOR SEQ ID NO: 4562:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

40 TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTcAGTT 60  
 GCCACAATTA CCATACCAAT TTTCTTTTTG TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120  
 TTAGCTCCGA TTGAAACGAT GTCTTGTTTT ACAGGACTAA CAGCCATTTc AGTTTGACCA 180  
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

(2) INFORMATION FOR SEQ ID NO: 4563:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60  
 5 TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT CTATGTTTCC ACCATTTTAA 120  
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180  
 10 nGACTCTGCT TTAAAATAAT TTAACTCATT GTCTGCTAAA CGTTT 225

## (2) INFORMATION FOR SEQ ID NO: 4564:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG 60  
 ATGGCCTAAC TGCTTTTAA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120  
 25 GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180  
 AATTATTICA GGTTTCTTTC TTTTGCATTT GGGTGCTTTA ACCATATCTT nTT 233

## (2) INFORMATION FOR SEQ ID NO: 4565:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60  
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120  
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTCAG 180  
 45 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

## (2) INFORMATION FOR SEQ ID NO: 4566:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAACCTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCAACCTAC 60  
 5 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120  
 TGGAGAnTGA CGGGTTCGAA CCGCCGAnCC TCTGCTTGTG AAGGCAGATG CTCTCCCAGC 180  
 TGAGCTAATT CTCCGATTTA AACTGGCCT GGGCAACGTT CTACTCTAGC GGGAAC 237

## (2) INFORMATION FOR SEQ ID NO: 4567:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60  
 GCCAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120  
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAC ACAGCTCATA ATATCAAAAA 180  
 GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240  
 TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAAC TAG TAATAAGTAT GTCAGTTTAA 300

## (2) INFORMATION FOR SEQ ID NO: 4568:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60  
 GTAGTTTAAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTCGA TTCCCATCAC 120  
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 180  
 TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240  
 AAACATTCCA 250

## (2) INFORMATION FOR SEQ ID NO: 4569:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

	GATCCCCTAG CTTTACGTTT AACTTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT	60
10	ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT	120
	AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT	180
	TCAGATTCTG ACCCAGGTTT AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT	235

15

(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

25	AATCTATTTT TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT	60
	TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTT GATTCGTGAT	120
30	TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC	180
	CAnCAATAAG ATTTTGCTTT AAACATTGAC TATGAAACTG GGA	223

(2) INFORMATION FOR SEQ ID NO: 4571:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

45	CATGATATTT TGAACCGCAT GGTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT	60
	GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG	120
	CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA	180
50	GGCAGCAGTA GGAATTTTTC CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG	240
	TGCTGCAGGT TCTTCGGATC GTAAAT	267

(2) INFORMATION FOR SEQ ID NO: 4572:

55



(A) LENGTH: 221 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTA<sup>2</sup>CTTACTA TCTAGTTT<sup>2</sup>TG AATGTATAAA TTACATT<sup>2</sup>CAT ATGTCTGGTG 60  
 ACTATAGCAA G<sup>2</sup>nGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120  
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180  
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 230 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60  
 30 TTCGGTGCA<sup>2</sup>n TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120  
 ATACCTGATG CGTATTGCTG TGTGCTAGTA C<sup>2</sup>nAGAGGGG AATTGCTTGA TCAACACAAG 180  
 GATGTAGCGC AAGATTTGTA CAAGGTTATA AAAAGTCTGG CTTTAAAATG 230

35

(2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 230 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

45

TCACATATCG ATAACATGAC ATA<sup>2</sup>ACTCATG CTGGGTTTCC CCATTCCGAA ATCTCTGGAT 60  
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120  
 50 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATA<sup>2</sup>ACTTAAT C<sup>2</sup>nATGTTTCC ACCATTTT<sup>2</sup>TA 180  
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

(2) INFORMATION FOR SEQ ID NO: 4575:

55

- (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60  
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120  
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180  
 15 CACTCCCCAA AAGACCGCAG TAGGATAATT CCATTGGAA ATACCTTACT GCCnGTTTTT 240  
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300  
 CCTTAAATT 309

20

(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

30

TGATTCTAGG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA 60  
 ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAA TAATGGTGGG CCTAAGTGGA 120  
 35 CTCGAACCAC CGACCTCAG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC 180  
 ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA 240

(2) INFORMATION FOR SEQ ID NO: 4577:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC 60  
 TGGGTAAAAA TnTATTAATT GGGTGGTTCG TGAAATGCAA TCTTTTAAAC GACTTCAGGG 120  
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

55

## (2) INFORMATION FOR SEQ ID NO: 4578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT 60  
 AACTCCCAAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC 120  
 CAAAATCTTC AAACCACGAT TTA CTTTg nC TACTAATTTT TTTTgAGCA ATGAGTACGC 180  
 GCCTTAGCAA TTTTAnGTAG CGTAGTCCGC TCCAAAATAA TATTAAACTG ACATACTTAT 240  
 TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA 300  
 CTTGATTACG CGCGCTCAAC ATTC 324

## (2) INFORMATION FOR SEQ ID NO: 4579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAA CTGATTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT 60  
 GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTTATG 120  
 GTATGCATAT CGTTTAAAC CTATTCTTTT GTTAnTAGGA CATATAAAAT CATCATTAAT 180  
 TCGTCATATT TCCAATTTTG AGTGThAAAA ATGTCACTTT TAACTTTC 229

## (2) INFORMATION FOR SEQ ID NO: 4580:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGCTTAACC GCTTGnACCA 60

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180  
 CGTAAGTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT 60  
 CGACTACAGG ATTATTACCT TCTTTGATTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120  
 CTTTGTA ACT CCGTATAGAG TGTCTACAA CCCCACAAG CAAGCTTGTT GTnTTGGGCT 180  
 CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60  
 AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120  
 TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCanCT 180  
 TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

ATTTTGGAAT CATTGTAAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGAAA 180  
 TAGGTCATAG GGTnAAAACh TTTTGTAGAA TTTGTCGCTA TTTGTAAAT TGTATCCCGG 240  
 5 CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTTCGTA GCTTCGCAGA 60  
 20 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120  
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180  
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATTA 60  
 TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120  
 40 CTATATTTAC TTAATTATCT AGTTTTCAAT GTACAATTnC TTTTGTAGTCA AGCGCTCGCA 180  
 TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGAATTCCAC TTTCCTCTTC TGCACCTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120  
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACCGCCTAC GCGCGCTTGT ACGCCCAATA 180  
 5 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCAGC TATThAGCCG 240  
 T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

20 CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60  
 TGAAGTGAAT AAGAAATCAA TCATTGCTC TTCTGTAAA TCATGTGTTT TTTCTAATTT 120  
 25 AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GCGGTTGCAC AAATAATACC 180  
 CATCGCAGCA TTGACTTCAT TGTTCGAAGG CACnTTGAC TGCGGCAATC ATTCATATCC 240  
 GACnAAGCAG ATG 253

(2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

40 ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60  
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120  
 45 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180  
 GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTTAACAGC CGATAGCTCT 60  
 5 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120  
 AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180  
 10 GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

(2) INFORMATION FOR SEQ ID NO: 4590:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60  
 ATCnCATTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT 120  
 25 CCTCGGCTAA GAACCTTTCT TGACTTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180  
 CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT 234

(2) INFORMATION FOR SEQ ID NO: 4591:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTTCGTTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC 60  
 ATTTAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT 120  
 45 TTCGTCGTCC CACCCCAACT TGnCACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180  
 TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

(2) INFORMATION FOR SEQ ID NO: 4592:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTh TTAGCCGTGG 60  
 5 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCCTAAT 120  
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180  
 10 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

## (2) INFORMATION FOR SEQ ID NO: 4593:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60  
 AGCTTTGATC CAGAGATTTC CGAATGGGGA AACCCAGCAT GAGTTATGTC ATGTTATCGA 120  
 25 TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180  
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

## (2) INFORMATION FOR SEQ ID NO: 4594:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60  
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120  
 45 TAATCGAAGG TGTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180  
 TTATCGGTTT AGGTGCCACA GnAAGTGGAT TCCAGGTTAG CCAAAGGGGT TAATCTGGAT 240  
 TAATTTTTTTT Th 252

## (2) INFORMATION FOR SEQ ID NO: 4595:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60  
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120  
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180  
 AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240  
 GTTACCCGGG AGnAAAGG 258

## (2) INFORMATION FOR SEQ ID NO: 4596:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCACTAG GATCTGCCGG TGCCGCACGT 60  
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAAGAA TTGCAACTAG CTCTGGTTTA 120  
 30 TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180  
 TnCATTTGTTT AGTTGGGTAC ATTAATGChG TATTATCGAC ACTACATCA 229

## (2) INFORMATION FOR SEQ ID NO: 4597:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60  
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120  
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180  
 50 TACTGCTTAG ACGTGCAATC CAATCGCACG CTTCGCCTAT CCTACTGnGG TCCCCCATC 240  
 GATTAA 246

## (2) INFORMATION FOR SEQ ID NO: 4598:

- (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

10 AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60  
 TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120  
 CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180  
 15 TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60  
 30 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA 120  
 TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180  
 CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGC 219

35

(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAKCCCCAG TAAACGGCGG 60  
 CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC 120  
 50 GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180  
 GTGAAGATGC AGGTTACCCG CGGACAGG 208

(2) INFORMATION FOR SEQ ID NO: 4601:

55

(A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTCA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60  
 AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120  
 CACTTGAACA ACATTTGTGA ACGGATTATT TGGCAATTCG TTATTGTCGA ACAnTGChAG 180  
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240  
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

(2) INFORMATION FOR SEQ ID NO: 4602:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGAThAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60  
 TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120  
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180  
 35 TGGTTCCACC CATTTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240  
 nTTAAACGGG GTATTAATCT TGTG 264

(2) INFORMATION FOR SEQ ID NO: 4603:

40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60  
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA 120  
 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT 180  
 55

TATCCn

246

## (2) INFORMATION FOR SEQ ID NO: 4604:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAACCTAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60  
 AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGGAAA GGTGTATGGA 120  
 CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180  
 GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240  
 TTTGATGG 248

## (2) INFORMATION FOR SEQ ID NO: 4605:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTTC AGTTTCCAAT GACCCTCCAC GGTGAGCCG GGACTTnTCA CATCAGACTT 60  
 AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATCCGG ATAACGCTTG CCACCTACGT 120  
 ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180  
 GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTTGTTTTn 240  
 TGGGTT 246

## (2) INFORMATION FOR SEQ ID NO: 4606:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTAAATGCT GTTAATGCGT TATCGACACG 120  
 ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180  
 5 TGCAGTTATT TCAGTTTCTG CTTACGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60  
 20 GACCCCGTAA CTTGCGGAGA GGGGTGCTCT TTAGGGTTAA CGCCGAGAAG AGCCGCATGA 120  
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT 180  
 AGGGGCTGAC GCCTGCCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240  
 25 GGAATCGAAG CCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAAGG TGTTAnATTa AAGCAGTTTC TGGATCTGGT 60  
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120  
 GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180  
 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

(2) INFORMATION FOR SEQ ID NO: 4609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGGTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTA AATCGAATCG 60  
 CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG 120  
 GTATCATTAT CTATAAAAT GAAACTCATT GATCCAGTTA CATTTTTAAC GCTTTTAAAT 180  
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCnGA ATnGATTAGC 240  
 C 241

(2) INFORMATION FOR SEQ ID NO: 4610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCAATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60  
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120  
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180  
 TTTCAnTTTCG CCAAGCCATT TTTCTTTGGT GnTTA 215

(2) INFORMATION FOR SEQ ID NO: 4611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60  
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGTGATA AATATGGCGT GCGTTTGGCA 120  
 ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180  
 TGCAGTACCG TGTTTGTGTA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240  
 TAAATTATCT TGTGATTGAG GTAAATCCAT CTTGTTAGCT ACTACGATTG GAGGTCTATC 300  
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360  
 GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4612:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60  
 TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120  
 TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180  
 15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCCTAATG 240  
 ACCGTTAAGG TThAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

20

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60  
 ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120  
 TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180  
 35 AGCTTTTTTTC TACAGCTTTT ACAATATTnn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

40

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60  
 50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120  
 ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180  
 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTAAAnTTTA 60  
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120  
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGACTGTATG 180  
 TCnTTGGATA GAGTTACAAA CTTATTTTG 209

## (2) INFORMATION FOR SEQ ID NO: 4616:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60  
 TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120  
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180  
 CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

## (2) INFORMATION FOR SEQ ID NO: 4617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCAATTC TGCGATTTCT 60  
 TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120  
 ATGTATCAAC ATATCGCGGT ATGTTTAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180  
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240



## (2) INFORMATION FOR SEQ ID NO: 4618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTh GAGGCTGGGA CATAAATCCC TAAATTTCAh 60  
 CAGTAAGATA ATTTTCAATT AGAAAATATC TTAGTGCTGT TCTCTATTTA TACAATACTT 120  
 CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180  
 GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT 216

## (2) INFORMATION FOR SEQ ID NO: 4619:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60  
 GCGATTnGTC GTCCTAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT 120  
 GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180  
 TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

## (2) INFORMATION FOR SEQ ID NO: 4620:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCATC ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60  
 GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120  
 CATTTTTCTT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG 180

TTGACCAGC

249

## (2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

15	TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG	60
	TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG	120
	TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA	180
20	AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC	240
	ACAGTCTCGG GCGATTGTCG AGTCCAC	267

## (2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

35	CAAAAGGTAG TTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT	60
	TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA	120
	TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC	180
40	GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C	231

## (2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

55	CGAAACCGGC CCGACCCGGA CnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA	60
----	--	----

CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180  
 CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240  
 5 AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA 300  
 A 301

(2) INFORMATION FOR SEQ ID NO: 4624:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

20 CGAGGTGCTG CAGAAGGTGT CATTGTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60  
 GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120  
 25 GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180  
 TTTGAAAAAG GGGnAAATCA TAATCATtng GCGATGCCCA AG 222

(2) INFORMATION FOR SEQ ID NO: 4625:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

35 TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC 60  
 40 CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120  
 AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180  
 45 CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240  
 CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300  
 A 301

(2) INFORMATION FOR SEQ ID NO: 4626:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60  
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120  
 10 CATTAATCCC ATTTTTCAnCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180  
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nAT 223

(2) INFORMATION FOR SEQ ID NO: 4627:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 221 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

25 TTGTTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG 60  
 GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120  
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180  
 30 AAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

(2) INFORMATION FOR SEQ ID NO: 4628:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60  
 45 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120  
 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180  
 TCCACCACAT GTTAAATATG CAGCAGAG 208

50 (2) INFORMATION FOR SEQ ID NO: 4629:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60  
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC 120  
 ACACAACATA GATTGATCAG CTAAAGCTTA CTTCAAATAA AAGAGATATA GCCATTAGTA 180  
 10 ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240  
 TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300  
 CACTG 305

15 (2) INFORMATION FOR SEQ ID NO: 4630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60  
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA 120  
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180  
 CAGCTCCACA TGTCACCATG CTTCAnCTn GAA 213

(2) INFORMATION FOR SEQ ID NO: 4631:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60  
 TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120  
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180  
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

(2) INFORMATION FOR SEQ ID NO: 4632:

(A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

10 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAT ATTCTGAACCA TTATTTACAG 60  
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG 120  
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCCAATA 180  
 15 TCGAAGCGAA CTTCAAGTTG CTTCA 205

(2) INFORMATION FOR SEQ ID NO: 4633:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60  
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTTCTn TAGAAATTAG 120  
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180  
 CTAATGTGTT AAGAACTACT ACAT 204

35

(2) INFORMATION FOR SEQ ID NO: 4634:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG 60  
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGC GTTACGT TAGCCCGTCT GATGTAGAAG 120  
 50 CTTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180  
 AAAAAGCATT CATTAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

55

(2) INFORMATION FOR SEQ ID NO: 4635:

(A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

10 CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC 60  
 GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTTG 120  
 AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG 180  
 15 GCTTAAGTTG GCCATTTTTC ATATGGTC 208

(2) INFORMATION FOR SEQ ID NO: 4636:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAAA GTAGACCTTG 60  
 30 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 120  
 CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC 180  
 TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG 228

35

(2) INFORMATION FOR SEQ ID NO: 4637:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA GATGGATCCG CGCTGCATTA 60  
 GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCCT GAGAGGGTGA 120  
 50 TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC 180  
 TTCCGCAATT GCGGAAAGCT GTACGGGCAA CG 212

55

(2) INFORMATION FOR SEQ ID NO: 4638:

(A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnThATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60  
 TTTTTTAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTC GATAATTTTT 120  
 CAGGAAGCAT TTAAATTTTA CTAATGAAGC CATATTTTGA GATTAACCAA AATTAATATT 180  
 15 TACATTTCTT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240  
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCT 60  
 GAGAAGTTTA AAATTTTATA TGTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120  
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATCCG TAAAATGCTA 180  
 35 AATCTAACCA TCTATTAAAT TTAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60  
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120  
 ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180  
 55 GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTAAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60  
 AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120  
 CGCTGAACTA CTTCTGCATA TCGGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG 180  
 ATCCTAAGTC TAGTGCGTCT GCCAA 205

## (2) INFORMATION FOR SEQ ID NO: 4642:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60  
 CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA 120  
 GACGGGCAAA GCGAACCAAT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180  
 ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTATGTn CCCAG 235

## (2) INFORMATION FOR SEQ ID NO: 4643:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60  
 CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120  
 GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180  
 ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

## (2) INFORMATION FOR SEQ ID NO: 4644:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60  
 TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120  
 ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180  
 GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAGC CTGTTACAAG CGATTTTTCGG 240  
 TTCAGTCCAC TACTGGCAAT ATAACCTGTA GAGCTAGGAC ATTGG 285

## (2) INFORMATION FOR SEQ ID NO: 4645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60  
 CGCTTGThTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120  
 TACGAACGTG TTAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180  
 ATTTAGATGG TGGCTTTTGA TAAACA 206

## (2) INFORMATION FOR SEQ ID NO: 4646:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60  
 CTTACGGATC ATGATGATTT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTCnGA TA

222

## (2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCG TGTGTGACAA TGTTCTTCCA GCATTGCTT AATGAATGCT TTTTCTTCGT 60  
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120  
 GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180  
 CCGAAATTAA TGACAGTCCA 200

## (2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60  
 ACGCAGGAnG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC 120  
 AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTAAA 180  
 TAAGCTTGGA ATTCATTAAG A 201

## (2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA 60  
 ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG 120

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGThAAAT

218

## (2) INFORMATION FOR SEQ ID NO: 4650:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTAA ATTAATGAAA GATACAGTAG GTGCTGATGT 60

AGAAGTAAAA GCCATCAGGT GCGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG 120

CAAGTGGCAG ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG 180

ATTCnGATTA CTAATATnTA TG 202

## (2) INFORMATION FOR SEQ ID NO: 4651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAACTGGnA TAACTTCnGG 60

AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC 120

TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGTAAGGT AACGGCTTAC 180

CAAGGCAACG ATGCATAGCC GACCTGAGA 209

## (2) INFORMATION FOR SEQ ID NO: 4652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG 60

ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

CCACTTATCG TGGTTGGAGA CA

202

## (2) INFORMATION FOR SEQ ID NO: 4653:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60  
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT 120  
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180  
 AACCGGTACG TGATCACTCA ACnGn 205

## (2) INFORMATION FOR SEQ ID NO: 4654:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60  
 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT 120  
 GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180  
 AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240  
 CTATTAATCC ACACGGGTTA GAnG 264

## (2) INFORMATION FOR SEQ ID NO: 4655:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG 180  
 AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

(2) INFORMATION FOR SEQ ID NO: 4656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60  
 GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120  
 GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180  
 ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTTGGG GGCTTAGCTC 60  
 AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TCGATCCCG CTATCTCCAC 120  
 CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAATA TAGATTTTAC CAAGCAAAAC 180  
 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTGGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180  
 AAAAn 185

(2) INFORMATION FOR SEQ ID NO: 4659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAAGC ACTCCGCCTG 60  
 GGGAGTACGA CCGCAAGTGT ATAAC TCAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120  
 GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180  
 AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

(2) INFORMATION FOR SEQ ID NO: 4660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTTAAAGTCA 60  
 CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120  
 GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTTCTA TTATTTATTT 180  
 GATAGAAATC ACTTTTGTAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTTCCTT 240  
 ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300  
 GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTCGTT 360  
 CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60  
 5 CCAATTCTCC TnATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120  
 CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTTTTATA GCCTATCCAT CATCTTTTCT 180  
 10 ACATGAAATT TTTCCAAGTG ATATATTTT 209

(2) INFORMATION FOR SEQ ID NO: 4662:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60  
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120  
 25 CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180  
 CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240  
 30 GCCTAA 246

(2) INFORMATION FOR SEQ ID NO: 4663:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 226 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60  
 45 TTAAGGAAGC GATTCACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120  
 CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180  
 AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT 226

(2) INFORMATION FOR SEQ ID NO: 4664:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 55 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60  
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120  
 GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTCGA ATCCTGTCTC 180  
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACTT 60  
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120  
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180  
 30 CATTTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60  
 TAGATTGTGG TTTTTTAGTT GGTGCCATGC TTAAACCTTT TCATTGATTT CAATAACAGG 120  
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn 180  
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTT 226

(2) INFORMATION FOR SEQ ID NO: 4667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60  
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120  
 10 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180  
 CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT 60  
 25 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA 120  
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180  
 30 TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTAAAAACA GTTACAACAG ATGAnAATGG 60  
 45 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120  
 AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180  
 TT 182

50 (2) INFORMATION FOR SEQ ID NO: 4670:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60  
 CACCTTTTAA AGTATTACGT AATGTTGTGT TGCGTTTACA TCTTACCCAA AGTGCTAATG 120  
 10 CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180  
 ATTGG 185

## (2) INFORMATION FOR SEQ ID NO: 4671:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

25 CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60  
 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTGCATGGTA 120  
 GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180  
 30 CATTGAGACC GCAAGGnTnT 200

## (2) INFORMATION FOR SEQ ID NO: 4672:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

40 CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60  
 45 ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTTCGC CATTAAAGCG nACGnTGCTG 120  
 GGTTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180  
 TGTCCCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCTG TGCCACGCAT 240  
 50 AGTGGGTAGT ATGTGTGGAC G 261

## (2) INFORMATION FOR SEQ ID NO: 4673:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60  
AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120  
ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180  
CGTT 184

15

(2) INFORMATION FOR SEQ ID NO: 4674:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

25

CCCAGTCAAA CTGCCCCGCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTTGAGAAA 60  
GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120  
CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180  
AAGCTCCACG GGGTTCTTTC CGT 203

30

(2) INFORMATION FOR SEQ ID NO: 4675:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

45

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60  
AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120  
GGATTGGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180  
TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTA 229

50

(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCAITTA TTACCTCAAT ATGCTTGTCA 60  
TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120  
TTACAAATTT AGTGTGChGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60  
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA 120  
TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180  
AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGhTCTCC TCCCGAAAAT AAGCCTTTTA 240  
GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAAh 286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTA TGGAGCGGAA GATAGGTTTA 60  
CACCTATACC TCGTTCCGGA AGGhTGTTC TAAAAGTGAA CTACTCCCGC AATATTAAAT 120  
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180  
AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACh 229

(2) INFORMATION FOR SEQ ID NO: 4679:

55

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

	ATGACTGCTT TTTATTATAC TTTACATTC TCCTTCGTC AGATTCAAAC GTTTTCACTT	60
10	CGCCAAGCCA TCTTTCTTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG	120
	ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC	173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 183 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

25	AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA	60
	TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT	120
	AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT	180
30	CCC	183

(2) INFORMATION FOR SEQ ID NO: 4681:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

	CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG	60
45	AGATGGTCCT CCCAGATTCC GACGAATTC ACGTGTCCG TCGTACTCAG GATCCACTCA	120
	AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA	180
	TTCGTCTAAT GTCGTCCTTT GTA	203

50

(2) INFORMATION FOR SEQ ID NO: 4682:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTACACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60  
 CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC 120  
 GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180  
 ACAAAGA 187

(2) INFORMATION FOR SEQ ID NO: 4683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60  
 TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120  
 CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180  
 TTAAATT 187

(2) INFORMATION FOR SEQ ID NO: 4684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60  
 AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120  
 AGCTTATTTA AAACCTCTTTA TTCACTCGGT TTTGTAAAT CTATATTT 168

(2) INFORMATION FOR SEQ ID NO: 4685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCGA 60  
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120  
 AGCGCCTGCT TThCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

## (2) INFORMATION FOR SEQ ID NO: 4686:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60  
 TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT CGCATACTGC 120  
 nTTATTTTCA AAAAATCAAA TGCTCATTTA CAAAAGTAAA CTCCGCTTTT AATT 174

## (2) INFORMATION FOR SEQ ID NO: 4687:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60  
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120  
 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

## (2) INFORMATION FOR SEQ ID NO: 4688:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60



GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180  
 GTGACAAAC 189

(2) INFORMATION FOR SEQ ID NO: 4689:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60  
 GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTCAC TGCGGCTCTT 120  
 CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180  
 CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTTCG 227

(2) INFORMATION FOR SEQ ID NO: 4690:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60  
 GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGA TTATGTGCAA 120  
 TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAAnA AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60  
 TTAAAGGGGG CCCAATTTTT CCCAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAA 120

GTTAAATTTT TTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240  
 TTAAGGGAAT TTAAAAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300  
 5 AAAATTAATT AAAAaACCCA TTTTTTTTTT TTAATTTTAA ACCCAAAGG GGGTAATTTG 360  
 GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

20 TAGTGTC AAT TTTATTGATA TTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60  
 nTTTACTTAA AGTAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA 120  
 25 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA 180  
 AAATAGGAAT ACATGAGTAA AACTCAnTGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60  
 40 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTAGGATCT 120  
 TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180  
 45 CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - 50 (D) TOPOLOGY: linear

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60  
 CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120  
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180  
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

(2) INFORMATION FOR SEQ ID NO: 4695:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

20 TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60  
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120  
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTTCG 159

25 (2) INFORMATION FOR SEQ ID NO: 4696:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

AATATGGTAG TTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60  
 ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT 120  
 40 TAACAGGTAA TTAAAACCA AATACGGATA GTAnTGCATT A 161

(2) INFORMATION FOR SEQ ID NO: 4697:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60  
 TTGGGCGTAA ACGCGCGTAG GnGTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120  
 GGGTCATTGG AAACCTGGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60  
 TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120  
 GGGCAAGGTC ATCTTGCAAA ATGGATTCTGA TTCAAGTGGG AGGnCGATG ATGGACGTGC 180  
 TGCATGCACT GATGACCCTT TTTGCCCATC CTGGCAAATC CCACCATGAA ATGACTGACG 240  
 CGGACGCh 248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 175 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

CCCAGCAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60  
 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

## (2) INFORMATION FOR SEQ ID NO: 4701:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60  
 AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT 120  
 AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

## (2) INFORMATION FOR SEQ ID NO: 4702:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60  
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA 120  
 GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

## (2) INFORMATION FOR SEQ ID NO: 4703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTC TGTTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60  
 GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120  
 AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

## (2) INFORMATION FOR SEQ ID NO: 4704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60  
ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120  
GGCAACGTTC TACTCTAGCG GAACGTAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60  
AATGCCAATT AATTAACTT GGAAGTCAG ACACATGGGT GATAAGGTCC GTATTCGAAA 120  
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAATATA TGT 163

30

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60  
CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTG ATTGGCTGCA GTCGCGATGG 120  
TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTTGACCh GTACCCGTCA GATATCCGCA 180  
GCAATGCAAT GTTGTGCAAG TTT 203

(2) INFORMATION FOR SEQ ID NO: 4707:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTTCCAGA GGAGGCTCGT CCGCTCTGGG 60  
 5 TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120  
 TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

20 nCTATAATGA ATAAATAATT TAGAAATATG CTTCGGATTG TTCGATGCTT TAATTCAGTT 60  
 AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120  
 TATGTCTTTG GATAGAGTTA CAAACTTATT 150

25 (2) INFORMATION FOR SEQ ID NO: 4709:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

35 AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60  
 TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120  
 40 TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

(2) INFORMATION FOR SEQ ID NO: 4711:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT	60
TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTTCAG AATCTTTTTC	120
AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG	160

(2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA	60
CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG	120
TAGAATGAAC CGGCGAGTTA CGATTTGATG C	151

(2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC	60
CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA	120
CCTGGGAGAT AGCTGGTTCT CTCCG	145

(2) INFORMATION FOR SEQ ID NO: 4714:



- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60  
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120  
 AAACCGACAG GCCTTAACGG GCCGCGGGG T 151

15 (2) INFORMATION FOR SEQ ID NO: 4715:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

25 TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60  
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAAACG TGTAATTTTA CTTTGnAATA 120  
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

40 GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60  
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCAATTGT TTGTAAAAGT GGCATTTCTA 120  
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 144 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGAnT AAATCTTTTA AGGCTTATAA 60  
 5 ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAGAC GATATACTAC GACACTCCTA 120  
 CGAACTTGTC CAAGGATTAC GAAA 144

(2) INFORMATION FOR SEQ ID NO: 4718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60  
 AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120  
 CTTAACCCAA CATCTCACGA CACGA 145

(2) INFORMATION FOR SEQ ID NO: 4719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60  
 CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACGTGA ATGGTGTCGT 120  
 ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60

TAAC TCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 146 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60  
 TTAATTAGCT TAAACGChGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120  
 TTACAGCTAT CTTAGCTAGT TTAGCC 146

(2) INFORMATION FOR SEQ ID NO: 4722:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGGCGCT AAGTAnATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC 60  
 CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120  
 TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCAC TTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60  
 GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120  
 AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

10 CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA 60  
 TTTCAACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120  
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

15 (2) INFORMATION FOR SEQ ID NO: 4725:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

25 GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCCC CTCAAGATGA nATTTCCTCAA 60  
 CTTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120  
 30 GACATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

TTGAATTTTT GAAAAAAAAA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60  
 45 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120  
 GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180  
 CAGCATGCCG GTGTTCTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240  
 50 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT	60
AACTCTATCC AAAGACATAC AGTCAATACA AACATTACG TATCTTTACA ACAGTAATCA	120
TGCATTCTAT GATGCTTCTA ACTGAATna	149

(2) INFORMATION FOR SEQ ID NO: 4728:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA	60
TGACAATTAA TAAAGAACCG TTCTTGCGC AGCACAATGG GCGCTCACTG GCAGACTTTT	120
GTGATGCTGA CTAAAGTAA ACTATTAGAT ATTGnGTG	158

30

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTA	60
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTG GAnCGCACGT	120
GCCCTCCCAT ACCTCGGG	138

45

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCCG ATTGTCTGA ATTCGTAACC 60  
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120  
 AAAGTATTTT GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180  
 GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60  
 AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTCCCTAT CCGTCGTGGG CGTAGGAAAT 120  
 TThAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60  
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120  
 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTTCAACTA AGTCACG

137

(2) INFORMATION FOR SEQ ID NO: 4734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA 60  
 ATTGCAAATT ATCCTACTGC TGTTCCTTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG 120  
 ACAAATTTTA TTTCGTCGTC CCACCCCAAC TTG 153

(2) INFORMATION FOR SEQ ID NO: 4735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAACTTGC ACATnATTGC 60  
 AAGCTGACTT TTCGTCACTT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120  
 TACTTTGATT GATGTCCAAG TT 142

(2) INFORMATION FOR SEQ ID NO: 4736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTGCAGAC TGATAAATCG CTTCAAGAAT 60  
 TTTTGTA ACT ACCATTGCTT GTTCCGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120  
 ATCAATCCAA GCTTTTG 137

(2) INFORMATION FOR SEQ ID NO: 4737:

- (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60  
 AGTTCAGGTA AACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAT GAGCGGATGA 120  
 ACTGAGGGTA GCGGAGAAAT TCCA 144

15

(2) INFORMATION FOR SEQ ID NO: 4738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25

GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60  
 TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTCGAGGTG 120  
 30 GAACATGGTG ACATGTAATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40

GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT 60  
 45 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAATG 120  
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60  
 5 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120  
 TTTCACTTCG CCAAGCCATT TTTCTTGTTGTT TTTATTTTATT TGACGTTTAG ACATAAAAAA 180  
 GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCGG AnTAGTGGCT ACCA 234

## (2) INFORMATION FOR SEQ ID NO: 4741:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GCGCATTAC CAGAGTTGCA 60  
 TGGTCAAAAT ATATTGTTGT CATTTGAAGA TGGACGTGTA CAAAAATGCG TGTACGTGA 120  
 25 TCATGATACT GTCAn 135

## (2) INFORMATION FOR SEQ ID NO: 4742:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60  
 40 AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATCCAAT CGAACCTGGA GAnAGCTGGT 120  
 TCTCTCCGAA ATAGCTTTAG GGCTA 145

## (2) INFORMATION FOR SEQ ID NO: 4743:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGATTATCAT GGGTGC GGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120  
TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

(2) INFORMATION FOR SEQ ID NO: 4744:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60  
AGGCGATAAA ATCAnAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120  
TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAAATTG AATGAACAAA CATTCAAAAC 60  
TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120  
AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60  
GATTCAGACA GCGATTGAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC 120  
GACAnTGACT CGGATTCA 138

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CAATTATTGTA AACTGAACTT TTCGTCACTT GCTGGTGnTT GGGGACCCCA CCAACTTGGC 60  
 ACATTATTGG TAAGCTGACT TTTCGTCACT TACTGTGTTG GGGCCCCGCC AACTTGCATT 120  
 GTCTGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180  
 GCCTG 185

## (2) INFORMATION FOR SEQ ID NO: 4748:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60  
 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120  
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

## (2) INFORMATION FOR SEQ ID NO: 4749:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60  
 CTAAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120  
 AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACCT ATTTTCATGG TGTCAAAAAT 180  
 TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

## (2) INFORMATION FOR SEQ ID NO: 4750:

(A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTTAAATAAG CTTGAATTCA 60  
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTTAAATCTT 120  
 TTTATAAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

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ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60  
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120  
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180  
 TCCG 184

(2) INFORMATION FOR SEQ ID NO: 4752:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45 GGGATCTTCC GCAATGGGCG AAAGTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60  
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTna 120  
 CGGTACCTAA TCA 133

50

(2) INFORMATION FOR SEQ ID NO: 4753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTCA TGTTCCGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60  
 ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120  
 TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG 162

## (2) INFORMATION FOR SEQ ID NO: 4754:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 134 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTGATTTC CCTAGTAGC GGCGACGAAA ACGGGAAnGA GCCCAAACCA ACAAGCTTGC 60  
 TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120  
 CTTGGGAAAG ATGA 134

## (2) INFORMATION FOR SEQ ID NO: 4755:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

35 AGAGTGCCTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60  
 ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120  
 TGAAGCATGn ATCGTAAGG 139

## (2) INFORMATION FOR SEQ ID NO: 4756:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120  
 ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

(2) INFORMATION FOR SEQ ID NO: 4757:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAGAG 60  
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAnGAT 120  
 TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60  
 GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120  
 ACTGCTGTTC TCTATTTATA CCAAnATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60  
 ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACnTTATGGG 120  
 ATTTGCT 127

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCTCG TCGGGTTACC GAATTCAGAC AAACCTCCGnA ATGCCAATTA ATTTAACTTG 60  
 GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120  
 AGTCCCAAAT ATATGTTAAT GAAAG 145

## (2) INFORMATION FOR SEQ ID NO: 4761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCACGTC GGCTCTTCTG GCGGTTAACC CTAAAGAGCA 60  
 CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120  
 CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180  
 TTAACACACC AAAACAGCTC CCACCACCAC TAnATCGAnC AACACTAG 228

## (2) INFORMATION FOR SEQ ID NO: 4762:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCACT 60  
 ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCGTT GCAACAGCTT GAATTGTATC 120  
 AGCAGGGTTG 130

## (2) INFORMATION FOR SEQ ID NO: 4763:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60  
GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120  
GTTACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION; SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60  
CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC 120  
TACTGCCA 128

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60  
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120  
TTTCCATGTG GnaAC 135

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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GATTCTCACC CGTCTTTCGC TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60  
 CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120  
 5 CACAGC 126

## (2) INFORMATION FOR SEQ ID NO: 4767:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60  
 20 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120  
 GATTTTAAAC 130

## (2) INFORMATION FOR SEQ ID NO: 4768:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 142 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

35 GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60  
 AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120  
 TAGGGCACCT ATTTTCCTAT CT 142

## (2) INFORMATION FOR SEQ ID NO: 4769:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

50 CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60  
 CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

## (2) INFORMATION FOR SEQ ID NO: 4770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60  
 ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120  
 TAGAGCTATT AAGCGTnGCC ATGAG 145

## (2) INFORMATION FOR SEQ ID NO: 4771:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60  
 GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120  
 ATGTGGGA 128

## (2) INFORMATION FOR SEQ ID NO: 4772:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTGGGCTA 60  
 ATGCCTCCAT CGTGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTGGTGT 120  
 GTACTT 126

## (2) INFORMATION FOR SEQ ID NO: 4773:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60  
 10 GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAGAn ACCTTGCGGT CTCAATGCGG 120  
 CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

25 ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60  
 TGCATCTTnA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120  
 TACG 124

30

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

40

ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60  
 ACCAACACCA CCGACACCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC 120  
 45 AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

CCCGCTAGTC TCCACCATTT ATTTTTCACA CGATGAACAT TGAAAACTnA ATACAATATG 60  
 CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120  
 5 AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60  
 20 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG GACGCTGGAT GTGCGAAACG 120  
 TTGGGGGTTC AACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60  
 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCACTGCTC 120  
 CCT 123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAACTATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60  
 AACAAATATAG CTCAGGTATT ACGTTTTCAT CTAAATATTT ATTAAGATT GCAATCATCC 120

## (2) INFORMATION FOR SEQ ID NO: 4780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCGACTAGT GAGCTATTAC 60  
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120  
 TCCTTTT 127

## (2) INFORMATION FOR SEQ ID NO: 4781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60  
 GTCTTATTTT TTAAAGTAT TTAAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120  
 CGAGACTCC 129

## (2) INFORMATION FOR SEQ ID NO: 4782:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCTG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60  
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTAT GTTTGnTTTG 120  
 GTCAGATTTA GGACCA 136

## (2) INFORMATION FOR SEQ ID NO: 4783:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60  
10 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60  
25 nATCCCATTG CATCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120  
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60  
40 ATGACAATTT TATCTGCAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnCAACAC TTTATCGTGG TGGGGAGACA GTGTTTCAGGC GGGCCAGTTT 60  
55

AATCATTTCAT AGAGTGT

137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTAAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AnATACCTTT 60

TTCATCTTGG TCTTGGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCAGT 60

TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCG 120

GCCACACATA GCTACCCAGC T 141

(2) INFORMATION FOR SEQ ID NO: 4789:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTTCAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60

AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120

GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATTT TTATGGAGAG TTTGATCCTG 60  
GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120  
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60  
TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCCTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60  
AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120  
CGn 123

45

(2) INFORMATION FOR SEQ ID NO: 4793:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

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AGTTTTGAAT GTTTGTTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120  
nCCCTGATAAC 130

(2) INFORMATION FOR SEQ ID NO: 4794:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60  
TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

(2) INFORMATION FOR SEQ ID NO: 4795:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAAA ATTCCCAATT TTTTTGGGG GGTGGAAT TTAAAAATTT GGTTTTTTAAC 60  
CCAAAGGCC TTTTCCCAA AATTTAAATT CCCTTAAAAA TTTAAATTT GGAATTTTT 120  
TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCA ATTTTTTAATT TAACCCTTAA 180  
AACCCCCAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA 224

(2) INFORMATION FOR SEQ ID NO: 4796:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60  
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGCAGAT 120

(2) INFORMATION FOR SEQ ID NO: 4797:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG 60  
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120  
 ATCTG 125

15 (2) INFORMATION FOR SEQ ID NO: 4798:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

25

CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60  
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

30 (2) INFORMATION FOR SEQ ID NO: 4799:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 116 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

40

CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60  
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

45 (2) INFORMATION FOR SEQ ID NO: 4800:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

55

TCAGTGCAT GATTCTGAA ATTGAAACGC AAGATTTCGA TATCGAnCAC CT

112

(2) INFORMATION FOR SEQ ID NO: 4801:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60  
 ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AnTCGTTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT 60  
 TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAATTT AACGTCTTCT GCAGTCGCAC 120  
 CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180  
 CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60  
 AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60

10 GTTAGGGGTT TCCGCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60

25 CCAGGAAAGT CGCCTTCGCC ACTGGTGTTT CTCCATATCT CTGCGCAT 108

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60

40 GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60

55 TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

## (2) INFORMATION FOR SEQ ID NO: 4808:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60

ATCATTGCTA GCTTTTCTTG TATTAACTGA TANTTACTAA TTGGTTTGCC GAATTGCT 118

## (2) INFORMATION FOR SEQ ID NO: 4809:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTTC 60

TCCnATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG 120

TACCTGACTT CAACTGACCA GGGTAGACAC 150

## (2) INFORMATION FOR SEQ ID NO: 4810:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA 60

AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

## (2) INFORMATION FOR SEQ ID NO: 4811:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCTG AGGAAGACAC 60  
 5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60  
 20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120  
 ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60  
 35 TAGCCCTAAA GCTATTTCGG AGAGAACCAG CTATCTCCAG GTTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60  
 50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GCGGGCGGTT GAACCCGTCA TTCTGCACCA 60  
 TTTATTCTTA CATATTGCCG GnCTAGCTCA ATTGGTAGAG CAACTGACCT TGTAATCAGT 120  
 AGGTT 125

## 15 (2) INFORMATION FOR SEQ ID NO: 4816:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60  
 CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT 104

## 30 (2) INFORMATION FOR SEQ ID NO: 4817:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

GTCGGGTAAAG TTCCGGCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG 60  
 ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

## 45 (2) INFORMATION FOR SEQ ID NO: 4818:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTC 120

A 121

(2) INFORMATION FOR SEQ ID NO: 4819:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

(2) INFORMATION FOR SEQ ID NO: 4820:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCCGGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

(2) INFORMATION FOR SEQ ID NO: 4821:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

TCGTAGTGGT TTCCAACCAA GTTTTATATA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

(2) INFORMATION FOR SEQ ID NO: 4822:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60

10 AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60

25 TTTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC 60

CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACTAGAGn 108

40

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60

nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT 116

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60  
 ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120  
 ATCCTTGTAT TCGTGTCAT AnAGTCTTTG CTCCTTGCAC 160

## (2) INFORMATION FOR SEQ ID NO: 4827:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60  
 AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

## (2) INFORMATION FOR SEQ ID NO: 4828:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATAATC CAAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60  
 TCAGAAAGCT TTTGATTAAAC TTAAAGTAT nCCCAATTAT AAT 103

## (2) INFORMATION FOR SEQ ID NO: 4829:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGACCGAACT GTCTCAGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60

GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTGTGTTGGGG CCCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60

TTTCGTTTCAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60

AGGTGCCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TThTAGAATG AACCGGCGAG TTACGATTTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60

TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60  
 CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120  
 TTTTCAGCAT CAATTTGATC AATC 144

10 (2) INFORMATION FOR SEQ ID NO: 4834:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60  
 GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

25 (2) INFORMATION FOR SEQ ID NO: 4835:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60  
 CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTTGnCTT GACCTCGCGG 60  
 TTTCGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAAA 109

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60  
 CGGAATTTC AATTGCAngC TACAGTAAAG CTCCACGGGG GTC 103

## (2) INFORMATION FOR SEQ ID NO: 4838:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAAATATTT 60  
 GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120

A 121

## (2) INFORMATION FOR SEQ ID NO: 4839:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60  
 ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG 104

## (2) INFORMATION FOR SEQ ID NO: 4840:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60  
 TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTGGGCTTT 120  
 CTAACCC 127

## (2) INFORMATION FOR SEQ ID NO: 4841:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTAGAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT 60  
 CATTCACTCA ACTACTGCCA ATATAATATT GnAAACTATA GGACATTTAT TAGTGTTC 120  
 GTTCT 125

## (2) INFORMATION FOR SEQ ID NO: 4842:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTACCCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60  
 CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

## (2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60  
 TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

## (2) INFORMATION FOR SEQ ID NO: 4844:

- (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

10 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60  
 AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

25 GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60  
 CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

40 CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60  
 AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATThTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

55 GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCTAA 60

## (2) INFORMATION FOR SEQ ID NO: 4848:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTTGGAAC GCACGTGnCC CTGCCCATAC 60  
 CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCATG 120  
 CCAGCAACGC GATTACC 137

## (2) INFORMATION FOR SEQ ID NO: 4849:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTAGTTACCG 60  
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

## (2) INFORMATION FOR SEQ ID NO: 4850:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60  
 TTATAGTTAC GGTCCGCCGT TTACTGGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA 120  
 CTCCT 125

## (2) INFORMATION FOR SEQ ID NO: 4851:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTTGG TGGGAGAACC 60  
TAAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC 96

(2) INFORMATION FOR SEQ ID NO: 4852:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

20 ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60  
GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

(2) INFORMATION FOR SEQ ID NO: 4853:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

35 CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTTA 60  
ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

(2) INFORMATION FOR SEQ ID NO: 4854:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

50 GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACGAGACC GTGAGGAAAG 60  
GTGAAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60  
 CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

25 CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60  
 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120  
 CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60  
 TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCCTG CGGCTT

106

(2) INFORMATION FOR SEQ ID NO: 4859:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAACTCGCC GGTTCATTCT ACAAAGGGC ACGCCAATCA CCCATTAAACG GGCTCCTGAA 60  
 CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCTA CTCCCCCTTT CCGGGGTnGC 120  
 TTTTTCACCC TTTTTCCTCC TCCACGGTTA CT 152

(2) INFORMATION FOR SEQ ID NO: 4860:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAGGAA TTCTAAGGTG AGCGAGCGAA 60  
 CTCTCGTTAA GGAACCTCGC AAACCTGACCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60  
 AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTC AAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60  
 CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60  
 TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120  
 GCAnTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60  
 TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 115 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60  
TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 90 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60  
CGGTTTAGCA GAGACCTGTG TTTTGATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 87 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTGCGT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60  
GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 165 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACTACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120  
 AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

(2) INFORMATION FOR SEQ ID NO: 4870:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTTT ATAACATTAA GTAATAACTT TTTTATCTT GTCCATTTTA TTTTnAACC 60  
 AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

(2) INFORMATION FOR SEQ ID NO: 4871:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCCTG CGGCTCTTCT 60  
 GGGCGTTAAC CCTAAAGAGC ACCC 84

(2) INFORMATION FOR SEQ ID NO: 4872:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGTA ACTGCATCTT CACAGGTACT 60  
 ATGATTTTAC CGATCTCTCh ATGAACAGTG CCAAATCGTA C 101

(2) INFORMATION FOR SEQ ID NO: 4873:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GGCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTTAATC 60  
GATGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

20 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTTCG ATCCCGCTAG TCTCCACCAT 60  
TATTTGTACA TTGAAACTA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

30 TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60  
35 CGAACTGAAT AAATAAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60  
50 TGGAACATAG ATTAAGTTAT TAAGGGC 87

(2) INFORMATION FOR SEQ ID NO: 4877:

(A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60  
 CGGGGAGGTT TgncCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

ATTATATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTGTCT 60  
 CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60  
 AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

CTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60



## (2) INFORMATION FOR SEQ ID NO: 4881:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60  
CTTCACGCTT CTTTCGCATTA 80

## (2) INFORMATION FOR SEQ ID NO: 4882:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCACGG CTCAACCGTG GAGGGTCATT GGAAACTGGA AACTTGAGT 60  
GCAGAAGAGG AAAGTGGGTT CCATGT 86

## (2) INFORMATION FOR SEQ ID NO: 4883:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60  
AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120  
CGGTAA 127

## (2) INFORMATION FOR SEQ ID NO: 4884:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60  
 CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60  
 GTGGATTGTC CTTTGGAAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTTCCG GTGGTGCACT TGCGACCAAC AATGGGTTGG AGATTGGATT 60  
 TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAAnTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 60  
 ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGTCCGA 60

25

GTTCCCTAAC GAGAGT 76

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACCTTA CCATTAATGT GGCAAGT 117

40

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

55

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 88 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60  
AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 102 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTTCG GCAGTTCGAA 60  
TCTGCCCCC TCCATTTATT ATTTTnAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 78 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60  
GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 141 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120  
 TTATACCGAG TnGGAATCTC A 141

(2) INFORMATION FOR SEQ ID NO: 4896:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTTCGGATTT AATTGATTC ATTTGTTGCG TAATTTTCAGA AGCCATTTTA TGAAAAGAGT 60  
 GATTTAATTC ATAAATTTCT 80

(2) INFORMATION FOR SEQ ID NO: 4897:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60  
 AAACCAATTA GTA 73

(2) INFORMATION FOR SEQ ID NO: 4898:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60  
 TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60  
 TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGCGGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60  
 CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60  
 AAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60  
 CAAAACCTAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60  
 AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 TCCTCTTCTT GGCTCTGCTT CTATTGCGCT CTAATGTGGC TTTTGTGTTGT AATAAGTTAT 120  
 GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

(2) INFORMATION FOR SEQ ID NO: 4905:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 75 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGAAGTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60  
 TTATCGTGGT GGGGA 75

(2) INFORMATION FOR SEQ ID NO: 4906:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

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ACTCAGACAG TGA CTCAGAT CAGATAGTGn CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGTACAC GTGCTACTAA  
 AGGTTTACCA

60

70

(2) INFORMATION FOR SEQ ID NO: 4908:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTTC GGTGGGACAC AATAGTGTG  
 ACTTTGAAGA AGATACACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC  
 C

60

120

121

(2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG  
 TTAAGTCCCG

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(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

GGACACCCGG AGAACTGAAA CATTGTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60  
 TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

nTCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60  
 TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT AACTTTGAT 120  
 GTAACTTTG GCACATCAGC TTTTAGTGTG TTTGCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60  
 AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA 60  
 GCGGAACGT 69

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 69 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60  
ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 70 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTTCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60  
CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 67 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTTCACTCC 60  
CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 161 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120  
 GGCGCACGTA GGCGATGATA CAGGTTATAT CCTnACACCT A 161

(2) INFORMATION FOR SEQ ID NO: 4918:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60  
 ACATATGT 68

(2) INFORMATION FOR SEQ ID NO: 4919:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60  
 AGTGACAATA CTTCAGGG 78

(2) INFORMATION FOR SEQ ID NO: 4920:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTTCGATTCG 60  
 TACTTCGC 68

(2) INFORMATION FOR SEQ ID NO: 4921:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60  
TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

20 GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60  
GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

35 GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60  
TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

50 GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60  
TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60  
 ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTG GGCAGTATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60  
 CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60  
 CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

## (2) INFORMATION FOR SEQ ID NO: 4929:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60  
GTGGGTCCCG ACACAGAGAA ATT 83

## (2) INFORMATION FOR SEQ ID NO: 4930:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGGITTT GGGACCAAGG GGTCGCAGTT CGAATCCTGT CTTCCCGATT 60  
ACTCTA 66

## (2) INFORMATION FOR SEQ ID NO: 4931:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60  
GACCG 65

## (2) INFORMATION FOR SEQ ID NO: 4932:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60  
 CACCAGTGGG CGA 73

(2) INFORMATION FOR SEQ ID NO: 4933:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60  
 GTCTG 65

(2) INFORMATION FOR SEQ ID NO: 4934:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60  
 TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

(2) INFORMATION FOR SEQ ID NO: 4935:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60  
 GGATAACGGT TG 72

(2) INFORMATION FOR SEQ ID NO: 4936:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT 60  
CTGC 64

(2) INFORMATION FOR SEQ ID NO: 4937:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

20 ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60  
TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

35 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60  
GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

50 TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60  
CCT 63

(2) INFORMATION FOR SEQ ID NO: 4940:



- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60  
TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCTTAG TAGCGGCGAG 60  
CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60  
TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

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## (2) INFORMATION FOR SEQ ID NO: 4944:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60  
 GACGAATACG TAATTGA 77

## (2) INFORMATION FOR SEQ ID NO: 4945:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT 60  
 CAGGTAACAC TGAAT 75

## (2) INFORMATION FOR SEQ ID NO: 4946:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60  
 TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120  
 TACAGCGCTG AACT 135

## (2) INFORMATION FOR SEQ ID NO: 4947:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTCC TTTCTCTTCC 60  
 5 T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAAT 60  
 20 TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60  
 35 CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60  
 50 TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GCGGAGGAA GAGGGATTG AACCCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

25

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

40

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTGGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

10

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

20

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 60

35

TTTCAATGTA CAATTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAA 59

50

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

5 GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

30 ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

55

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG 60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG 59

(2) INFORMATION FOR SEQ ID NO: 4965:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG 59

(2) INFORMATION FOR SEQ ID NO: 4966:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTT TCAGTTCGG 59

(2) INFORMATION FOR SEQ ID NO: 4967:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTCGCT ATGTATATCG CATTAAACGT 60

## (2) INFORMATION FOR SEQ ID NO: 4968:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTT TAGAGG CGACGCCAG TCAA CTGCC CGCTGACACT GTCTCCACC 60

## (2) INFORMATION FOR SEQ ID NO: 4969:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

## (2) INFORMATION FOR SEQ ID NO: 4970:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACG 65

## (2) INFORMATION FOR SEQ ID NO: 4971:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60



## (2) INFORMATION FOR SEQ ID NO: 4972:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60  
AGGTAGG 67

## (2) INFORMATION FOR SEQ ID NO: 4973:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACATGC ATAAGAAATA CTAATTTTC 58

## (2) INFORMATION FOR SEQ ID NO: 4974:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

## (2) INFORMATION FOR SEQ ID NO: 4975:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

## (2) INFORMATION FOR SEQ ID NO: 4976:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTTCGA CCCTGACTCG ACTTG TAGGT CTCGCAGTCA AGCTCCCTT 59

## (2) INFORMATION FOR SEQ ID NO: 4977:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT 58

## (2) INFORMATION FOR SEQ ID NO: 4978:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

## (2) INFORMATION FOR SEQ ID NO: 4979:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

## (2) INFORMATION FOR SEQ ID NO: 4980:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTGA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

AAGATGAATC AAAGT 75

25

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

55

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60  
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTGGATCG TAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTTG CGCAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA 57

10

(2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

20

TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG 57

(2) INFORMATION FOR SEQ ID NO: 4990:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT 60

35

G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTC 60

50

ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT 57

10

(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

20

CCAATGCCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG 57

(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG 57

35

(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

45

CAAACCTCTCG TGGTGTGACG GGCGGTGTGG TACAAGCCCC GGAACGTAT TCACCGTAGC 60

ATGCCGGTCT ACG 73

50

(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

5 ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60  
TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

20 ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

45 GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

(2) INFORMATION FOR SEQ ID NO: 5000:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC

56

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC

56

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCCGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG

56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA

56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:



## (2) INFORMATION FOR SEQ ID NO: 5005:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCAC TAGAA GCCGATG 57

## (2) INFORMATION FOR SEQ ID NO: 5006:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCTG 57

## (2) INFORMATION FOR SEQ ID NO: 5007:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA 60

AACCAAAGA 69

## (2) INFORMATION FOR SEQ ID NO: 5008:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT 57

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC

56

(2) INFORMATION FOR SEQ ID NO: 5010:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC

60

TTGGG

65

(2) INFORMATION FOR SEQ ID NO: 5011:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA

56

(2) INFORMATION FOR SEQ ID NO: 5012:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 60 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTGTATAA ACAGTCGCTT

60

(2) INFORMATION FOR SEQ ID NO: 5013:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60  
ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCCACCACT GGCCTCCACG TAAGCTAGCG CTTACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTGGGA nCAGACATGG GTGATAAGGT CGTGTTTCGAA 60  
40 GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT 56

55

(2) INFORMATION FOR SEQ ID NO: 5017:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT 60  
TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

40

(2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50 TACGGCGTTT AGTATTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA 55

10

(2) INFORMATION FOR SEQ ID NO: 5022:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

AGAGTTCACA TCGACGGGGA GGT TTGGCAC CTCGATGTCG GCTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

35

(2) INFORMATION FOR SEQ ID NO: 5024:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGGAATT 60  
CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60  
AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

(2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTA CTTACTT ATCTAGTTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

## (2) INFORMATION FOR SEQ ID NO: 5034:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC 54

## (2) INFORMATION FOR SEQ ID NO: 5035:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA 54

## (2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAACCTCTG TGTTCGGCAT GGGAACAGGT GTGA 54

## (2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG 56

## (2) INFORMATION FOR SEQ ID NO: 5038:



- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

10 GACCGGGATG GACATACCTC TGGTGTACCA GTTGTCTGTG CCAACGCATA AGCT 54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG 54

25 (2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35

TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

40 (2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

50

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

10

(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT

59

35

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

60

TT

62

50

(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTTTGTAC CCGCAGTCAA CTTAGAGTGC CCA

53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG

53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA

53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT

59

(2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAGAC GTACTTCATG 60  
TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
10     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
25     (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

30 CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

(2) INFORMATION FOR SEQ ID NO: 5053:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
35     (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

- 45 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
50     (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

## (2) INFORMATION FOR SEQ ID NO: 5055:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG

53

## (2) INFORMATION FOR SEQ ID NO: 5056:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA

60

CAA

63

## (2) INFORMATION FOR SEQ ID NO: 5057:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC

54

## (2) INFORMATION FOR SEQ ID NO: 5058:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG

53

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA 59

(2) INFORMATION FOR SEQ ID NO: 5060:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT 53

(2) INFORMATION FOR SEQ ID NO: 5061:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC 55

(2) INFORMATION FOR SEQ ID NO: 5062:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 52 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT CA 52

(2) INFORMATION FOR SEQ ID NO: 5063:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 52 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTTGAC GTTTTAGACA TA

52

10

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

20

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAAC

60

TTGGAGCGCC TCCGTT

76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

35

CCACCGCTTG TCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG

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(2) INFORMATION FOR SEQ ID NO: 5067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCCGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA

52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CAC TTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA

52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGCCTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCCT TTGG

74

(2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA

52

(2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGTTGG CACTGTCTCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5079:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGACC AGAAATGATG GTATTTAATA AT

52

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 52 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG

52

(2) INFORMATION FOR SEQ ID NO: 5081:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 52 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

52

(2) INFORMATION FOR SEQ ID NO: 5082:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

56

(2) INFORMATION FOR SEQ ID NO: 5083:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 62 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTCCTA

60

CG

62

(2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10

GTGTACCACT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG

52

(2) INFORMATION FOR SEQ ID NO: 5085:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC

60

CCGAGGAGCG GATTAACA

25

78

(2) INFORMATION FOR SEQ ID NO: 5086:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT

52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50

AAGTTGTTCT CAGTTCGGAT TGTAAGTCTGC AACTCGACTA CATGAAGCTG G

51

(2) INFORMATION FOR SEQ ID NO: 5088:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T 51

10

(2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20

AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G 51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGGTC C 51

35

(2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

45

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T 51

(2) INFORMATION FOR SEQ ID NO: 5092:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA

55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A

51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT

60

ATTGTGCCAC CGATTGA

77

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 64 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60  
CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 58 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:



- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10 ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT

50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA

50

(2) INFORMATION FOR SEQ ID NO: 5107:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA

50

(2) INFORMATION FOR SEQ ID NO: 5109:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCGGT CTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCCGCCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCAATTG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

50

(2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 60 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

60

(2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

50

(2) INFORMATION FOR SEQ ID NO: 5121:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

60

T

61

(2) INFORMATION FOR SEQ ID NO: 5122:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

10 TAGCGACTCA GATTGAGACA GCGATTGAGA CAGCGACTCA GACTGAGATA

50

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT

50

(2) INFORMATION FOR SEQ ID NO: 5124:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

35

CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCAGAGAAG GTCTCTATCT

60

(2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT

60

50

AGAA

64

(2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT

57

10

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

20

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG

50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCAGTTGTTG CTCGTTCAA TTTTATGGGG CCATTTATGG

50

35

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A

51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

## (2) INFORMATION FOR SEQ ID NO: 5135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

## (2) INFORMATION FOR SEQ ID NO: 5136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

## (2) INFORMATION FOR SEQ ID NO: 5137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

## (2) INFORMATION FOR SEQ ID NO: 5138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

50

## (2) INFORMATION FOR SEQ ID NO: 5139:



- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10 GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC 52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT 56

25 (2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT 56

50

(2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAAC AATTTCATC CAAACCTTCA TCACTCACGC GCGTTGCTC CGTCAGCTTT 60  
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAAACTG AAACATCTTA AGTACCCGGA GnaAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

## (2) INFORMATION FOR SEQ ID NO: 5152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAATT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

## (2) INFORMATION FOR SEQ ID NO: 5153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60

ATACA 65

## (2) INFORMATION FOR SEQ ID NO: 5154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

## (2) INFORMATION FOR SEQ ID NO: 5155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

## (2) INFORMATION FOR SEQ ID NO: 5156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC 58

## (2) INFORMATION FOR SEQ ID NO: 5157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT G 51

## (2) INFORMATION FOR SEQ ID NO: 5158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC 50

## (2) INFORMATION FOR SEQ ID NO: 5159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T 51

## (2) INFORMATION FOR SEQ ID NO: 5160:

- (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTCGCTG CCCTTTGTAT 60

T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

25 AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

35 CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

(2) INFORMATION FOR SEQ ID NO: 5163:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

50 CTTGATCTGT ATTTAAATG ATATTTTCTA TCITTTCTTT ATTATTAACG TCTATGACGT 60

CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

55

- (A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60  
AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAAGTG CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60  
AA 62

40

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10 TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAACTAG ATAAGTAGTA AATATA 56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA 55

(2) INFORMATION FOR SEQ ID NO: 5170:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35

CTACTGCTGC ATATGCCGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA 52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAAGTTC TnAGGCAATG TAAAAAGCT GATTCTATT 50

(2) INFORMATION FOR SEQ ID NO: 5172:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

5 AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTCGAAG 60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn 50

(2) INFORMATION FOR SEQ ID NO: 5174:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

30 CAACTCTCGT TAAGGAACTC GGCAAATAC CCCGTAAGTT CGGAGTAGGT CTCTTTA 57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA 60

(2) INFORMATION FOR SEQ ID NO: 5176:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

55

GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTC TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCGGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAAGTTC ATACCTTTTA ACATATTTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAAGTGT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

GTTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC

GCAATAT

(2) INFORMATION FOR SEQ ID NO: 5182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCACTAG CGAAGGCAAC TTTCT

(2) INFORMATION FOR SEQ ID NO: 5183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

(2) INFORMATION FOR SEQ ID NO: 5184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

CC

62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAAGTTGGGCACT CTAAGTTGAC TGCCGnGnC ACCnAAGAAG

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

54

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGACCG ACTACAGCCC AGATCGATGA

50

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

60

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu  
 1 5 10 15

## EP 0 786 519 A2

	20	25	30
5	Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45		
	Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60		
10	Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80		
	Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95		
15	Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110		
	Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125		
20	Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140		
	Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160		
25	Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175		
	Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190		
30	Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205		
	Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220		
	Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240		
40	Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255		
	Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270		
45	Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285		
	Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300		
50	Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320		

55

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

Met	Asn	Lys	Val	Ile	Lys	Met	Leu	Val	Val	Thr	Leu	Ala	Phe	Leu	Leu	1	5	10	15
Val	Leu	Ala	Gly	Cys	Ser	Gly	Asn	Ser	Asn	Lys	Gln	Ser	Ser	Asp	Asn	20	25	30	
Lys	Asp	Lys	Glu	Thr	Thr	Ser	Ile	Lys	His	Ala	Met	Gly	Thr	Thr	Glu	35	40	45	
Ile	Lys	Gly	Lys	Pro	Lys	Arg	Val	Val	Thr	Leu	Tyr	Gln	Gly	Ala	Thr	50	55	60	
Asp	Val	Ala	Val	Ser	Leu	Gly	Val	Lys	Pro	Val	Gly	Ala	Val	Glu	Ser	65	70	75	80
Trp	Thr	Gln	Lys	Pro	Lys	Phe	Glu	Tyr	Ile	Lys	Asn	Asp	Leu	Lys	Asp	85	90	95	
Thr	Lys	Ile	Val	Gly	Gln	Glu	Pro	Ala	Pro	Asn	Leu	Glu	Glu	Ile	Ser	100	105	110	
Lys	Leu	Lys	Pro	Asp	Leu	Ile	Val	Ala	Ser	Lys	Val	Arg	Asn	Glu	Lys	115	120	125	
Val	Tyr	Asp	Gln	Leu	Ser	Lys	Ile	Ala	Pro	Thr	Val	Ser	Thr	Asp	Thr	130	135	140	
Val	Phe	Lys	Phe	Lys	Asp	Thr	Thr	Lys	Leu	Met	Gly	Lys	Ala	Leu	Gly	145	150	155	160
Lys	Glu	Lys	Glu	Ala	Glu	Asp	Leu	Leu	Lys	Lys	Tyr	Asp	Asp	Lys	Val	165	170	175	
Ala	Ala	Phe	Gln	Lys	Asp	Ala	Lys	Ala	Lys	Tyr	Lys	Asp	Ala	Trp	Pro	180	185	190	
Leu	Lys	Ala	Ser	Val	Val	Asn	Phe	Arg	Ala	Asp	His	Thr	Arg	Ile	Tyr	195	200	205	
Ala	Gly	Gly	Tyr	Ala	Gly	Glu	Ile	Leu	Asn	Asp	Leu	Gly	Phe	Lys	Arg	210	215	220	
Asn	Lys	Asp	Leu	Gln	Lys	Gln	Val	Asp	Asn	Gly	Lys	Asp	Ile	Ile	Gln	225	230	235	240
Leu	Thr	Ser	Lys	Glu	Ser	Ile	Pro	Leu	Met	Asn	Ala	Asp	His	Ile	Phe	245	250	255	

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys  
260 265 270

Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala  
275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn  
290 295 300

Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr  
305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys  
325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile  
1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly  
20 25 30

Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr  
35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe  
50 55 60

Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val  
65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val  
85 90 95

Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala  
100 105 110

Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly  
115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile  
130 135 140

Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn  
145 150 155 160



Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn  
 165 170 175  
 5 Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala  
 180 185 190  
 Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr  
 195 200 205  
 10 Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu  
 210 215 220  
 Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp  
 225 230 235 240  
 15 Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu  
 245 250 255  
 Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val  
 260 265 270  
 20 Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly  
 275 280 285  
 Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn  
 290 295 300  
 25 Lys Asn Leu Arg Leu Xaa Ser His Lys Gln  
 305 310

## (2) INFORMATION FOR SEQ ID NO:5195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala  
 1 5 10 15  
 45 Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser  
 20 25 30  
 Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp  
 35 40 45  
 50 Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn  
 50 55 60  
 55 Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe  
 65 70 75 80

Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser  
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys  
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro  
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala  
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys  
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala  
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn  
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile  
195 200 205

25 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile  
210 215 220

Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile  
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp  
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys  
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys  
275 280

## (2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val  
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys  
20 25 30

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys  
 35 40 45  
 5 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr  
 50 55 60  
 Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile  
 65 70 75 80  
 10 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys  
 85 90 95  
 Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro  
 100 105 110  
 15 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys  
 115 120 125  
 Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe  
 130 135 140  
 20 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val  
 145 150 155 160  
 Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp  
 165 170 175  
 25 Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr  
 180 185 190  
 Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile  
 195 200 205  
 Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala  
 210 215 220  
 35 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln  
 225 230 235 240  
 Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp  
 245 250 255  
 40 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala  
 260 265 270  
 Lys

## (2) INFORMATION FOR SEQ ID NO:5197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

5	Met	Lys	Lys	Ile	Lys	Tyr	Ile	Leu	Val	Val	Phe	Val	Leu	Ser	Leu	Thr	1	5	10	15
	Val	Leu	Ser	Gly	Cys	Ser	Leu	Pro	Gly	Leu	Gly	Ser	Lys	Ser	Thr	Lys	20	25	30	
10	Asn	Asp	Val	Lys	Ile	Thr	Ala	Leu	Ser	Thr	Ser	Glu	Ser	Gln	Ile	Ile	35	40	45	
	Ser	His	Met	Leu	Arg	Leu	Leu	Ile	Glu	His	Asp	Thr	His	Gly	Lys	Ile	50	55	60	
15	Lys	Pro	Thr	Leu	Val	Asn	Asn	Leu	Gly	Ser	Ser	Thr	Ile	Gln	His	Asn	65	70	75	80
	Ala	Leu	Ile	Asn	Gly	Asp	Ala	Asn	Ile	Ser	Gly	Val	Arg	Tyr	Asn	Gly	85	90	95	
20	Thr	Asp	Leu	Thr	Gly	Ala	Leu	Lys	Glu	Ala	Pro	Ile	Lys	Asn	Pro	Lys	100	105	110	
	Lys	Ala	Met	Ile	Ala	Thr	Gln	Gln	Gly	Phe	Lys	Lys	Lys	Phe	Asp	Gln	115	120	125	
25	Thr	Phe	Phe	Asp	Ser	Tyr	Gly	Phe	Ala	Asn	Thr	Tyr	Ala	Phe	Met	Val	130	135	140	
	Thr	Lys	Glu	Thr	Ala	Lys	Lys	Tyr	His	Leu	Glu	Thr	Val	Ser	Asp	Leu	145	150	155	160
30	Ala	Lys	His	Ser	Lys	Asp	Leu	Arg	Leu	Gly	Met	Asp	Ser	Ser	Trp	Met	165	170	175	
	Asn	Arg	Lys	Gly	Asp	Gly	Tyr	Glu	Gly	Phe	Lys	Lys	Glu	Tyr	Gly	Phe	180	185	190	
35	Asp	Phe	Gly	Thr	Val	Arg	Pro	Met	Gln	Ile	Gly	Leu	Val	Tyr	Asp	Ala	195	200	205	
40	Leu	Asn	Ser	Glu	Lys	Leu	Asp	Val	Ala	Leu	Gly	Tyr	Ser	Thr	Asp	Gly	210	215	220	
	Arg	Ile	Ala	Ala	Tyr	Asp	Leu	Lys	Val	Leu	Lys	Asp	Asp	Lys	Gln	Phe	225	230	235	240
45	Phe	Pro	Pro	Tyr	Ala	Ala	Ser	Ala	Val	Ala	Thr	Asn	Glu	Leu	Leu	Arg	245	250	255	
	Gln	His	Pro	Glu	Leu	Lys	Thr	Thr	Ile	Asn	Lys	Leu	Thr	Gly	Lys	Ile	260	265	270	
50	Ser	Thr	Ser	Glu	Met	Gln	Arg	Leu	Asn	Tyr	Glu	Ala	Asp	Gly	Lys	Gly	275	280	285	
55	Lys	Glu	Pro	Ala	Val	Val	Ala	Glu	Glu	Phe	Leu	Lys	Lys	His	His	Tyr	290	295	300	

Phe Asp Lys Gln Lys Gly Gly His Lys  
305 310

## (2) INFORMATION FOR SEQ ID NO:5198:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala  
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys  
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr  
25 35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu  
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala  
30 65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala  
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp  
35 100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile  
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys  
40 130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala  
45 145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp  
165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile  
50 180 185 190

Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala  
195 200 205

Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys  
55 210 215 220

Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu  
 225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys  
 245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu  
 260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu  
 275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala  
 1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys  
 20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr  
 35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu  
 50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala  
 65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala  
 85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp  
 100 105 110

Met Lys Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile  
 115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys  
 130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala  
 145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp  
 165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile  
 180 185 190  
 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala  
 195 200 205  
 Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys  
 210 215 220  
 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu  
 225 230 235 240  
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys  
 245 250 255  
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu  
 260 265 270  
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu  
 275 280

## (2) INFORMATION FOR SEQ ID NO:5200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu  
 1 5 10 15  
 Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn  
 20 25 30  
 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn  
 35 40 45  
 Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn  
 50 55 60  
 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys  
 65 70 75 80  
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu  
 85 90 95  
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn  
 100 105 110  
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys  
 115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn  
130 135 140

5 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile  
145 150 155 160

Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro  
165 170 175

10 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu  
180 185 190

Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys  
195 200 205

15

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

20 (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

30 Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile  
1 5 10 15

Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser  
20 25 30

35 Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn  
35 40 45

Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu  
40 50 55 60

Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn  
65 70 75 80

45 Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp  
85 90 95

Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu  
100 105 110

50 Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser  
115 120 125

Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser  
130 135 140

55 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr



Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys  
                                   165                                  170                                  175

Arg Ala Cys Glu Pro Asp Lys Tyr  
                                   180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile  
   1                                  5                                  10                                  15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr  
                                   20                                  25                                  30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys  
                                   35                                  40                                  45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu  
                                   50                                  55                                  60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu  
   65                                  70                                  75                                  80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser  
                                   85                                  90                                  95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser  
                                   100                                  105                                  110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu  
                                   115                                  120                                  125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn  
                                   130                                  135                                  140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile  
   145                                  150                                  155                                  160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val  
                                   165                                  170                                  175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile  
                                   180                                  185                                  190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys

## (2) INFORMATION FOR SEQ ID NO:5203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

```

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
1           5           10           15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
20           20           25           30

Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
35           40           45

Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
50           55           60

Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
65           70           75           80

Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
85           90           95

Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
100          105          110

Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
115          120          125

Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
130          135          140

Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
145          150          155          160

Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
165          170          175

Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
180          185          190

Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
195          200          205

Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
210          215          220

```

225                      230                      235                      240  
 Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro  
                                  245                      250                      255  
 Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln  
                                  260                      265                      270  
 Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile  
                                  275                      280

## (2) INFORMATION FOR SEQ ID NO:5204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly  
 1                      5                      10                      15  
 Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu  
                                  20                      25                      30  
 Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln  
                                  35                      40                      45  
 Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys  
                                  50                      55                      60  
 His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe Lys Asp Asn  
 65                      70                      75                      80  
 Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly  
                                  85                      90                      95  
 Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala  
                                  100                      105                      110  
 Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg  
                                  115                      120                      125  
 Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu  
                                  130                      135                      140  
 Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr  
 145                      150                      155                      160  
 Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr  
                                  165                      170                      175

180 185 190  
 Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr  
 195 200 205  
 5 Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met  
 210 215 220  
 Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val  
 10 225 230 235 240  
 Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val  
 245 250 255  
 Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys  
 15 260 265 270  
 Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn  
 275 280 285  
 20 Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val  
 290 295 300  
 His Ser Lys Asp Glu  
 305

(2) INFORMATION FOR SEQ ID NO:5205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly  
 1 5 10 15  
 Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu  
 20 25 30  
 Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln  
 35 40 45  
 Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys  
 50 55 60  
 Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met  
 65 70 75 80  
 Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser  
 85 90 95

100 105 110  
 Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His  
 115 120 125  
 5 Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp  
 130 135 140  
 Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His  
 10 145 150 155 160  
 Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln  
 165 170 175  
 15 Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys  
 180 185 190  
 Ser

20 (2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 amino acids  
 (B) TYPE: amino acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala  
 1 5 10 15  
 35 Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser  
 20 25 30  
 Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe  
 40 35 40 45  
 His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys  
 50 55 60  
 45 Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser  
 65 70 75 80  
 Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile  
 85 90 95  
 50 Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe  
 100 105 110  
 Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn  
 115 120 125  
 55

130                      135                      140  
 Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala  
 145                      150                      155                      160  
 Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu  
 165                      170                      175  
 Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp  
 180                      185                      190  
 Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn  
 195                      200                      205  
 Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp  
 210                      215                      220  
 Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn  
 225                      230                      235                      240  
 Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser  
 245                      250                      255  
 Lys Ser Lys

(2) INFORMATION FOR SEQ ID NO:5207:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 203 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile  
 1                      5                      10                      15  
 Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn  
 20                      25                      30  
 Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln  
 35                      40                      45  
 Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser  
 50                      55                      60  
 Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly  
 65                      70                      75                      80  
 Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp  
 85                      90                      95

100 105 110  
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu  
 115 120 125  
 5  
 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp  
 130 135 140  
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys  
 10 145 150 155 160  
 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu  
 165 170 175  
 15 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val  
 180 185 190  
 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr  
 195 200

20 (2) INFORMATION FOR SEQ ID NO:5208:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 amino acids  
 (B) TYPE: amino acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu  
 1 5 10 15  
 35 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp  
 20 25 30  
 40 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile  
 35 40 45  
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys  
 50 55 60  
 45 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile  
 65 70 75 80  
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu  
 85 90 95  
 50 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys  
 100 105 110  
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe  
 115 120 125  
 55

130                      135                      140  
 Ala Lys Thr Trp Lys Asp Val Asn Ser Lys Trp Pro Asp Lys Lys Ile  
 145                      150                      155                      160  
 Asn Ala Val Ser Pro Asn Ser Ser His Gly Thr Tyr Asp Phe Phe Glu  
 165                      170                      175  
 Asn Glu Val Met Asn Lys Glu Asp Ile Lys Ala Glu Lys Asn Ala Asp  
 180                      185                      190  
 Thr Asn Ala Ile Val Ser Ser Val Thr Lys Asn Lys Glu Gly Ile Gly  
 195                      200                      205  
 Tyr Phe Gly Tyr Asn Phe Tyr Val Gln Asn Lys Asp Lys Leu Lys Glu  
 210                      215                      220  
 Val Lys Ile Lys Asp Glu Asn Gly Lys Ala Thr Glu Pro Thr Lys Lys  
 225                      230                      235                      240  
 Thr Ile Gln Asp Asn Ser Tyr Ala Leu Ser Arg Pro Leu Phe Ile Tyr  
 245                      250                      255  
 Val Asn Glu Lys Ala Leu Lys Asp Asn Lys Val Met Ser Glu Phe Ile  
 260                      265                      270  
 Lys Phe Val Leu Glu Asp Lys Gly Lys Ala Ala Glu Glu Ala Gly Tyr  
 275                      280                      285  
 Val Ala Ala Pro Glu Lys Thr Tyr Lys Ser Gln Leu Asp Asp Leu Lys  
 290                      295                      300  
 Ala Phe Ile Asp Lys Asn Gln Lys Ser Asp Asp Lys Lys Ser Asp Asp  
 305                      310                      315                      320  
 Lys Lys Ser Glu Asp Lys Lys  
 325

## (2) INFORMATION FOR SEQ ID NO:5209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr  
 1                      5                      10                      15  
 Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln  
 20                      25                      30



	35	40	45
5	Asn Leu Met Met Thr Lys Lys Leu Leu Ser Gln Tyr Asn His Pro Lys 50 55 60		
	Tyr Lys Leu Glu Leu Val Lys Phe Asn Asn Trp Pro Asp Leu Met Asp 65 70 75 80		
10	Ala Leu Asn Ser Gly Arg Ile Asp Gly Ala Ser Thr Leu Ile Glu Leu 85 90 95		
	Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu 100 105 110		
15	Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu 115 120 125		
	Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His 130 135 140		
20	Arg Tyr Ser Thr His Tyr Leu Leu Leu Glu Glu Leu Arg Lys Gln Leu 145 150 155 160		
	Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu 165 170 175		
25	Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala 180 185 190		
	Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu 195 200 205		
30	Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val 210 215 220		
	Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe 225 230 235 240		
35	Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln 245 250 255		
	Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu 260 265 270		
40	Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro 275 280 285		
	Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe 290 295 300		
45	Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu 305 310 315 320		
50	Ala Ser Arg Ser		

## (2) INFORMATION FOR SEQ ID NO:5210:

55 (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val  
 1 5 10 15  
 Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser  
 15 20 25 30  
 Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys  
 35 40 45  
 Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly  
 20 50 55 60  
 Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu  
 65 70 75 80  
 Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys  
 25 85 90 95  
 Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp  
 100 105 110  
 Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys  
 30 115 120 125  
 Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln  
 35 130 135 140  
 Val Asp Tyr Trp  
 145

(2) INFORMATION FOR SEQ ID NO:5211:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp  
 1 5 10 15

55

20

25

30

His

5

## (2) INFORMATION FOR SEQ ID NO:5212:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys  
1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn  
20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly  
35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp  
50 55 60

30

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn  
65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser  
85 90 95

35

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr  
100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp  
115 120 125

40

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg  
130 135 140

45

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe  
145 150 155 160

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro  
165 170 175

50

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile  
180 185 190

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn  
195 200 205

55

EP 0 786 519 A2

	210	215	220
	Ala Glu Ala Tyr Arg	Asn Gly Leu Val	Asn Ala Pro Leu Ser Arg Leu
5	225	230	235 240
	Glu Ala Gly Ile Ala His Ser Tyr Val	Ser Gly Asn Thr Val	Trp Gln
	245	250	255
10	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly		
	260	265	270
	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp		
	275	280	285
15	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala		
	290	295	300
	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg		
	305	310	315 320
20	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val		
	325	330	335
	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp		
	340	345	350
25	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr		
	355	360	365
	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala		
	370	375	380
30	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys		
	385	390	395 400
	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn		
	405	410	415
35	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val		
	420	425	430
	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met		
	435	440	445
40	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg		
	450	455	460
	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln		
	465	470	475 480
45	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser		
	485	490	

50 (2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

55

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

5  
 10 Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu  
 1 5 10 15  
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala  
 20 25 30  
 15 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile  
 35 40 45  
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val  
 50 55 60  
 20 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly  
 65 70 75 80  
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys  
 85 90 95  
 25 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu  
 100 105 110  
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe  
 115 120 125  
 30 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val  
 130 135 140  
 35 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp  
 145 150 155 160  
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr  
 165 170 175  
 40 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His  
 180 185 190  
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln  
 195 200 205  
 45 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu  
 210 215 220  
 50 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala  
 225 230 235 240  
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe  
 245 250 255  
 55 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn  
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys  
 290 295

## (2) INFORMATION FOR SEQ ID NO:5214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn  
 1 5 10 15  
 Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr  
 20 25 30  
 Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro  
 35 40 45  
 Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn  
 50 55 60  
 Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro  
 65 70 75 80  
 Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp  
 85 90 95  
 Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala  
 100 105 110  
 Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln  
 115 120 125  
 Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg  
 130 135 140  
 Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys  
 145 150 155 160  
 Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu  
 165 170 175  
 Val Lys

## (2) INFORMATION FOR SEQ ID NO:5215:

## (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys	Glu	Arg	Val	Leu	Met	Lys	Lys	Leu	Leu	Thr	Ala	Ser	Ile	Ile	Ala	1	5	10	15
Cys	Ser	Val	Val	Met	Gly	Val	Gly	Leu	Val	Asn	Thr	Ser	Ala	Glu	Ala	20	25	30	
Ala	Ser	Gly	Asn	Ser	Ile	Asp	Thr	Val	Lys	Gln	Leu	Ile	Lys	Gly	Asp	35	40	45	
Gln	Ser	Leu	Glu	Asn	Val	Lys	Ile	Gly	Glu	Ser	Ile	Lys	Asp	Val	Leu	50	55	60	
Thr	Lys	Tyr	Lys	Asn	Pro	Met	Tyr	Ser	Tyr	Asn	Glu	Asp	Gly	Thr	Glu	65	70	75	80
His	Tyr	Tyr	Glu	Phe	His	Thr	Lys	Lys	Gly	Met	Leu	Leu	Val	Thr	Thr	85	90	95	
Asp	Gly	Lys	Lys	Asn	Asn	Gly	Lys	Val	Thr	His	Ile	Ser	Met	Met	Tyr	100	105	110	
Asn	Asp	Ala	Asn	Gly	Pro	Thr	Tyr	Gln	Ala	Val	Lys	Asn	Tyr	Val	Gly	115	120	125	
Lys	Ala	Val	Thr	His	Thr	Glu	Tyr	Ser	Lys	Val	Ala	Gly	Asn	Phe	Gly	130	135	140	
Tyr	Ile	Glu	Lys	Gly	Lys	Thr	Thr	Tyr	Gln	Phe	Ala	Ser	Ala	Pro	Lys	145	150	155	160
Asp	Lys	Asn	Ile	Lys	Leu	Tyr	Arg	Ile	Asp	Leu	Glu	Lys	165	170					

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

1                      5                      10                      15  
 Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val  
                          20                      25                      30  
 5 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile  
                          35                      40                      45  
 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn  
 10                      50                      55                      60  
 Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu  
 65                      70                      75                      80  
 15 Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu  
                          85                      90                      95  
 Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr  
                          100                      105                      110  
 20 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala  
                          115                      120                      125  
 Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys  
 25                      130                      135                      140  
 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr  
 145                      150                      155                      160  
 30 Asp Asp Asn Lys Gln Pro Ala  
                          165

## (2) INFORMATION FOR SEQ ID NO:5217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

45 Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser  
 1                      5                      10                      15  
 50 Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys  
                          20                      25                      30  
 Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val  
                          35                      40                      45  
 55 Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val  
                          50                      55                      60



[illegible]

(2) INFORMATION FOR SEQ ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

	Asn	Phe	Lys	Met	Gln	Glu	Val	Lys	Tyr	Met	Thr	Glu	Ile	Thr	Phe	Lys
	1				5					10						15
30	Gly	Gly	Pro	Ile	His	Leu	Lys	Gly	Gln	Gln	Ile	Asn	Glu	Gly	Asp	Phe
				20					25					30		
	Ala	Pro	Asp	Phe	Thr	Val	Leu	Asp	Asn	Asp	Leu	Asn	Gln	Val	Thr	Leu
			35					40					45			
35	Ala	Asp	Tyr	Ala	Gly	Lys	Lys	Lys	Leu	Ile	Ser	Val	Val	Pro	Ser	Ile
		50					55					60				
	Asp	Thr	Gly	Val	Cys	Asp	Gln	Gln	Thr	Arg	Lys	Phe	Asn	Ser	Asp	Ala
	65					70					75					80
40	Ser	Lys	Glu	Glu	Gly	Ile	Val	Leu	Thr	Ile	Ser	Ala	Asp	Leu	Pro	Phe
					85					90					95	
	Ala	Gln	Lys	Arg	Trp	Cys	Ala	Ser	Ala	Gly	Leu	Asp	Asn	Val	Ile	Thr
				100					105					110		
45	Leu	Ser	Asp	His	Arg	Asp	Leu	Ser	Phe	Gly	Glu	Asn	Tyr	Gly	Val	Val
			115					120					125			
	Met	Glu	Glu	Leu	Arg	Leu	Leu	Ala	Arg	Ala	Val	Phe	Val	Leu	Asp	Ala
50		130					135					140				
	Asp	Asn	Lys	Val	Val	Tyr	Lys	Glu	Ile	Val	Ser	Glu	Gly	Thr	Asp	Phe
	145					150					155					160
55	Pro	Asp	Phe	Asp	Ala	Ala	Leu	Ala	Ala	Tyr	Lys	Asn	Ile			
				165						170						

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr  
 1 5 10 15  
 Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp  
 20 25 30  
 Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His  
 35 40 45  
 Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu  
 50 55 60  
 Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala  
 65 70 75 80  
 Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr  
 85 90 95  
 Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val  
 100 105 110  
 Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln  
 115 120 125  
 Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys  
 130 135

## (2) INFORMATION FOR SEQ ID NO:5220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val  
 1 5 10 15

[illegible]

(2) INFORMATION FOR SEQ ID NO:5221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

Ile	Met	Ala	Tyr	Asp	Gly	Leu	Phe	Thr	Lys	Lys	Met	Val	Glu	Ser	Leu
1				5					10					15	
Gln	Phe	Leu	Thr	Thr	Gly	Arg	Val	His	Lys	Ile	Asn	Gln	Pro	Asp	Asn
			20					25					30		
Asp	Thr	Ile	Leu	Met	Val	Val	Arg	Gln	Asn	Arg	Gln	Asn	His	Gln	Leu
		35					40					45			
Leu	Leu	Ser	Ile	His	Pro	Asn	Phe	Ser	Arg	Leu	Gln	Leu	Thr	Thr	Lys
	50					55					60				
Lys	Tyr	Asp	Asn	Pro	Phe	Asn	Pro	Pro	Met	Phe	Ala	Arg	Val	Phe	Arg
65					70					75					80

	85	90	95
5	Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp 100 105 110		
	Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn 115 120 125		
10	Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His 130 135 140		
	Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn 145 150 155 160		
15	Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr 165 170 175		
	Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala 180 185 190		
20	Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn 195 200 205		
	Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu 210 215 220		
25	Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile 225 230 235 240		
	Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys 245 250 255		
30	Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp 260 265 270		
	Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys 275 280 285		
35	Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys 290 295 300		
40	Tyr Gln Asn Lys Leu Ala Ser 305 310		

## (2) INFORMATION FOR SEQ ID NO:5222:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

	1	5	10	15
	Glu	Gln	Leu	Tyr
		Gly	Glu	Leu
			Ile	Thr
				Ala
				Asn
				Ile
				Tyr
				Arg
				Ile
				Lys
5				
	Gln	Gly	Asp	Lys
			Glu	Val
			Thr	Ala
				Leu
				Asn
				Tyr
				Tyr
				Thr
				Asn
				Glu
				Glu
10				
	Val	Val	Ile	Pro
			Leu	Asn
			Pro	Thr
			Lys	Ser
			Pro	Ser
				Ala
				Asn
				Ala
				Gln
	Tyr	Tyr	Tyr	Lys
			Gln	Tyr
			Xaa	Arg
			Met	Lys
			Thr	Arg
			Xaa	Arg
			Glu	Leu
15				
	Gln	His	Gln	Ile
			Gln	Leu
			Thr	Lys
			Asp	Asn
			Ile	Asp
			Tyr	Phe
			Ser	Thr
	Ile	Glu	Gln	Gln
			Leu	His
			His	Ile
			Ser	Val
			His	Asp
			Ile	Asp
			Glu	Ile
20				
	Arg	Asp	Glu	Leu
			Ala	Glu
			Gln	Gly
			Phe	Met
			Lys	Gln
			Arg	Lys
			Asn	Gln
	Thr	Lys	Lys	Lys
			Ala	Gln
			Ile	Gln
			Leu	Gln
			His	Tyr
			Val	Ser
			Thr	
25				
	Asp	Gly	Asp	Asp
			Ile	Tyr
			Val	Gly
			Lys	Asn
			Asn	Lys
			Gln	Asn
			Asp	Tyr
30				
	Leu	Thr	Asn	Lys
			Lys	Ala
			Lys	Lys
			Thr	His
			Thr	Trp
			Leu	His
			Thr	Lys
	Asp	Ile	Pro	Gly
			Ser	His
			Val	Val
			Ile	Phe
			Asn	Asp
			Ala	Pro
			Ser	Asp
35				
	Thr	Thr	Ile	Lys
			Glu	Ala
			Ala	Met
			Leu	Ala
			Gly	Tyr
			Phe	Ser
			Lys	Ala
40				
	Gly	Asn	Ser	Gly
			Gln	Ile
			Pro	Val
			Asp	Tyr
			Thr	Leu
			Ile	Lys
			Asn	Val
	His	Lys	Pro	Ser
			Gly	Ala
			Lys	Pro
			Gly	Phe
			Val	Thr
			Tyr	Asp
			Asn	Gln
45				
	Lys	Thr	Leu	Tyr
			Ala	

## (2) INFORMATION FOR SEQ ID NO:5223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser  
 1 5 10 15  
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg  
 20 25 30  
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu  
 35 40 45  
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn  
 50 55 60  
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe  
 65 70 75 80  
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr  
 85 90 95  
 Asp Leu Lys

## (2) INFORMATION FOR SEQ ID NO:5224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu  
 1 5 10 15  
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn  
 20 25 30  
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn  
 35 40 45  
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu  
 50 55 60  
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu  
 65 70 75 80  
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr  
 85 90 95  
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly  
 100 105 110

115

120

125

His Ser Ile

130

## (2) INFORMATION FOR SEQ ID NO:5225:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

Asn	His	Leu	Thr	Ala	Arg	Ile	Ile	Asn	Gln	Glu	Asp	Asp	Leu	Met	Asn	1	5	10	15
Leu	Phe	Arg	Gln	Gln	Lys	Phe	Ser	Ile	Arg	Lys	Phe	Asn	Val	Gly	Ile	20	25	30	
Phe	Ser	Ala	Leu	Ile	Ala	Thr	Val	Thr	Phe	Ile	Ser	Thr	Asn	Pro	Thr	35	40	45	
Thr	Ala	Ser	Ala	Ala	Glu	Gln	Asn	Gln	Pro	Ala	Gln	Asn	Gln	Pro	Ala	50	55	60	
Gln	Pro	Ala	Asp	Ala	Asn	Thr	Gln	Pro	Asn	Ala	Asn	Ala	Gly	Ala	Gln	65	70	75	80
Ala	Asn	Pro	Thr	Ala	Gln	Pro	Ala	Ala	Pro	Ala	Asn	Gln	Gly	Gln	Pro	85	90	95	
Ala	Val	Gln	Pro	Ala	Asn	Gln	Gly	Gly	Gln	Ala	Asn	Pro	Ala	Gly	Gly	100	105	110	
Ala	Ala	Gln	Pro	Asn	Thr	Gln	Pro	Ala	Gly	Gln	Gly	Asp	Gln	Ala	Asp	115	120	125	
Pro	Asn	Asn	Ala	Ala	Gln	Ala	Gln	Pro	Gly	Asn	Gln	Ala	Thr	Pro	Ala	130	135	140	
Asn	Gln	Ala	Gly	Gln	Gly	Asn	Asn	Gln	Ala	Thr	Pro	Asn	Asn	Asn	Ala	145	150	155	160
Thr	Pro	Ala	Asn	Gln	Thr	Gln	Pro	Ala	Asn	Ala	Pro	Ala	Ala	Ala	Gln	165	170	175	
Pro	Ala	Ala	Pro	Val	Ala	Ala	Asn	Ala	Gln	Thr	Gln	Asp	Pro	Asn	Ala	180	185	190	
Ser	Asn	Thr	Gly	Glu	Gly	Ser	Ile	Asn	Thr	Thr	Leu	Thr	Phe	Asp	Asp	195	200	205	

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	210	215	220
5	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly 225 230 235 240		
	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn 245 250 255		
10	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val 260 265 270		
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys 275 280 285		
15	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr 290 295 300		
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp 305 310 315 320		
20	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly 325 330 335		
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu 340 345 350		
25	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr 355 360 365		
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly 370 375 380		
30	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro 385 390 395 400		
	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn 405 410 415		
	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu 420 425 430		
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr 435 440 445		
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr 450 455 460		
45	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly 465 470 475 480		
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp 485 490 495		
50	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr 500 505 510		
55	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser 515 520 525		



530

535

540

## (2) INFORMATION FOR SEQ ID NO:5226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His  
 1 5 10 15  
 Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val  
 20 25 30  
 Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile  
 35 40 45  
 Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His  
 50 55 60  
 Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe  
 65 70 75 80  
 Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe  
 85 90 95  
 Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu  
 100 105 110  
 Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly  
 115 120 125  
 Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro  
 130 135 140  
 Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile  
 145 150 155 160  
 Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val  
 165 170 175  
 Lys

## (2) INFORMATION FOR SEQ ID NO:5227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala  
1 5 10 15  
Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln  
20 25 30  
His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro  
35 40 45  
Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly  
50 55 60  
Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu  
65 70 75 80  
Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu  
85 90 95  
Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met  
100 105 110  
Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp  
115 120 125  
Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln  
130 135 140  
Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys  
145 150 155 160  
Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe  
165 170 175  
Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe  
180 185 190  
Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr  
195 200 205  
Cys

45

(2) INFORMATION FOR SEQ ID NO:5228:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 256 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5 Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg  
 1 5 10 15  
 Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys  
 20 25 30  
 10 Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp  
 35 40 45  
 Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val  
 50 55 60  
 15 Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly  
 65 70 75 80  
 Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys  
 85 90 95  
 20 Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln  
 100 105 110  
 Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala  
 115 120 125  
 25 Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His  
 130 135 140  
 30 Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys  
 145 150 155 160  
 His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys  
 165 170 175  
 35 Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu  
 180 185 190  
 Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu  
 195 200 205  
 40 Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp  
 210 215 220  
 45 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu  
 225 230 235 240  
 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu  
 245 250 255

## (2) INFORMATION FOR SEQ ID NO:5229:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10 Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys  
 1 5 10 15  
 Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr  
 20 25 30  
 15 Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp  
 35 40 45  
 Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn  
 50 55 60  
 20 Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp  
 65 70 75 80  
 Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser  
 85 90 95  
 25 Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly  
 100 105 110  
 Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val  
 115 120 125  
 30 Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala  
 130 135 140  
 35 Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg  
 145 150 155 160  
 Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln  
 165 170 175  
 40 Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile  
 180 185 190  
 Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly  
 195 200 205  
 45 Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr  
 210 215 220  
 Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly  
 225 230 235 240  
 Leu Gly Ala Trp Gly Phe  
 245

55 (2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys	Glu	Pro	His	Lys	Met	Lys	Lys	Ile	Tyr	Lys	Ser	Leu	Thr	Val	Ser	1	5	10	15
Ala	Ile	Val	Ala	Thr	Val	Ser	Leu	Ser	Ala	Leu	Pro	Gln	Ser	Leu	Ala	20	25	30	
Ile	Thr	His	Glu	Ser	Gln	Pro	Thr	Lys	Gln	Gln	Arg	Thr	Val	Leu	Phe	35	40	45	
Asp	Arg	Ser	His	Gly	Gln	Thr	Ala	Gly	Ala	Ala	Asp	Trp	Val	Ser	Asp	50	55	60	
Gly	Ala	Phe	Ser	Asp	Tyr	Ala	Asp	Ser	Ile	Gln	Lys	Gln	Gly	Tyr	Asp	65	70	75	80
Val	Lys	Ala	Ile	Asp	Gly	His	Ser	Asn	Ile	Thr	Glu	Ala	Ser	Leu	Lys	85	90	95	
Ser	Ser	Lys	Ile	Phe	Val	Ile	Pro	Glu	Ala	Asn	Ile	Pro	Phe	Lys	Glu	100	105	110	
Ser	Glu	Gln	Ala	Ala	Ile	Val	Lys	Tyr	Val	Lys	Gln	Gly	Gly	Asn	Val	115	120	125	
Val	Phe	Ile	Ser	Asp	His	Tyr	Asn	Ala	Asp	Arg	Asn	Leu	Asn	Arg	Ile	130	135	140	
Asp	Ser	Ser	Glu	Ala	Met	Asn	Gly	Tyr	Arg	Arg	Gly	Ala	Tyr	Glu	Asp	145	150	155	160
Met	Ser	Lys	Gly	Met	Asn	Ala	Glu	Glu	Lys	Ser	Ser	Thr	Ala	Met	Gln	165	170	175	
Gly	Val	Lys	Ser	Ser	Asp	Trp	Leu	Ser	Thr	Asn	Phe	Gly	Val	Arg	Phe	180	185	190	
Arg	Tyr	Asn	Ala	Leu	Gly	Asp	Leu	Asn	Thr	Ser	Asn	Ile	Val	Ser	Ser	195	200	205	
Lys	Glu	Ser	Phe	Gly	Ile	Thr	Glu	Gly	Val	Lys	Ser	Val	Ser	Met	His	210	215	220	
Ala	Gly	Ser	Thr	Leu	Ala	Ile	Thr	Asn	Pro	Glu	Lys	Ala	Lys	Gly	Ile	225	230	235	240
Val	Tyr	Thr	Pro	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Lys	Trp	Ser	His	Ala	245	250	255	

Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr  
 260 265 270  
 5 Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp  
 275 280 285  
 Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn  
 290 295 300  
 10 Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly  
 305 310 315 320  
 Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly  
 325 330 335  
 15 Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu  
 340 345 350  
 Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro  
 355 360 365  
 20 Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe  
 370 375 380  
 Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn  
 385 390 395 400  
 25 Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe  
 405 410 415  
 30 Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile  
 420 425 430  
 His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val  
 435 440 445  
 35 Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys  
 450 455 460  
 Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys  
 465 470 475 480  
 Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu  
 485 490 495  
 45 Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr  
 500 505 510  
 Leu Ile Thr Thr Asp Phe Lys  
 515

(2) INFORMATION FOR SEQ ID NO:5231:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5	Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	1	5	10	15
	Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	20	25	30	
10	Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	35	40	45	
	Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	50	55	60	
15	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	65	70	75	80
	Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	85	90	95	
20	Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	100	105	110	
	Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	115	120	125	
25	Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	130	135	140	
	Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	145	150	155	160
30	Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	165	170	175	
35	Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	180	185	190	
	Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	195	200	205	
40	His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	210	215	220	
45	Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu	225	230	235	240
	Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala	245	250	255	
50	Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His	260	265	270	
	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu	275	280	285	

Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe  
 290 295 300

5 Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:5232:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 433 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

20 Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr  
 1 5 10 15  
 25 Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr  
 20 25 30  
 30 Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala  
 35 40 45  
 30 Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu  
 50 55 60  
 35 Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys  
 65 70 75 80  
 40 Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu  
 85 90 95  
 45 Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser  
 100 105 110  
 40 Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp  
 115 120 125  
 45 Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala  
 130 135 140  
 50 Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe  
 145 150 155 160  
 55 Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr  
 165 170 175  
 His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe  
 180 185 190  
 55 Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg  
 195 200 205



Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile  
 210 215 220  
 5 Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr  
 225 230 235 240  
 Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly  
 245 250 255  
 10 Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His  
 260 265 270  
 Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met  
 275 280 285  
 15 Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met  
 290 295 300  
 Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val  
 305 310 315 320  
 20 Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr  
 325 330 335  
 Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys  
 340 345 350  
 25 Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro  
 355 360 365  
 Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His  
 370 375 380  
 30 Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu  
 385 390 395 400  
 35 Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly  
 405 410 415  
 Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg  
 420 425 430  
 40 Lys

## (2) INFORMATION FOR SEQ ID NO:5233:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val  
 1 5 10 15  
 Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly  
 5 20 25 30  
 Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys  
 35 40 45  
 Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile  
 10 50 55 60  
 Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu  
 65 70 75 80  
 Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu  
 15 85 90 95  
 Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr  
 20 100 105 110  
 Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys  
 115 120 125  
 Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile  
 25 130 135 140  
 Asp Ile Asn Val Lys Thr Lys  
 145 150

## (2) INFORMATION FOR SEQ ID NO:5234:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 497 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe  
 1 5 10 15  
 Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His  
 20 25 30  
 Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His  
 35 40 45  
 Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala  
 50 55 60  
 Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln  
 55 65 70 75 80

	Val	His	Asn	Glu	Ser	Gln	Thr	Ser	Glu	Asp	Asn	Val	Gln	Asn	Glu	Ala	
					85					90					95		
5	Gly	Thr	Ile	Asp	Asp	Arg	Gln	Val	Glu	Ser	Ser	His	Ser	Thr	Glu	Ser	
				100					105					110			
	Gln	Glu	Pro	Ser	His	Gln	Asp	Ser	Thr	Pro	Gln	His	Glu	Glu	Glu	Tyr	
			115					120					125				
10	Tyr	Asn	Lys	Asn	Ala	Phe	Ala	Met	Asp	Lys	Ser	His	Pro	Glu	Pro	Ile	
		130					135					140					
	Glu	Asp	Asn	Asp	Lys	His	Asp	Thr	Ile	Lys	Asn	Ala	Glu	Asn	Asn	Thr	
	145					150					155					160	
15	Glu	His	Ser	Thr	Val	Ser	Asp	Lys	Ser	Glu	Ala	Glu	Gln	Ser	Gln	Gln	
					165					170					175		
	Pro	Lys	Pro	Tyr	Phe	Thr	Thr	Gly	Ala	Asn	Gln	Ser	Glu	Thr	Ser	Lys	
20				180					185					190			
	Asn	Glu	His	Asp	Asn	Asp	Ser	Val	Lys	Gln	Asp	Gln	Asp	Glu	Pro	Lys	
			195					200					205				
25	Glu	His	His	Asn	Gly	Lys	Lys	Ala	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	
		210					215					220					
	Gly	Val	Ala	Gly	Ala	Ala	Gly	Ala	Met	Ala	Ala	Ser	Lys	Ala	Lys	Lys	
	225					230					235					240	
30	His	Ser	Asn	Asp	Ala	Gln	Asn	Lys	Ser	Asn	Ser	Gly	Lys	Ala	Asn	Asn	
					245					250					255		
	Ser	Thr	Glu	Asp	Lys	Ala	Ser	Gln	Asp	Lys	Ser	Lys	Asp	His	His	Asn	
				260					265					270			
35	Gly	Lys	Lys	Gly	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	Gly	Leu	Ala	Gly	
			275					280					285				
	Gly	Ala	Ala	Ser	Lys	Ser	Ala	Ser	Ala	Ala	Ser	Lys	Pro	His	Ala	Ser	
		290					295					300					
40	Asn	Asn	Ala	Ser	Gln	Asn	His	Asp	Glu	His	Asp	Asn	His	Asp	Arg	Asp	
	305					310					315					320	
	Lys	Glu	Arg	Lys	Lys	Gly	Gly	Met	Ala	Lys	Val	Leu	Leu	Pro	Leu	Ile	
45					325					330					335		
	Ala	Ala	Val	Leu	Ile	Ile	Gly	Ala	Leu	Ala	Ile	Phe	Gly	Gly	Met	Ala	
				340					345					350			
	Leu	Asn	Asn	His	Asn	Asn	Gly	Thr	Lys	Glu	Asn	Lys	Ile	Ala	Asn	Thr	
50			355					360					365				
	Asn	Lys	Asn	Asn	Ala	Asp	Glu	Ser	Lys	Asp	Lys	Asp	Thr	Ser	Lys	Asp	
		370					375					380					
55	Ala	Ser	Lys	Asp	Lys	Ser	Lys	Ser	Thr	Asp	Ser	Asp	Lys	Ser	Lys	Glu	
	385					390					395					400	

Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn  
 405 410 415  
 Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln  
 5 420 425 430  
 Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln  
 435 440 445  
 Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln  
 10 450 455 460  
 Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala  
 465 470 475 480  
 Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile  
 15 485 490 495  
 Pro

(2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn  
 1 5 10 15  
 Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr  
 20 25 30  
 Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser  
 35 40 45  
 Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile  
 50 55 60  
 Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp  
 65 70 75 80  
 Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn  
 85 90 95  
 Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala  
 100 105 110  
 Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe  
 115 120 125

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	Gln	Leu	Leu	Asp	Lys	Asn	Asn	Glu	Thr	Gln	Tyr	Tyr	His	Phe	Phe	Ser	
	130						135					140					
5	Ile	Lys	Asp	Pro	Ala	Asp	Val	Tyr	Tyr	Thr	Lys	Lys	Lys	Ala	Glu	Val	
	145					150					155					160	
	Glu	Leu	Asp	Ile	Asn	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr	
					165					170					175		
10	Glu	Asn	Asn	Gln	Lys	Leu	Pro	Val	Arg	Leu	Val	Ser	Tyr	Ser	Pro	Val	
				180					185					190			
	Pro	Glu	Asp	His	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asp	Gly	Thr	Gln	
			195					200					205				
15	Glu	Leu	Lys	Ile	Val	Ser	Ser	Thr	Gln	Ile	Asp	Asp	Gly	Glu	Glu	Thr	
	210						215					220					
	Asn	Tyr	Asp	Tyr	Thr	Lys	Leu	Val	Phe	Ala	Lys	Pro	Ile	Tyr	Asn	Asp	
	225					230					235					240	
20	Pro	Ser	Leu	Val	Lys	Ser	Asp	Thr	Asn	Asp	Ala	Val	Val	Thr	Asn	Asp	
					245					250					255		
	Gln	Ser	Ser	Ser	Val	Ala	Ser	Asn	Gln	Thr	Asn	Thr	Asn	Thr	Ser	Asn	
25				260					265					270			
	Gln	Asn	Ile	Ser	Thr	Ile	Asn	Asn	Ala	Asn	Asn	Gln	Pro	Gln	Ala	Thr	
			275					280					285				
	Thr	Asn	Met	Ser	Gln	Pro	Ala	Gln	Pro	Lys	Ser	Ser	Thr	Asn	Ala	Asp	
30		290					295					300					
	Gln	Ala	Ser	Ser	Gln	Pro	Ala	His	Glu	Thr	Asn	Ser	Asn	Gly	Asn	Thr	
	305					310					315					320	
35	Asn	Asp	Lys	Thr	Asn	Glu	Ser	Ser	Asn	Gln	Ser	Asp	Val	Asn	Gln	Gln	
					325					330					335		
	Tyr	Pro	Pro	Ala	Asp	Glu	Ser	Leu	Gln	Asp	Ala	Ile	Lys	Asn	Pro	Ala	
				340					345					350			
40	Ile	Ile	Asp	Lys	Glu	His	Thr	Ala	Asp	Asn	Trp	Arg	Pro	Ile	Asp	Phe	
			355					360					365				
	Gln	Met	Lys	Asn	Asp	Lys	Gly	Glu	Arg	Gln	Phe	Tyr	His	Tyr	Ala	Ser	
45		370					375					380					
	Thr	Val	Glu	Pro	Ala	Thr	Val	Ile	Phe	Thr	Lys	Thr	Gly	Pro	Ile	Ile	
	385					390					395					400	
	Glu	Leu	Gly	Leu	Lys	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr	
50					405					410					415		
	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Val	Glu	Leu	Val	Ser	Tyr	Asp	Ser	Asp	
				420					425					430			
55	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asn	Gly	Thr	Arg	Glu	
			435					440					445				

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	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His	Glu	Asp	
	450						455					460					
5	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn	Asn	Pro	
	465					470					475					480	
	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu	Leu	Ala	
					485					490					495		
10	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Glu	
				500					505					510			
	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	Lys	Lys	
			515					520					525				
15	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	Ser	Ala	
	530						535					540					
	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	Thr	Asp	
20	545					550					555					560	
	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	Ser	Glu	
					565					570					575		
	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	Thr	Leu	
25				580					585					590			
	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	Tyr	Trp	
		595						600					605				
30	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	Lys	Asp	
	610						615					620					
	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro	Asp	Lys	
	625					630					635					640	
35	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile	Gly	Tyr	
					645					650					655		
	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn	Thr	Lys	
				660					665					670			
40	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn	Val	Gln	
			675					680					685				
	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu	Asn	Ser	
45		690					695					700					
	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp	Val	Ile	
	705					710					715					720	
	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile	Asp	Lys	
50					725					730					735		
	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp	Asn	Asn	
				740					745					750			
55	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile	Ala	Lys	
		755						760					765				

Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met  
 770 775 780  
 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys  
 5 785 790 795 800  
 Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys  
 805 810 815  
 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys  
 10 820 825 830  
 Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys  
 835 840 845  
 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser  
 15 850 855 860  
 Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg  
 20 865 870 875 880  
 Asn Asn Xaa Gln Ala Asn  
 885

## (2) INFORMATION FOR SEQ ID NO:5236:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 236 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:  
 Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile  
 1 5 10 15  
 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser  
 20 25 30  
 Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys  
 35 40 45  
 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val  
 50 55 60  
 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn  
 65 70 75 80  
 Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys  
 85 90 95  
 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys  
 55 100 105 110

Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu  
 115 120 125  
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys  
 130 135 140  
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr  
 145 150 155 160  
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly  
 165 170 175  
 Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser  
 180 185 190  
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly  
 195 200 205  
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro  
 210 215 220  
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:5237:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr  
 1 5 10 15  
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr  
 20 25 30  
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val  
 35 40 45  
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly  
 50 55 60  
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr  
 65 70 75 80  
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala  
 85 90 95  
 Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr  
 100 105 110



Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr  
                   115                                  120                                  125  
 5 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser  
                   130                                  135                                  140  
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln  
 145                                  150                                  155                                  160  
 10 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu  
                                   165                                  170                                  175  
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln  
 180                                  185                                  190  
 15 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val  
                   195                                  200                                  205  
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu  
 210                                  215                                  220  
 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val  
 225                                  230                                  235                                  240  
 25 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile  
                                   245                                  250                                  255  
 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile  
                                   260                                  265                                  270  
 30 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr  
                   275                                  280                                  285  
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu  
 290                                  295                                  300  
 35 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser  
 305                                  310                                  315                                  320  
 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu  
 325                                  330                                  335  
 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly  
 340                                  345                                  350  
 45 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys  
                   355                                  360

## (2) INFORMATION FOR SEQ ID NO:5238:

- 50 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 150 amino acids  
     (B) TYPE: amino acid  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val  
 1 5 10 15  
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala  
 20 25 30  
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser  
 35 40 45  
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn  
 50 55 60  
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys  
 65 70 75 80  
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile  
 85 90 95  
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr  
 100 105 110  
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr  
 115 120 125  
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn  
 130 135 140  
 Val Asp Thr Lys Lys Gln  
 145 150  
 30

## (2) INFORMATION FOR SEQ ID NO:5239:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp  
 1 5 10 15  
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly  
 20 25 30  
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile  
 35 40 45  
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly  
 50 55 60  
 55

Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met  
 65 70 75 80  
 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu  
 5 85 90 95  
 Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr  
 100 105 110  
 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser  
 10 115 120 125  
 Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys  
 130 135 140  
 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu  
 15 145 150 155 160  
 Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser  
 165 170 175  
 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val  
 180 185 190  
 Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile  
 195 200 205  
 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr  
 210 215 220  
 Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:5240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val  
 1 5 10 15  
 Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser  
 20 25 30  
 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys  
 35 40 45  
 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val  
 50 55 60

Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu  
65 70 75 80

5 Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys  
85 90 95

Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe  
100 105 110

10 Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu  
115 120 125

Phe Asp Val Lys Ala  
130

15 (2) INFORMATION FOR SEQ ID NO:5241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 amino acids

(B) TYPE: amino acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

30 Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val  
1 5 10 15

Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly  
20 25 30

35 Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro  
35 40 45

Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp  
50 55 60

40 Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser  
65 70 75 80

Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp  
85 90 95

45 Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn  
100 105 110

50 Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala  
115 120 125

Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly  
130 135 140

55 Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu  
145 150 155 160

	Pro	Ile	Gly	Val	Val	Gly	Ala	Val	Val	Ala	Trp	Asn	Phe	Pro	Met	Leu	
						165					170				175		
5	Leu	Ala	Ala	Trp	Lys	Ile	Ala	Pro	Ala	Ile	Ala	Ala	Gly	Asn	Thr	Ile	
						180				185				190			
	Val	Ile	Gln	Pro	Ser	Ser	Ser	Thr	Pro	Leu	Ser	Leu	Leu	Glu	Val	Ala	
						195				200				205			
10	Lys	Ile	Phe	Gln	Glu	Val	Leu	Pro	Lys	Gly	Val	Val	Asn	Ile	Leu	Thr	
						210				215			220				
	Gly	Lys	Gly	Ser	Glu	Ser	Gly	Asn	Ala	Ile	Phe	Asn	His	Asp	Gly	Val	
							230					235				240	
15	Asp	Lys	Leu	Ser	Phe	Thr	Gly	Ser	Thr	Asp	Val	Gly	Tyr	Gln	Val	Ala	
							245				250				255		
	Glu	Ala	Ala	Ala	Lys	His	Leu	Val	Pro	Ala	Thr	Leu	Glu	Leu	Gly	Gly	
							260				265				270		
20	Lys	Ser	Ala	Asn	Ile	Ile	Leu	Asp	Asp	Ala	Asn	Leu	Asp	Leu	Ala	Val	
							275						285				
	Glu	Gly	Ile	Gln	Leu	Gly	Ile	Leu	Phe	Asn	Gln	Gly	Glu	Val	Cys	Ser	
25							290						300				
	Ala	Gly	Ser	Arg	Leu	Leu	Val	His	Glu	Lys	Ile	Tyr	Asp	Gln	Leu	Val	
							310					315				320	
30	Pro	Arg	Leu	Gln	Glu	Ala	Phe	Ser	Asn	Ile	Lys	Val	Gly	Asn	Pro	Gln	
							325				330				335		
	Asp	Glu	Ala	Thr	Gln	Met	Gly	Ser	Gln	Thr	Gly	Lys	Asp	Gln	Leu	Asp	
							340				345			350			
35	Lys	Ile	Gln	Ser	Tyr	Ile	Asp	Ala	Ala	Lys	Glu	Ser	Asp	Ala	Gln	Ile	
							355						365				
	Leu	Ala	Gly	Gly	His	Arg	Leu	Thr	Glu	Asn	Gly	Leu	Asp	Lys	Gly	Phe	
							370						380				
40	Phe	Phe	Glu	Pro	Thr	Leu	Ile	Ala	Val	Pro	Asp	Asn	His	His	Lys	Leu	
							390					395				400	
	Ala	Gln	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Thr	Val	Ile	Lys	Val	Lys	
							405				410				415		
45	Asp	Asp	Gln	Glu	Ala	Ile	Asp	Ile	Ala	Asn	Asp	Ser	Glu	Tyr	Gly	Leu	
							420				425			430			
	Ala	Gly	Gly	Val	Phe	Ser	Gln	Asn	Ile	Thr	Arg	Ala	Leu	Asn	Ile	Ala	
							435						445				
50	Lys	Ala	Val	Arg	Thr	Gly	Arg	Ile	Trp	Ile	Asn	Thr	Tyr	Asn	Gln	Val	
							450				455			460			
	Pro	Glu	Gly	Ala	Pro	Phe	Gly	Gly	Tyr	Lys	Lys	Ser	Gly	Ile	Gly	Arg	
55							465				475					480	

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile  
 485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr  
 500 505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn  
 1 5 10 15  
 Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile  
 20 25 30  
 Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr  
 35 40 45  
 Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala  
 50 55 60  
 Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln  
 65 70 75 80  
 Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro  
 85 90 95  
 Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly  
 100 105 110  
 Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp  
 115 120 125  
 Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala  
 130 135 140  
 Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala  
 145 150 155 160  
 Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln  
 165 170 175  
 Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala  
 180 185 190  
 Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp  
 195 200 205

## EP 0 786 519 A2

Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val  
 210 215 220  
 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly  
 5 225 230 235 240  
 Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn  
 245 250 255  
 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val  
 10 260 265 270  
 Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys  
 275 280 285  
 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr  
 15 290 295 300  
 Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp  
 305 310 315 320  
 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly  
 20 325 330 335  
 Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu  
 25 340 345 350  
 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr  
 355 360 365  
 Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly  
 30 370 375 380  
 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro  
 385 390 395 400  
 Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn  
 35 405 410 415  
 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu  
 420 425 430  
 Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr  
 40 435 440 445  
 Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr  
 450 455 460  
 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly  
 45 465 470 475 480  
 Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp  
 485 490 495  
 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr  
 50 500 505 510  
 Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser  
 55 515 520 525

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His  
 530 535 540

## (2) INFORMATION FOR SEQ ID NO:5243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln  
 1 5 10 15  
 Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln  
 20 25 30  
 Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly  
 25 35 40 45  
 Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp  
 50 55 60  
 Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe  
 30 65 70 75 80  
 Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln  
 85 90 95  
 Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala  
 35 100 105 110  
 Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr  
 115 120 125  
 Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser  
 40 130 135 140  
 Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala  
 145 150 155 160  
 Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val  
 45 165 170 175  
 Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser  
 50 180 185 190  
 Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr  
 195 200 205  
 Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu  
 55 210 215 220



His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val  
 225 230 235 240  
 Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro  
 245 250 255  
 Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn  
 260 265 270  
 Asn Asp

## (2) INFORMATION FOR SEQ ID NO:5244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val  
 1 5 10 15  
 Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile  
 20 25 30  
 Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly  
 35 40 45  
 Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr  
 50 55 60  
 Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe  
 65 70 75 80  
 Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys  
 85 90 95  
 Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys  
 100 105 110  
 Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val  
 115 120 125  
 Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr  
 130 135 140  
 Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr  
 145 150 155 160  
 Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu  
 165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu  
180 185 190

5 Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gly Ser Thr Lys Gly Ser  
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr  
210 215 220

10 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser  
225 230 235 240

Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr  
15 245 250 255

Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile  
260 265 270

20 Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn  
275 280 285

Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly  
290 295 300

25 Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser  
305 310 315 320

Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys  
325 330 335

30 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala  
340 345 350

Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln  
35 355 360 365

Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp  
370 375 380

40 Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp  
385 390 395 400

Val Gln Leu Gly Leu Gly Asn Ala Ala Thr Ala Tyr Gly Cys Asp  
405 410 415

45 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr  
420 425 430

## (2) INFORMATION FOR SEQ ID NO:5245:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 469 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5	Asn	Pro	Ala	Leu	Thr	Val	Phe	Ala	Phe	Ile	Met	Ile	Ile	Ser	Ile	Leu	1	5	10	15
	Leu	Ala	Tyr	Val	Phe	Lys	Trp	Leu	Gly	Leu	Val	Asp	Asp	Val	Leu	Leu	20	25	30	
10	Met	Val	Ile	Ile	Ile	Ser	Thr	Ile	Ser	Leu	Gly	Val	Val	Val	Pro	Thr	35	40	45	
	Leu	Lys	Glu	Met	Asn	Ile	Met	Arg	Thr	Thr	Ile	Gly	Gln	Phe	Ile	Leu	50	55	60	
15	Leu	Val	Ala	Val	Leu	Ala	Asp	Leu	Val	Thr	Met	Ile	Leu	Leu	Thr	Val	65	70	75	80
	Tyr	Gly	Ala	Ile	Asn	Gly	Gln	Gly	Gly	Ser	Thr	Ile	Trp	Leu	Ile	Gly	85	90	95	
20	Ile	Leu	Val	Val	Phe	Thr	Ala	Ile	Ser	Tyr	Ile	Leu	Gly	Val	Gln	Phe	100	105	110	
	Lys	Arg	Met	Ser	Phe	Leu	Gln	Lys	Leu	Met	Asp	Gly	Thr	Thr	Gln	Ile	115	120	125	
25	Gly	Ile	Arg	Ala	Val	Phe	Ala	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Ala	130	135	140	
30	Glu	Gly	Val	Gly	Ala	Glu	Asn	Ile	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Val	145	150	155	160
	Val	Val	Ser	Leu	Leu	Asn	Pro	Asp	Glu	Glu	Met	Val	Glu	Lys	Leu	Asp	165	170	175	
35	Ser	Phe	Gly	Tyr	Gly	Phe	Phe	Ile	Pro	Ile	Phe	Phe	Ile	Met	Xaa	Gly	180	185	190	
	Val	Asp	Leu	Asn	Ile	Pro	Ser	Leu	Ile	Lys	Glu	Pro	Lys	Leu	Leu	Ile	195	200	205	
40	Ile	Ile	Pro	Ile	Leu	Ile	Val	Ala	Phe	Ile	Ile	Ser	Lys	Leu	Ile	Pro	210	215	220	
	Val	Met	Phe	Ile	Arg	Arg	Trp	Phe	Asp	Met	Lys	Thr	Thr	Ile	Ala	Ser	225	230	235	240
45	Ala	Phe	Leu	Leu	Thr	Ser	Thr	Leu	Ser	Leu	Val	Ile	Ala	Ala	Ala	Lys	245	250	255	
	Ile	Ser	Glu	Arg	Leu	Asn	Ala	Ile	Ser	Ala	Glu	Thr	Ser	Gly	Ile	Leu	260	265	270	
50	Ile	Leu	Ser	Ala	Val	Ile	Thr	Cys	Val	Phe	Val	Pro	Ile	Ile	Phe	Lys	275	280	285	
55	Lys	Leu	Phe	Pro	Val	Pro	Asp	Glu	Phe	Asn	Arg	Lys	Ile	Glu	Val	Ser	290	295	300	

Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr  
 305 310 315 320  
 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp  
 5 325 330 335  
 Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr  
 340 345 350  
 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val  
 10 355 360 365  
 Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu  
 370 375 380  
 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr  
 15 385 390 395 400  
 Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser  
 20 405 410 415  
 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn  
 420 425 430  
 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln  
 25 435 440 445  
 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe  
 450 455 460  
 Gly Gly Asp Ile Ile  
 30 465

## (2) INFORMATION FOR SEQ ID NO:5246:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 414 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala  
 1 5 10 15  
 Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala  
 50 20 25 30  
 Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu  
 35 40 45  
 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu  
 55 50 55 60

	Asn	Ile	Tyr	Arg	Arg	Leu	Thr	Asp	Ser	Glu	Glu	Gln	Leu	Lys	Gly	Glu	65	70	75	80
5	Asn	Leu	Ile	Ile	Ser	Ala	Thr	Thr	Glu	Val	Phe	Lys	Pro	Ile	Met	Ser	85	90	95	
	Ser	Thr	Leu	Val	Thr	Ile	Ile	Val	Phe	Leu	Pro	Leu	Val	Phe	Val	Ser	100	105	110	
10	Gly	Ser	Val	Gly	Glu	Met	Phe	Arg	Pro	Phe	Ala	Leu	Ala	Ile	Ala	Phe	115	120	125	
	Ser	Leu	Leu	Ala	Ser	Leu	Leu	Val	Ser	Ile	Thr	Leu	Val	Pro	Ala	Leu	130	135	140	
15	Ala	Ala	Thr	Leu	Phe	Lys	Lys	Gly	Val	Lys	Arg	Arg	Asn	Lys	Gln	His	145	150	155	160
	Gln	Glu	Gly	Leu	Gly	Val	Val	Ser	Thr	Thr	Tyr	Lys	Lys	Val	Leu	His	165	170	175	
20	Trp	Ser	Leu	Asn	His	Lys	Trp	Ile	Val	Ile	Ile	Leu	Ser	Thr	Leu	Ile	180	185	190	
	Leu	Val	Ala	Thr	Ile	Val	Phe	Gly	Gly	Pro	Arg	Leu	Gly	Thr	Ser	Phe	195	200	205	
25	Ile	Ser	Ala	Gly	Asp	Asp	Lys	Phe	Leu	Ala	Ile	Thr	Tyr	Thr	Pro	Lys	210	215	220	
	Pro	Gly	Glu	Thr	Glu	Gln	Ala	Val	Leu	Asn	His	Ala	Lys	Asp	Val	Glu	225	230	235	240
30	Lys	Tyr	Leu	Lys	Gln	Lys	Lys	His	Val	Lys	Thr	Ile	Gln	Tyr	Ser	Val	245	250	255	
	Gly	Gly	Ser	Ser	Pro	Val	Asp	Pro	Thr	Gly	Ser	Thr	Asn	Ser	Met	Ala	260	265	270	
35	Ile	Met	Val	Glu	Tyr	Asp	Asn	Asp	Thr	Pro	Asn	Phe	Asp	Val	Glu	Ala	275	280	285	
40	Asp	Lys	Val	Ile	Lys	His	Ala	Asp	Gly	Phe	Lys	His	Pro	Gly	Glu	Trp	290	295	300	
	Lys	Asn	Gln	Asp	Leu	Gly	Thr	Gly	Ala	Gly	Asn	Lys	Ser	Val	Glu	Val	305	310	315	320
45	Thr	Val	Lys	Gly	Pro	Ser	Met	Asp	Ala	Ile	Lys	Ser	Thr	Val	Lys	Asp	325	330	335	
	Ile	Glu	Gln	Lys	Met	Lys	Gln	Val	Lys	Gly	Leu	Ala	Asn	Val	Lys	Ser	340	345	350	
50	Asp	Leu	Ser	Gln	Thr	Tyr	Asp	Gln	Tyr	Glu	Ile	Lys	Val	Asp	Gln	Asn	355	360	365	
55	Lys	Ala	Ala	Glu	Asn	Gly	Ile	Ser	Ala	Ser	Gln	Leu	Ala	Met	His	Leu	370	375	380	

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly  
 385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala  
 405 410

## (2) INFORMATION FOR SEQ ID NO:5247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu  
 1 5 10 15  
 Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu  
 20 25 30  
 Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile  
 35 40 45  
 Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp  
 50 55 60  
 Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Leu Arg Ala Thr Val  
 65 70 75 80  
 Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys  
 85 90 95  
 His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile  
 100 105 110  
 Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro  
 115 120 125  
 Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro  
 130 135 140  
 Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu  
 145 150 155 160  
 Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe  
 165 170 175  
 Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn  
 180 185 190  
 Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu  
 195 200 205

	Lys	Leu	Phe	Asn	Arg	Thr	Glu	Gln	Thr	Glu	Lys	His	Ile	Tyr	Asp	Asp	
	210						215					220					
5	Ser	Thr	Gln	Phe	Arg	Thr	Leu	Thr	Met	Arg	Ile	Leu	Arg	Ser	Ala	Phe	
	225					230					235					240	
	Leu	Ser	Gly	Leu	Met	Leu	Glu	Phe	Ile	Ser	Met	Leu	Gly	Ile	Gly	Leu	
					245					250					255		
10	Val	Ala	Leu	Glu	Ala	Thr	Leu	Ser	Leu	Val	Val	Phe	His	Asn	Ile	Asp	
				260					265					270			
	Phe	Lys	Thr	Ala	Ala	Ile	Ala	Ile	Ile	Leu	Ala	Pro	Glu	Phe	Tyr	Asn	
				275				280					285				
15	Ala	Ile	Lys	Asp	Leu	Gly	Gln	Ala	Phe	His	Thr	Gly	Lys	Gln	Ser	Glu	
		290					295					300					
	Gly	Ala	Ser	Asp	Val	Val	Phe	Glu	Phe	Leu	Glu	Gln	Pro	Asn	Tyr	Asn	
	305					310					315					320	
20	Asn	Glu	Phe	Leu	Leu	Lys	Tyr	Glu	Glu	Asn	Gln	Lys	Pro	Phe	Ile	Gln	
					325					330					335		
	Leu	Thr	Asp	Ile	Ser	Phe	Arg	Tyr	Asp	Asp	Ser	Asp	Arg	Leu	Val	Leu	
25				340					345					350			
	Asn	Asp	Leu	Asn	Leu	Glu	Ile	Phe	Lys	Gly	Asp	Gln	Ile	Ala	Leu	Val	
			355					360					365				
	Gly	Pro	Ser	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Thr	His	Leu	Ile	Ala	Gly	
30		370					375					380					
	Val	Tyr	Gln	Pro	Thr	Ile	Gly	Thr	Ile	Ser	Thr	Asn	Gln	Arg	Asp	Leu	
	385					390					395					400	
	Asn	Ile	Gly	Ile	Leu	Ser	Gln	Gln	Pro	Tyr	Ile	Phe	Ser	Ala	Ser	Ile	
35					405					410					415		
	Lys	Glu	Asn	Ile	Thr	Met	Phe	Lys	Asp	Ile	Glu	Asn	Asn	Thr	Ile	Glu	
				420					425					430			
40	Glu	Val	Leu	Asp	Glu	Val	Gly	Leu	Leu	Asp	Lys	Val	Gln	Ser	Phe	Thr	
		435						440					445				
	Lys	Gly	Ile	Asn	Thr	Ile	Ile	Gly	Glu	Gly	Gly	Glu	Met	Leu	Ser	Gly	
		450					455					460					
45	Gly	Gln	Met	Arg	Arg	Ile	Glu	Leu	Cys	Arg	Leu	Leu	Val	Met	Lys	Pro	
	465					470					475					480	
	Asp	Leu	Val	Ile	Phe	Asp	Glu	Pro	Ala	Thr	Gly	Leu	Asp	Ile	Gln	Thr	
					485					490					495		
50	Glu	His	Met	Ile	Gln	Asn	Val	Leu	Phe	Gln	His	Phe	Lys	Asp	Thr	Thr	
				500					505					510			
	Met	Ile	Val	Ile	Ala	His	Arg	Asp	Asn	Thr	Ile	Arg	His	Leu	Gln	Arg	
55			515					520					525				

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile  
 530 535 540

5 Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu  
 545 550 555

## (2) INFORMATION FOR SEQ ID NO:5248:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 393 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

20 Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe  
 1 5 10 15  
 Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu  
 25 20 25 30  
 Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met  
 35 35 40 45  
 Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr  
 30 50 55 60  
 Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr  
 65 70 75 80  
 Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp  
 35 85 90 95  
 Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val  
 100 105 110  
 40 Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala  
 115 120 125  
 Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val  
 130 135 140  
 45 Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile  
 145 150 155 160  
 Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu  
 50 165 170 175  
 Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr  
 180 185 190  
 55 Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp  
 195 200 205



Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe  
 210 215 220  
 5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val  
 225 230 235 240  
 Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly  
 245 250 255  
 10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu  
 260 265 270  
 Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala  
 275 280 285  
 15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr  
 290 295 300  
 Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn  
 305 310 315 320  
 20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr  
 325 330 335  
 Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn  
 340 345 350  
 25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg  
 355 360 365  
 Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn  
 370 375 380  
 30 Gln Ile Asn Gln Ile Met Gln Tyr Lys  
 385 390

## (2) INFORMATION FOR SEQ ID NO:5249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu  
 1 5 10 15  
 Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val  
 20 25 30  
 Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala  
 35 40 45

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	Ser Glu Asn Ser Val Thr Gln Ser Asp Ser Ala Ser Asn Glu Ser Lys	
	50	55 60
5	Ser Asn Asp Ser Ser Ser Val Ser Ala Ala Pro Lys Thr Asp Asp Thr	
	65	70 75 80
	Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu Thr	
		85 90 95
10	Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser	
		100 105 110
	Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr	
		115 120 125
15	Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn	
		130 135 140
	Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Ser	
		145 150 155 160
20	Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr	
		165 170 175
	Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr	
		180 185 190
25	Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys	
		195 200 205
	Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala	
		210 215 220
30	Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Val Ala Gly Thr Asp	
		225 230 235 240
	Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr	
		245 250 255
	Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe	
		260 265 270
40	Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val	
		275 280 285
	Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro	
		290 295 300
45	Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser	
		305 310 315 320
	Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp	
		325 330 335
50	Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu Asn	
		340 345 350
	Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr	
		355 360 365

	Thr	Ala	Asn	Lys	Thr	Val	Leu	Val	Asp	Tyr	Glu	Lys	Tyr	Gly	Lys	Phe	
	370						375					380					
5	Tyr	Asn	Leu	Ser	Ile	Lys	Gly	Thr	Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn	
	385					390					395					400	
	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Gly	Asp	Asn	Val	
				405						410					415		
10	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn	
				420					425					430			
	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp	
			435					440					445				
15	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe	
		450					455					460					
	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln	
	465				470						475					480	
20	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr	
				485					490						495		
	Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu	
25				500					505					510			
	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg	
			515					520					525				
30	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser	
		530					535					540					
	Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	Val	Pro	Glu	Gln	Pro	Asp	Glu	Pro	
	545				550						555					560	
35	Gly	Glu	Ile	Glu	Pro	Ile	Pro	Glu	Asp	Ser	Asp	Ser	Asp	Pro	Gly	Ser	
				565					570						575		
	Asp	Ser	Gly	Ser	Asp	Ser	Asn	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Gly	Ser	
			580					585					590				
40	Asp	Ser	Thr	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	
			595				600						605				
	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	
		610					615					620					
45	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Ser	Asp	Ser	
	625				630					635						640	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
			645					650					655				
50	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
			660				665						670				
55	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
		675					680					685					

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 690 695 700

5 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 705 710 715 720

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 725 730 735

10 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 740 745 750

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 755 760 765

15 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser  
 770 775 780

20 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 785 790 795 800

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 805 810 815

25 Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 820 825 830

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser  
 835 840 845

30 Asp Ser Asp Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser  
 850 855 860

Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro  
 865 870 875 880

35 Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys  
 885 890 895

40 Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu  
 900 905 910

Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg  
 915 920 925

45 Lys Lys Glu Asn Lys Asp Lys Lys  
 930 935

## (2) INFORMATION FOR SEQ ID NO:5250:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 194 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

5 Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala  
 1 5 10 15  
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro  
 20 25 30  
 10 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu  
 35 40 45  
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys  
 50 55 60  
 15 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys  
 65 70 75 80  
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr  
 85 90 95  
 20 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn  
 100 105 110  
 Leu Lys His Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys  
 115 120 125  
 25 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys  
 130 135 140  
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala  
 145 150 155 160  
 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln  
 165 170 175  
 35 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys  
 180 185 190  
 Ile Leu

## (2) INFORMATION FOR SEQ ID NO:5251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

55 Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp  
 1 5 10 15

	Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser	20	25	30
5	Leu Asn Phe Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr	35	40	45
	Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His	50	55	60
10	Leu Phe Gly Tyr Tyr Asn Tyr Tyr Tyr Thr Ser Asn Leu Thr Trp Lys	65	70	75
	Asn Gly Val Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp	85	90	95
15	Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu	100	105	110
	Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile	115	120	125
20	Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala	130	135	140
	Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu	145	150	155
25	Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys	165	170	175
	His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly	180	185	190
30	Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser	195	200	205
	Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu	210	215	220
35	Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp	225	230	235
	Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile	245	250	255
40	Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn	260	265	270
	Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His	275	280	285
45	Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly	290	295	300
	Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu	305	310	315
50	Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile	325	330	335

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys  
 340 345 350  
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe  
 355 360 365  
 Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile  
 370 375 380  
 Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His  
 385 390 395 400  
 Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His  
 405 410 415  
 Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val  
 420 425 430  
 Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro  
 435 440 445  
 Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro  
 450 455 460  
 Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala  
 465 470 475 480  
 Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val  
 485 490 495  
 Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro  
 500 505 510  
 Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly  
 515 520 525  
 Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile  
 530 535 540  
 Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala  
 545 550 555

## (2) INFORMATION FOR SEQ ID NO:5252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu  
 1 5 10 15

Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val  
 20 25 30  
 5 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn  
 35 40 45  
 Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp  
 50 55 60  
 10 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu  
 65 70 75 80  
 Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro  
 85 90 95  
 15 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile  
 100 105 110  
 Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys  
 115 120 125  
 20 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr  
 130 135 140  
 25 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu  
 145 150 155 160  
 Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg  
 165 170 175  
 30 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys  
 180 185 190  
 Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln  
 195 200 205  
 35 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys  
 210 215 220  
 Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser  
 225 230 235 240  
 40 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala  
 245 250

## (2) INFORMATION FOR SEQ ID NO:5253:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:



1 Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr  
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr  
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu  
 10 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser  
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp  
 15 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser  
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys  
 20 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys  
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser  
 25 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln  
 Arg Lys Lys

## (2) INFORMATION FOR SEQ ID NO:5254:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1027 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

1 Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr  
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr  
 20 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu  
 35 Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn  
 50

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	Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu	65	70	75	80
5	Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala	85	90	95	
	Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln	100	105	110	
10	Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys	115	120	125	
	Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn	130	135	140	
15	Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln	145	150	155	160
	Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala	165	170	175	
20	Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala	180	185	190	
	Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser	195	200	205	
25	Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn	210	215	220	
	Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu	225	230	235	240
30	Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu	245	250	255	
	Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro	260	265	270	
35	Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu	275	280	285	
40	Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val	290	295	300	
	Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr	305	310	315	320
45	Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu	325	330	335	
	Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn	340	345	350	
50	Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn	355	360	365	
	Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr	370	375	380	

	Thr	Ser	Val	Thr	Val	Thr	Gly	Thr	Leu	Met	Lys	Gly	Ser	Asn	Gln	Asn	385		390		395		400
5	Gly	Asn	Gln	Pro	Lys	Val	Arg	Ile	Phe	Glu	Tyr	Leu	Gly	Asn	Asn	Glu		405		410		415	
	Asp	Ile	Ala	Lys	Ser	Val	Tyr	Ala	Asn	Thr	Thr	Asp	Thr	Ser	Lys	Phe		420		425		430	
10	Lys	Glu	Val	Thr	Ser	Asn	Met	Ser	Gly	Asn	Leu	Asn	Leu	Gln	Asn	Asn		435		440		445	
	Gly	Ser	Tyr	Ser	Leu	Asn	Ile	Glu	Asn	Leu	Asp	Lys	Thr	Tyr	Val	Val		450		455		460	
15	His	Tyr	Asp	Gly	Glu	Tyr	Leu	Asn	Gly	Thr	Asp	Glu	Val	Asp	Phe	Arg		465		470		475	
	Thr	Gln	Met	Val	Gly	His	Pro	Glu	Gln	Leu	Tyr	Lys	Tyr	Tyr	Tyr	Asp		485		490		495	
20	Arg	Gly	Tyr	Thr	Leu	Thr	Trp	Asp	Asn	Gly	Leu	Val	Leu	Tyr	Ser	Asn		500		505		510	
	Lys	Ala	Asn	Gly	Asn	Glu	Lys	Asn	Gly	Pro	Ile	Ile	Gln	Asn	Asn	Lys		515		520		525	
25	Phe	Glu	Tyr	Lys	Glu	Asp	Thr	Ile	Lys	Glu	Thr	Leu	Thr	Gly	Gln	Tyr		530		535		540	
	Asp	Lys	Asn	Leu	Val	Thr	Thr	Val	Glu	Glu	Glu	Tyr	Asp	Ser	Ser	Thr		545		550		555	
30	Leu	Asp	Ile	Asp	Tyr	His	Thr	Ala	Ile	Asp	Gly	Gly	Gly	Gly	Tyr	Val		565		570		575	
	Asp	Gly	Tyr	Ile	Glu	Thr	Ile	Glu	Glu	Thr	Asp	Ser	Ser	Ala	Ile	Asp		580		585		590	
35	Ile	Asp	Tyr	His	Thr	Ala	Val	Asp	Ser	Glu	Ala	Gly	His	Val	Gly	Gly		595		600		605	
40	Tyr	Thr	Glu	Ser	Ser	Glu	Glu	Ser	Asn	Pro	Ile	Asp	Phe	Glu	Glu	Ser		610		615		620	
	Thr	His	Glu	Asn	Ser	Lys	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu		625		630		635	
45	Asp	Thr	Asn	Pro	Gly	Gly	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val		645		650		655	
	Glu	Phe	Asp	Glu	Glu	Ser	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser		660		665		670	
50	Asp	His	Thr	Thr	Val	Glu	Asp	Thr	Lys	Glu	Tyr	Thr	Thr	Glu	Ser	Asn		675		680		685	
	Leu	Ile	Glu	Leu	Val	Asp	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln		690		695		700	

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	Gly	Pro	Val	Glu	Glu	Ile	Thr	Lys	Asn	Asn	His	His	Ile	Ser	His	Ser	705	710	715	720
5	Gly	Leu	Gly	Thr	Glu	Asn	Gly	His	Gly	Asn	Tyr	Asp	Val	Ile	Glu	Glu	725	730	735	
	Ile	Glu	Glu	Asn	Ser	His	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu	740	745	750	
10	Gly	Gly	Gln	Asn	Ser	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu	755	760	765	
	Asp	Lys	Pro	Lys	Tyr	Glu	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe	770	775	780	
15	Asp	Ser	Val	Pro	Gln	Ile	His	Gly	Gln	Asn	Lys	Gly	Asn	Gln	Ser	Phe	785	790	795	800
	Glu	Glu	Asp	Thr	Glu	Lys	Asp	Lys	Pro	Lys	Tyr	Glu	His	Gly	Gly	Asn	805	810	815	
20	Ile	Ile	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	His	Ile	His	Gly	Phe	Asn	820	825	830	
	Lys	His	Thr	Glu	Ile	Ile	Glu	Glu	Asp	Thr	Asn	Lys	Asp	Lys	Pro	Ser	835	840	845	
25	Tyr	Gln	Phe	Gly	Gly	His	Asn	Ser	Val	Asp	Phe	Glu	Glu	Asp	Thr	Leu	850	855	860	
30	Pro	Lys	Val	Ser	Gly	Gln	Asn	Glu	Gly	Gln	Gln	Thr	Ile	Glu	Glu	Asp	865	870	875	880
	Thr	Thr	Pro	Pro	Ile	Val	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	885	890	895	
35	Ser	Glu	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	900	905	910	
	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	915	920	925	
40	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ala	Glu	Pro	Gly	Lys	Pro	930	935	940	
	Val	Pro	Pro	Ala	Lys	Glu	Glu	Pro	Lys	Lys	Pro	Ser	Lys	Pro	Val	Glu	945	950	955	960
45	Gln	Gly	Lys	Val	Val	Thr	Pro	Val	Ile	Glu	Ile	Asn	Glu	Lys	Val	Lys	965	970	975	
	Ala	Val	Ala	Pro	Thr	Lys	Lys	Pro	Gln	Ser	Lys	Lys	Ser	Glu	Leu	Pro	980	985	990	
50	Glu	Thr	Gly	Gly	Glu	Glu	Ser	Thr	Asn	Lys	Gly	Met	Leu	Phe	Gly	Gly	995	1000	1005	
55	Leu	Phe	Ser	Ile	Leu	Gly	Leu	Ala	Leu	Leu	Arg	Arg	Asn	Lys	Lys	Asn	1010	1015	1020	

His Lys Ala  
1025

(2) INFORMATION FOR SEQ ID NO:5255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

Gly	Glu	Lys	Cys	Met	Phe	Leu	Ala	Trp	Asn	Glu	Ile	Arg	Arg	Asn	Lys	1	5	10	15
Leu	Lys	Phe	Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Met	Ile	Ser	Tyr	Leu	20	25	30	
Leu	Phe	Leu	Leu	Ser	Gly	Leu	Ala	Asn	Gly	Leu	Ile	Asn	Met	Asn	Lys	35	40	45	
Glu	Gly	Ile	Asp	Lys	Trp	Gln	Ala	Asp	Ala	Ile	Val	Leu	Asn	Lys	Asp	50	55	60	
Ala	Asn	Gln	Thr	Val	Gln	Gln	Ser	Val	Phe	Asn	Lys	Lys	Asp	Ile	Glu	65	70	75	80
Asn	Lys	Tyr	Lys	Lys	Gln	Ala	Thr	Leu	Lys	Gln	Thr	Gly	Glu	Ile	Val	85	90	95	
Ser	Asn	Gly	His	Gln	Lys	Asp	Asn	Val	Leu	Val	Phe	Gly	Val	Glu	Lys	100	105	110	
Ser	Ser	Phe	Leu	Val	Pro	Ser	Leu	Ile	Glu	Gly	His	Lys	Ala	Thr	Lys	115	120	125	
Asp	Asn	Glu	Val	Leu	Ala	Asp	Glu	Thr	Leu	Lys	Asn	Lys	Gly	Leu	Lys	130	135	140	
Leu	Gly	Asp	Thr	Leu	Ser	Leu	Ser	Xaa	Xaa	Arg						145	150	155	

Claims

- Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
- Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:

(a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;

(b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

(c) retrieval means for obtaining said homologous sequence(s) of step (b).

6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.

9. The nucleic acid fragment of claim 8 which is DNA.

10. The nucleic acid fragment of claim 8 which is RNA.

11. A vector comprising a fragment of claim 8.

12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.

13. A vector comprising a fragment of claim 12.

14. A organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.

15. A method for producing a polypeptide in a host cell comprising the steps of:

(a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and

(b) isolating said protein.

16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.

18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:

- (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;
- (b) identifying members of said library which contain sequences that hybridize to said target sequence;
- (c) isolating the nucleic acid molecules from said members identified in step (b).

19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:

- (a) isolating mRNA, DNA, or cDNA produced from an organism;
- (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
- (c) isolating said amplified sequences produced in step (b).

20. A polypeptide encoded by a fragment of claim 8.

21. An antibody which selectively binds to any one of the polypeptides of claim 20.

22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.

23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.

24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.

25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.

26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.

27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising

- (a) an isolated polypeptide antigen of claim 24, and
- (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.

28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.

29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

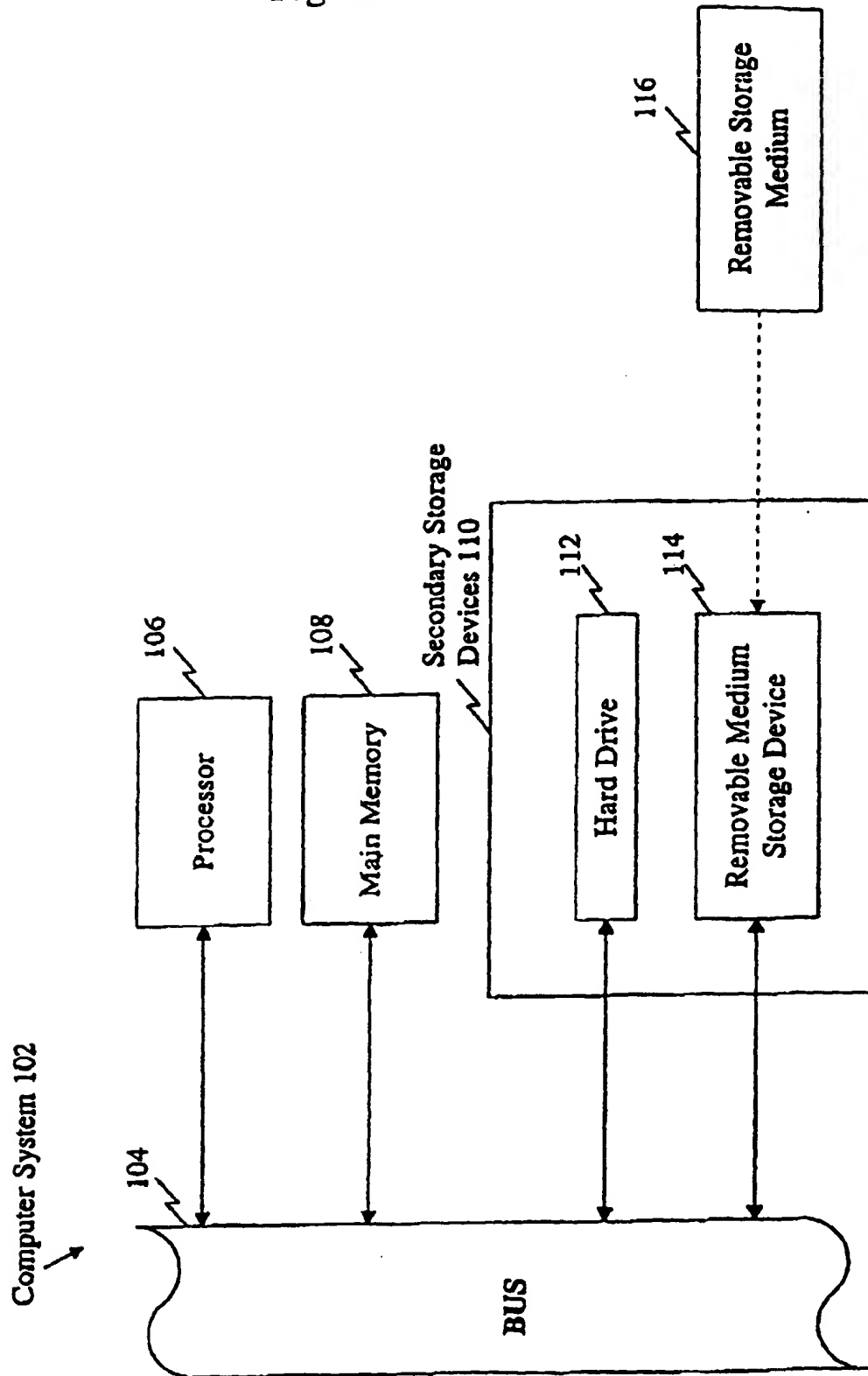
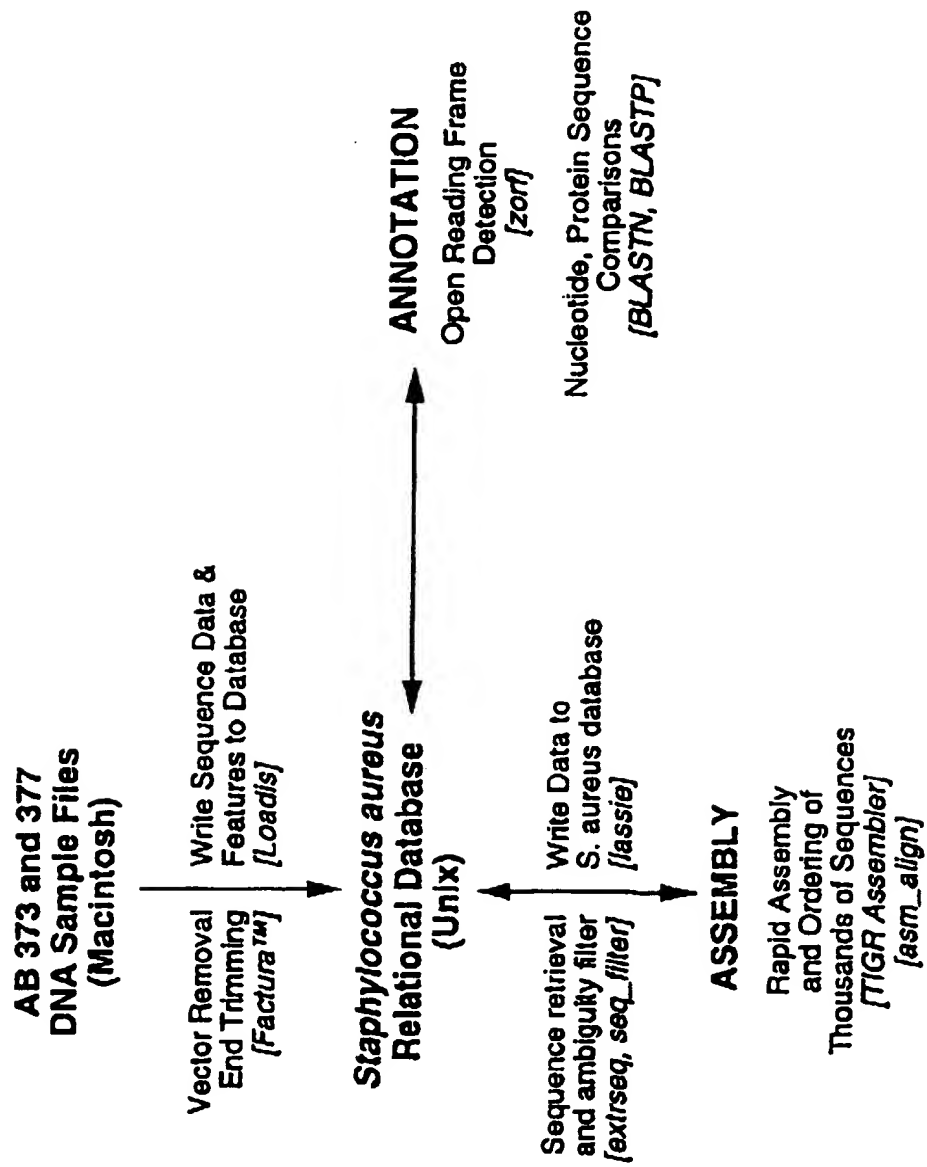
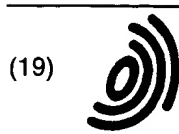




Figure 2





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(11) **EP 0 786 519 A3**

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(30) Priority: 05.01.1996 US 9861

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(54) **Staphylococcus aureus polynucleotides and sequences**

(57) The present invention provides polynucleotide sequences of the genome of *Staphylococcus aureus*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynu-

cleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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# PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention EP 97 10 0117 shall be considered, for the purposes of subsequent proceedings, as the European search report

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
X	"EMBL Database entry SA5SRR, accession no. L36472, 17th November 1994, C.J. GREEN AND B.S. VOLD: "An unusual rRNA-tRNA gene organization in Staphylococcus aureus" EMBL NUCLEOTIDE SEQUENCE, XP002036821 ---	1-29	C12N15/31 G06F17/30 C12N1/21 C12P21/02 C12Q1/68 C07K16/12
Y	BURKS C. ET AL.: "GenBank" NUCLEIC ACIDS RESEARCH., vol. 20, 1992, OXFORD GB, pages 2065-2069, XP002036820 * the whole document * ---	1-29	C07K14/31 A61K39/085 //(C12N1/21, C12R1:445)
Y	US 5 292 874 A (GEN-PROBE INC.) 8 March 1994 *whole document* ---	1-29	
Y	US 5 187 775 A (DNASTAR, INC.) 16 February 1993 *whole document* ---	1-29	
-/--			TECHNICAL FIELDS SEARCHED (Int.Cl.6)
			C12N G06F C12P C12Q C07K A61K
<b>INCOMPLETE SEARCH</b>			
<p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search:</p> <p>Article 52 (2)(d) EPC - Presentation of information - Claims 1-4 concerns computer readable media characterised solely by the information stored thereon. However, search has been carried out as far as possible.</p>			
Place of search <b>MUNICH</b>		Date of completion of the search <b>31 July 1998</b>	Examiner <b>Chakravarty, A</b>
<b>CATEGORY OF CITED DOCUMENTS</b> X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

EPO FORM 1503 03/82 (P/M/C/D)

## PARTIAL EUROPEAN SEARCH REPORT

Application Number

EP 97 10 0117

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (InLC1.8)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
Y	FLEISCHMANN R D ET AL: "WHOLE-GENOME RANDOM SEQUENCING AND ASSEMBLY OF HAEMOPHILUS INFLUENZAE RD" SCIENCE, vol. 269, no. 5223, 28 July 1995, pages 496-498, 507 - 512, XP000517090 * the whole document *	1-29	
X	DATABASE EMBL European Bioinformatics Institute Accession No. U21636, 21 November 1995 ZHANG Q. ET AL.: XP002073245 * abstract *	1-29	
X	DATABASE PIR Accession No. S15269, 13 January 1995 KONTINEN V.P. ET AL.: XP002073246 * abstract *	1-29	TECHNICAL FIELDS SEARCHED (InLC1.6)
X	DATABASE GENESEQ DERWENT Accession No. Q24523, 10 November 1992 YAMAZAKI H. ET AL.: XP002073247 * abstract *	1-29	
X	DATABASE PIR Accession No. S54820, 8 July 1995 MAHE B. ET AL.: XP002073248 * abstract *	1-29	



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Application Number  
EP 97 10 0117

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (InCL6)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
X	DATABASE EMBL European Bioinformatics Institute Accession No. X56347, 6 March 1991 HOCH J.A.: XP002073249 * abstract *	1-29	
X	--- DATABASE PIR Accession number: A53310, 8 September 1995 TANIMOTO K. ET AL.: XP002073250 * abstract *	1-29	
X	--- DATABASE EMBL European Bioinformatics Institute Accession number: U38418, 9 December 1995 CHUNG Y.J. ET AL.: XP002073251 * abstract *	1-29	TECHNICAL FIELDS SEARCHED (Int.Cl.6)
A	--- DATABASE SWISSPROT Accession number: P33362, 1 February 1994 RICHTERICH P. ET AL.: XP002073252 * abstract *	1-29	
A	--- DATABASE PIR Accession number: S29683, 7 October 1994 GLASER P. ET AL.: XP002073253 * abstract *	1-29	
A	--- DATABASE PIR Accession number: S14508, 31 December 1991 SCHREIBER L. ET AL.: XP002073254 * abstract *	1-29	
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EPO FORM 1500 03.92 (P04C10)



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## PARTIAL EUROPEAN SEARCH REPORT

**Application Number**

EP 97 10 0117

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
A	DATABASE PIR Accession number: Pc1253, 30 September 1993 STUCKA R. ET AL.: XP002073255 * abstract *	1-29	
A	DATABASE EMBL European Bioinformatics Institute Accession number: Z54398, 4 October 1995 ODELL. C ET AL.: XP002073256 * abstract *	1-29	
A	DATABASE EMBL European Bioinformatics Institute Accession number: U32788, 9 August 1995 FLEISCHMANN R.D. ET AL.: XP002073258 * abstract *	1-29	TECHNICAL FIELDS SEARCHED (Int.Cl.6)
A	DATABASE PIR Accession number: I64181, 18 August 1995 FLEISCHMANN ET AL.: XP002073259 * abstract *	1-29	
A	DATABASE EMBL European Bioinformatics Institute Accession number: U32744, 9 August 1995 FLEISCHMANN R.D. ET AL.: XP002073260 * abstract *	1-29	
	-/--		



European Patent  
Office

## PARTIAL EUROPEAN SEARCH REPORT

Application Number  
EP 97 10 0117

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
A	DATABASE PIR Accession number: P31728, 1 July 1993 CHANYANGAM M. ET AL.: XP002073261 * abstract * -----	1-29	
			TECHNICAL FIELDS SEARCHED (Int.Cl.6)

EPO FORM 1503 03/12 (P4/C10)





(C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578:

AAATTGTCAC TnCAGGTCAT AACCAACCAG GTGGGACTGC ACGAGCGTTA CTAATGATCC 60

10 AACGGTCTTG CTTTGTGATG AGGCAACAAG TGCACCTGAT CCGC 104

(2) INFORMATION FOR SEQ ID NO: 1579:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579:

GCTCAATAGA TACAATATT AGGACAACGG ACTATCGTTT ACAATTTATT CCAGATAAGG 60

25 ATCGCGCAGG TCGTATGCGT AACTATGCA 89

(2) INFORMATION FOR SEQ ID NO: 1580:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580:

TTGTCTCTAA TAATGGnTTT GGCTTTTCT AAAATTTTCTAG ATGTGGGTGC TGGTGAAGCA 60

40 CCGACTGGTT AATTTTCTTG TCGTCACGGC CACTTTTGT TT 102

(2) INFORMATION FOR SEQ ID NO: 1581:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581:

AAGGTGCTGT TATTAGGATA ATGnATTAA ACCCCATGGT ATGAAGGATA TCTGGAAGTT 60

55 AGATTGGATA TCCCTTAACC ATGGGGGGTT TTATTTTGG GG 102

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582:

TTCAGGGGAG CTGAACATAT TGACGACTTT TGGGTCAATT CATTTTGCAT TTTACTTTTA 60  
 AATGCGTTGT TGCATGTAAT TGTATTAACG ACATACATGG TGGGGCTCTA AATnAATGCT 120  
 TGACTAATTT CTTGGATGGA GACCACGATT TACCAACTCA 160

## (2) INFORMATION FOR SEQ ID NO: 1583:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583:

TAAAAGCAAG TACATTAGAG GTTAGATCAC AAGCTACTCA AGACTTGAGT GAATATTATA 60  
 ATAGACCGTT CTTTGAGTAT ACAAATCAGT CAGGATATAA AGAGGAAGGA AAAGTGACGT 120  
 TTACTCCTAA TTATCAACTT ATAGATGTAA CTTTAACTGG GAATGAAAAG CAAAATTTTG 180  
 GTGAAGATAT TTCTAATGTA GATATATTTG TTGTAAGAGA AAATTCTGAT AGATCTGGTA 240  
 ATACAGCTTC AATTGGTGGT ATTACTAAAA CAAACGGTTC AAATTATATT GATAAAGTAA 300  
 AAGATGTAAA TTTAATAATT ACTAAAAACA TCGATAGTGT TACATCAA 348

## (2) INFORMATION FOR SEQ ID NO: 1584:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584:

AGCCAGCAGT AGATAGATAT ATTAATGAAT TCTTGAGAGAA AGGTAGCTCA AATTGTCCAA 60  
 TTGAGATATT GAA 73

## (2) INFORMATION FOR SEQ ID NO: 1585:

(A) LENGTH: 255 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585:

10 GTAAGGAATG GTCACGTATT CCACACTTCT ATATGAATTA TTATGTATAT CAATACGCAA 60  
 mTGGTTACAG TGCAGCTCAA AGCTTAAGTC ATCAAATTTT AnCAGAAGGT AAGCCAGCAG 120  
 TAGATnGATA TATTAATGAA TTCTTGAAAA AAGGTAGCTC AAATTATCCA ATTGAGATAT 180  
 15 TAAAAAATGC TGGTGTAGAT ATGACAACAC CTGAACCAAT TGAACAAGCT TGTGAAGTTT 240  
 TTGAACAAAA ATTGA 255

(2) INFORMATION FOR SEQ ID NO: 1586:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586:

30 TTATTAGGTG AnTCCATTGG CAACATTGAT TGGTTTGTC TTAGGACAAA TTTTATTATA 60  
 CATGGCGTT ATTTTACTA TCTTATCTGG TATTGAATAC TTTTATAAAG GTAGAGATGT 120  
 TTTTAAACAA AAATAAATAT TTGTTTATAC TAGATTTTCAT TTTCATATGG AATCTAGTTT 180  
 35 TTTTAATCCC AATTTTAGAA ATTAGCCACG CAATTGTTTA TAATGATATA TTGTAAACA 240  
 ATATTTGTTT ATTTTTTTAG GGAAATCTG TAGTAGCATC TGATACATTG AATCTAAAAT 300  
 40 TGATGTGAAT TTTTAAATGA AATACATGAA AAAATGAATT AAACGATACA AGGGGGATAT 360  
 AAATGTCAAT TGCCATTATT GCTGTAGGCT CAGAACTATT 400

(2) INFORMATION FOR SEQ ID NO: 1587:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 561 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587:

55 CAAAGCGTCT ATTATTGTTT GATTTTGATG AAACATATTT TAAACATAAT ACAAATGAAG 60

AAGTGATCAC TGCTGTATTG ACAGGAAGTA CATTTCAAAG TGTCATGGAT AAaATGGATC 180  
 AAGTTAATAT GACGTTTAAA CCATTACATA TCTTTTCTGA TTTGAGTTCT AAAATGTTCA 240  
 5 CTTGGAATAA TGGCGAATAT GTTGAATCAG AAACATATAA AAAGAAAGTC TTGAGCGAAC 300  
 CATTTTTATT TGAAGATATT GAAGATATAT TACGTCATAT TTCTGCGCAA TATAATGTCG 360  
 10 AATTTATTCC ACAAAGAGCA TTTGAAGGTA ATGAAACACA TTATAATTTT TATTTTCATT 420  
 CAACAGGTAA TCACAACAAT GATAGTCGTA TCCTAGAAGC ACTnnTCAGA TACGCAAATG 480  
 ACCAAACTA TACAGCGAGA TTTAGTCGAA GCAATCCATT AGCTGGTGAT CCTGAAAATG 540  
 15 CGTATGATAT TGACTTCACA C 561

(2) INFORMATION FOR SEQ ID NO: 1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588:

CCAACAGTTT TATCATTATG GCAAGTTCTG TTAAACCTGC TGAGAGTTAT TTTGCACTGA 60  
 30 TTGCAAAACC AGAAATTGG 79

(2) INFORMATION FOR SEQ ID NO: 1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589:

GCAGATATGC AGCAATTTAT AGAGGACTAG TAAACGCATA TATGACTTAC AGCTTTCAGA 60  
 45 CAAATAGCTT TGC 73

(2) INFORMATION FOR SEQ ID NO: 1590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TCAATTTATG GTTGATCATA GGCCTCGTCT TTTTCCTTGG GGATTTTATC TTAAATACA 60  
CAGATTGGCG C 71

(2) INFORMATION FOR SEQ ID NO: 1591:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591:

ATACAATACA ATTCACACCA TATATGGATA AAATGCAAGA TGCAATTACT GCAGTTGCAC 60  
AGTGCAAGTA GCAATACC 78

(2) INFORMATION FOR SEQ ID NO: 1592:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592:

CCAATTAATT AAAAACCGGA AAACCAATTT TTAAACCAA TTAAGTTAAA AATTTTTTAA 60  
AATTGGGCCC CAAACCTTGG AAAAAGGTTT AATTTTCCTT TCCCAATTTT CCCAAAATTT 120  
TTAAACCCAA AATTCCCGG TTTTGGGTTA AATTTCCCTn GGTAAAT 168

(2) INFORMATION FOR SEQ ID NO: 1593:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593:

TGCTAGAAAG TATAGAACCT GGTTCAAACG CATGGTTTTA TGTCCCTTTT TAAACnGATG 60  
TTTATTAAAA AAATATGGAA ATTGGCCACG TCCGCCAATT TCCTTAGAAA AGAACGT 117

(2) INFORMATION FOR SEQ ID NO: 1594:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594:

AGACGAAGCC AAAAAGTTAT TCGCCAAATC TGAAATATTT TCAAAGACCT TAAAGGCGTA 60

10

AAATAC 66

(2) INFORMATION FOR SEQ ID NO: 1595:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595:

ATTTTATTTA GGCCAATAAC TGNCTACTTC TGAAATAAGT TGCTTTGCAT AGTCTGACGC 60

25

GGGATGTTTG GATAATATCT TCTGTGTTAT TGCATTGCAA 100

(2) INFORMATION FOR SEQ ID NO: 1596:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596:

GACCAGACGG CCGTAAACCT GGATGAAACC GTCCATTAGA TTCTGAAGTT GGTATTTTAC 60

40

CTAGAACGCA TGG 73

(2) INFORMATION FOR SEQ ID NO: 1597:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597:

CTTTATAAAA TTGTCITTGA CTAACAGGAT TTTCAACGCT ATTCACAAAC CATGGTTTAA 60

55

CATATT 66

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598:

TATGGCACCC TCTTTGATnT TGTGACCGTT TTTGGTAATT CACCATTATT GTACGAACCA 60  
 TGGAAATTCGC TGCCTTCCTT TAGGCAATAA CATAATTATA TTTATCCCCT TCTTGTCACT 120  
 AGAGGTGCTG ACAACACCA 139

## (2) INFORMATION FOR SEQ ID NO: 1599:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599:

CTCCTCTGCA TGCACATCTT GTTGTAGCAA GGTTCACATG TAATTTATTA AATCGAACT 60  
 CTATCCAAC TATGTTATAAA GTTCATTCTA AACAAATnAG T 101

## (2) INFORMATION FOR SEQ ID NO: 1600:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600:

TTGTACCAAG GTTCACATGT AATTTATTAA AGCGAAACGC GTATCCAAC TATGTTATAAA 60  
 GTTCATTTCGT AAACAAATAA GTATAAAAAAT TCAATATTTT TATTACTAGA ATATGGTTAA 120  
 ATACATTTAT TTCTTATAAn AATTTGATGT TTAAGATATT TTGCCAAATT GA 172

## (2) INFORMATION FOR SEQ ID NO: 1601:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601:

5 TTGGCACTGG CCGTCGTTTT ACAACGTCGT GCACTGGGAA AACCAAA<sub>n</sub>CA CGACGTTGTA 60  
 AAACGACGGC CAGTGCCAAG CTTGCATGCC TGCAGGTCGA CTCTAAGAAG GA 112

## (2) INFORMATION FOR SEQ ID NO: 1602:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 679 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602:

20 TGCAATGGTT AATCATCTCA TATAACAACA CATAATTTGT ATCCTTAGGA GGAAAACAAC 60  
 ATGACAAAAC ATTATTTAAA CAGTAAGTAT CAATCAGAAC AACGTTTCATC AGCTATGAAA 120  
 AAGATTACAA TGGGTACAGC ATCTATCATT TTAGGTTCCC TTG<sub>n</sub>ATACAT AGGCGCAGAC 180  
 25 AGCCAACAAG TCAATGCGGC AACAGAAGCT ACGAACGCAA CTAATAATCA AAGCACACAA 240  
 GTTTCTCAAG CAACATCACA ACCAATTAAT TTCCAAGTGC AAAAAGATGG gCTCTTCAGA 300  
 GAAGTCACAC ATGGATGACT ATATGCAACA CCCTGGTAAA GTa<sub>a</sub>TTAAAC mAAATAATAA 360  
 30 ATATTATTTT CAAACCGTGT TAAACAATGC ATCATTCTGG AAAGAATACA AATTTTACAA 420  
 TGCAAACAAT CAAGAATTAG CAACAAC<sub>T</sub>GT TGTTAACGAT AATAAAAAAG CGGATACTAG 480  
 AACAATCAAT GTTGCAGTTG AACCTGGATA TAAGAGCTTA ACTACTAAAG TACATATTGT 540  
 35 CGTGCCACAA ATTAATTACA ATCATAGATA TACTACGCAT TTGGAATTTG AAAAAGCAAT 600  
 TCCTACATTA GCTGACGCAG CAAAACCAA CAATGT<sub>T</sub>AAA CCGGTTCAAC CAAAACCAGC 660  
 40 TCAACCTAAA ACACCTACT 679

## (2) INFORMATION FOR SEQ ID NO: 1603:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 85 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603:

50 CATTTTAATT GATATAATTT AGACTTTAAC ATTTCATGCT GTTCACGGTT TTAATTTGAG 60  
 55 ACGTCATTTG GTATAACAAC TATAC 85



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604:

ACTGGTGTGA ATAGCTCCAG CAATTTCTTT AACCGCGATC ATAATCAACG TCACCTTTTA 60

ATTTGCCA 68

(2) INFORMATION FOR SEQ ID NO: 1605:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605:

TGGGGGGTnT TTTTGGGTTG GGTAAAAAA AGGGAATTGG CCCAAGGGGG GAATTCCTT 60

AAAAAAACCC CCAACCCCT TGGGAAATTA AAAATTGGGT TAACCGGA 109

(2) INFORMATION FOR SEQ ID NO: 1606:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606:

GCTTATATAC ATGTTCCATT ATAAAAGGAG TACGAACGAA AGTAACGCAT GACGTTAATT 60

TAAAAATATT GTAATAATTA TGGATTAAAT TTAAAACCAh GGGGTATTCC AT 112

(2) INFORMATION FOR SEQ ID NO: 1607:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607:

GTTCAAGTTG GTAACCTAAC AACACGnAAT TAGTTTAAAC GTTTGG

106

(2) INFORMATION FOR SEQ ID NO: 1608:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608:

CACACTGATA CCATAGGATT TATGATAGAT CAACAGCATG ACCAAATGTA TGACCTAAAT 60  
 TTAAAAATTT ACGTACACCT TGT 83

(2) INFORMATION FOR SEQ ID NO: 1609:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609:

AAAAGAATAA AGTCACTGAA CAATGGTCTT TCACAATGAT GTTGCGTCAA TGCACAAGCG 60  
 CATTATGTnT GTGACTTGGG CAITTTGGCT TATCAGCTGA ATATTATACG CATTTACATC 120  
 CCAATTAACG TA 132

(2) INFORMATION FOR SEQ ID NO: 1610:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610:

TTTAATGCAT ACGCTTCTCG CTTAGCAATT TCTTTGCACG TCTAACAAGC ATTAACGCTC 60  
 TTAnTACTAT AATCACAACA AAACCAGCGA AATATAACAT GCGTATA 107

(2) INFORMATION FOR SEQ ID NO: 1611:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611:

5 TTCGCACCTG GTATCGTTCA AACCACCAAT GATGGCCCGT CTCGCCGTGG CAACAGCCGA 60  
 AGACCGCAGG TAAACCCTGA ACGC 84

## (2) INFORMATION FOR SEQ ID NO: 1612:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612:

20 ACTCACATGT ACGATAACAC CCTTCGTAAA TCCATCTTTG GTTTGCCAAG TTCGTCGTTG 60  
 TAAACTGTCT ATACTCGTTA AACCGCTACA TGTTTTCTTA AAnCCTGTGC CTAAATGCTT 120  
 TACTGAA 127

## (2) INFORMATION FOR SEQ ID NO: 1613:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613:

35 CGTTCAACTT TTTCAATTTT TAACGGCGTT TTACTATCTT TATCTGTAAC TAATTCAACT 60  
 CCAAACATTA AGCCTCGTCC TCTTACATCA CCAACATTTT GATGACGCTT CAGCGCATGT 120  
 40 AACTGTTTC 129

## (2) INFORMATION FOR SEQ ID NO: 1614:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614:

50 nCAACTAGTG GATTTAAnAT AnACATAATT ATAAATGCAA ATGCTAATAG CTGAATACCC 60

55

GCACTAGGTG CATAATTTGT GTATTGAGCA AATAAGCTA ATACAATGAT TGTAATTCCT 180  
 TTAATGACAA ATAAAGGTAA ATTTAATCGT TTTAAAGGTT GGTAAATTAA AAATACAATT 240  
 5 GCAGCTATAT GCGAGCCACT AACTGCCAGC AAATGATATA TACCTATCTC TTAAACACGT 300  
 TCCTTAAATT GCTCATTAAAC TTCTTTTACG TCACCAGTAA TCAATGCC 348

(2) INFORMATION FOR SEQ ID NO: 1615:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615:

20 GAGCTCCACC GCGGTGTCGC CCGCTCTAGA ACTACTGGAT CCCCCGGGCT GCAGGAATTC 60  
 GGCACAGCAT AT 72

(2) INFORMATION FOR SEQ ID NO: 1616:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616:

35 CATCACGTTA AATCATAACG CGTGACGTGC TTTTGCTATT TGTCTCTCGG TATCTCTATA 60  
 TCT 63

(2) INFORMATION FOR SEQ ID NO: 1617:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617:

50 ATTGAATTCA AGGGTGGAAC TCATGAATTG GCTGGAAAAA GGTAGATTTA ACTGGATGGT 60  
 TGnAGCCATA TATCGGTGCG TTTATTTATT TGGTATTTTA AAAATCAACC TCG 113

(2) INFORMATION FOR SEQ ID NO: 1618:

- (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618:

10 GTACAATAAA GTGGTAAACA ACATGCCAAT GGAAAAAGGG ATTAAAGGTG TTTATGTCAT 60  
 TCTTAAAGAT AGTAACGGTA 80

(2) INFORMATION FOR SEQ ID NO: 1619:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619:

25 ATCTTATGTT TTTTTCCTAA AACTTCTGCT ACTTCATTTA TTTGATGTAT GGTAGATAAT 60  
 TCTGTTTGGA TACTCATATC AACTTTTTTCT ATCATATCTG AAATCTCTTT TnTGGCA 117

(2) INFORMATION FOR SEQ ID NO: 1620:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620:

40 CGATAAACCC TTCGTAATCA ATCTTTGGTT TGCCAAGTTC GTCGTTGTAA CAGTCTATAT 60  
 CGTTAAAAGC TACATGnTTT CCTAAGCCTG TGCCTAATGC TTTACTG 107

(2) INFORMATION FOR SEQ ID NO: 1621:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621:

55 AATATCGTGT CTCTGTCCAG TGCTGTCCAA TCAATTTTGA TCCACCGATT GTCATACGTA 60

## (2) INFORMATION FOR SEQ ID NO: 1622:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622:

ACCATCTGAC ATCATCAATT ATGAATTAAT GATGATATTA AAAATAAATT TGAAACATTG 60  
CCAATTGATA GTGCC 75

## (2) INFORMATION FOR SEQ ID NO: 1623:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623:

TACCTGTGTA TCAGCTCTAT TAACAACCTA ACATATGTGA ATAATTTGCG ATCCTTGTTG 60  
ATAATGCTGT AATTGAC 78

## (2) INFORMATION FOR SEQ ID NO: 1624:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624:

GCAAGCTTTT GCGGCTTCTG ATGCACCATT AACTTCTGTA ATTAAACACA CAAAGTGAAA 60  
CAGGTAGGTA ATGCAAAACT GCAACGGACA ATCGA 95

## (2) INFORMATION FOR SEQ ID NO: 1625:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

ATTGCGATTA CACAGTAGTG AATGAGATAT TTGACATGAA AGCTCCTGCA GCTTCTAAAG 60  
 AAGAGTTAGC AGGTTT 76

(2) INFORMATION FOR SEQ ID NO: 1626:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626:

AAAAGCTAAA AAAGATTATC AGGTGTATCA CAAACTCAAA TTCTCATTAC CATTATCTC 60  
 AGTGTGAACG TCTTAATTGA GAACTAATCT AAATTGAGAT ATTAGTCATA TAAGGATGGA 120  
 CAAGCA 126

(2) INFORMATION FOR SEQ ID NO: 1627:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627:

TGATACGATA GAACATAGTT CAGCACATTG TTTGTTGAAA TTGGATATTA CCGCCATTTT 60  
 TTCACAATAT CAATAATACC TGAACGTGTT GGTtTTCCA CATTATGATT GTACAT 116

(2) INFORMATION FOR SEQ ID NO: 1628:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 91 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628:

ATTTTGTCTT ATCTTGAACA AATCCGATTT TTCTCAGACA CTGAATCCAA AGTATTCATG 60  
 TACCATAAAC CATCTGCATG TTGATTTATG C 91

(2) INFORMATION FOR SEQ ID NO: 1629:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629:

ACAGAAAGTC AAACAGTAAA AGCGGCAGAA TCAACTCAAG GTCAACACAA TTATAAATCG	60
TTAAAATACT ACTATAGCAA GCCAAGTATA GAGTTAAAAA ATCTTGATGG TTTGTATAGA	120
CAGAAAGTGA CAGATAAAGG AGTATATGTT TGGAAGGATC GAAAAGATTA TTTTGTGGC	180
TTGCTTGATA AAGATATTGA AAAATACCCT CAAGGTGAGC ATGATAAGCA AGATGCATT	240
TTAGTCATCG AGGAGGAAAC TGTTAATGGA AGACAATATT CAATTGGTGG TTTAAGTAAG	300
ACAAATAGTA AAGAATTTAG TAAAGAAGTC GATGTTAAAG TAACAAGAAA AATTGATGAA	360
TCATCGGAAA AGTCTAAAGA TAGTAAATTT AAAATTACTA	400

20

(2) INFORMATION FOR SEQ ID NO: 1630:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630:

GCTTTCCTTT TCGAAATCTA TAAATCTAAT CCATTGAAGT AAATAATTA TGATAATTAT	60
TAATTCTATA ATTGTnGTTA TCTTTAAATA ATTTGGAAAC CTTTCATAAT CTAAACCAAA	120
AAAGAAAGTT AGACATGAAA AAAGTATCAT AAATAATGAT GCTAAACTTA AGGCTTGTGC	180
ACCTGGCTTT CGAAGAATGT CTATATTTTC CTTAGTAGTC ATATTTACCT ATCTCCTATA	240
CATTGATTTT GTAATAGCAT ATTAAGTATT TAAAGTTATA AGTACTTAGA TTCTTTTCGA	300
TTAAAAGTAT AAAAGCCTAA AATTATCTTT ATATTATTAT TTGATGACAA CTTTATGGTC	360
TCTATTGTTT TTTACTTAAA CGCTAAAAAG CTAnACAAAG	400

40

(2) INFORMATION FOR SEQ ID NO: 1631:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631:

55



TCTAGAGCGA

70

## (2) INFORMATION FOR SEQ ID NO: 1632:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632:

CAACGAAGAT ATTCAAGTGT TCAGTCATTA TTTTGTACTG CTAATGAAAC TGATTCTTGT 60  
 GG 62

## (2) INFORMATION FOR SEQ ID NO: 1633:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 81 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633:

CTAATGATTA GATTCAAAC AATAAAGACT ACAAAAACAA GTTGATAATG GTAAAGATAT 60  
 TATCCAACCTT GACATCTAAA G 81

## (2) INFORMATION FOR SEQ ID NO: 1634:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634:

AATTCACCT TTGTCTAGTA ATTTATTTGT GTAGTGTAAT CATTAATTGT TTTAATATCT 60  
 AGT 63

## (2) INFORMATION FOR SEQ ID NO: 1635:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 579 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635:

ACCAACTAGC TAAATGCCAG CGCGGnATCC ATCTCAnAAG TGCACAGCAA GACCGTCTTT 60  
 5 CCAACTTTTG AACCATGCGG TTCAAAATAT TATCCGGTAT TnAGCTACGG TTTCCCGAAG 120  
 TTATCCCACT CTTATAGGTA GGTtATCCCC AGTGTtACTC ACCCGTCCGC CGCTAACATC 180  
 cAGAGAAGCA AGCTTCTCGT CCGTTCGCTC GACTTGCATG TATTaGGCAc GCCGCCAGCG 240  
 10 TTCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 300  
 TACTAAATAA TGTTTGTAAC TAATAGTTAC GTTTTTGGAA TTAACGTTGA CATATTGTCA 360  
 15 TTCAGTTTTT AATGTTcATT AATGTTCAAT CTCTTTTATT CTACTTCATT TATTTCTTGA 420  
 AGTCAATAAC TTTTtGAACG ATTACTTTAT TTATTCTATA TTGTTTTTAT AGTTATTTCa 480  
 ATGGtAAGTn TTACACTTTT GaaATTCTTC TTTAAAAACA ACTGCGTCGt TTTTGaCGcT 540  
 20 TTATCaTATT ATCmACTTTG GGaATTtAAA GTCAATAAC 579

## (2) INFORMATION FOR SEQ ID NO: 1636:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636:

TCGACATTAA GCAACGTTCT TCGCAAAGG TAGCGAGCGA CACGAGTTAA CTTTGCACGT 60  
 35 TTCATTATT 69

## (2) INFORMATION FOR SEQ ID NO: 1637:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637:

CTGTGACTTC GTCGCGATGA CCTTCGCCGT TGTTCTCATG GTAAGCTTTA AGTATCGTCG 60  
 50 ATGCAGTCnG TTCGCCATGT GCGCCAGCAG ACTGGTTGTA ATGTCGCCTC GTCCGT 116

## (2) INFORMATION FOR SEQ ID NO: 1638:

## (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 71 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638:

ACAACATTTA GGTACTTTCA CGCATATCAC TACAGCTCAA CGTGATGATT TACCAAATCA 60

10

AATTTACAAA G 71

(2) INFORMATION FOR SEQ ID NO: 1639:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639:

GCGTGGCTTT GTGATTAACA TTGACAAGCA CGTGCAACAA CATATTCGAC GCGATAAAGC 60

25

GACATCTAAT ATT 73

(2) INFORMATION FOR SEQ ID NO: 1640:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640:

CGCGATCATT TTCATTTCTA ATTAATCTTC CAAGTCCTTG TCTAAAACGT GTAACGTCAT 60

40

CAGGTAATAC ATATTCCTTG AAAGTTGAAG TGAATTCAGA ATCCATAAGC CAATATTTTG 120

CATTATGCTT GTTCATAAAC GGTAACCTCG CTATCATCAC ACATTTAATA CCATTTGCTT 180

GAAAATCAAA ACCTTCAAAA AATGTTGACG TACCAAGCAG TATGGCCTTA TCAAAATTAT 240

45

TAAACTGTTG TACTATTTTA TAATTTTGGT TCTGCTGTTG TGTTAATACA ACATAATCTT 300

CAAATTCTGG CAATTCATTT AAGCATATCT TGTACCATAT GCATCATTTT ATAACGTA 360

AATAAGACTA AACATTTTGA TGACGTTATA GTCGTATATn 400

50

(2) INFORMATION FOR SEQ ID NO: 1641:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641:

ATTGTTGTAC CATGTATACT AACAAATTGTA ATGTCTCATT TCAGTAAACA AAAAGCGAAA 60  
GACATT 66

(2) INFORMATION FOR SEQ ID NO: 1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642:

ATTTTCGTCGG GAATAAATTT TGCCATTACA TAGAAATATC TAATAGATAA CGAAAAAGTA 60  
TCGTATGTAT TTTTAATATA GTGTAAAATA TTATATGTAA AATAAAATGT AGGTTTTTTAG 120  
TTAGAGGCAT TATAAGAnAA TTTTGAGTAT AGGTTAGCTT TTAATTATGA ATCTTATTGA 180  
AATTTGATTA ATAAAAATAT GATAGGGGAT TAAAATGAAA CTATTTTATA TCGTATTTCT 240  
TATTATTATA TGGCTGAATA TATTTTTAGG AAATGAAATC ATCCATACAC TGACTGTTTT 300  
AATAACAACA TTGTATATTG TTAATTCACG AnAGGGGATT AAAAATGACA GAGTTGAATA 360  
ATATTATAAA CGCGCnTGCA ATCnTTGTTT GAGTCCGGAA 400

(2) INFORMATION FOR SEQ ID NO: 1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643:

AACTAGAGGA GGACATCCTA ATGGAAGCAA AACCCGTTGC TAGAACAATA AGAATCGCAC 60  
CTCGTA 66

(2) INFORMATION FOR SEQ ID NO: 1644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644:

TATCAATTTC ATATGCGATT TGGCCTTGCA ATAATTAGGT CTCACCTTGC CATATCTTTA 60

CCTAAGCAAT ACTTG 75

(2) INFORMATION FOR SEQ ID NO: 1645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645:

CATTCTCCTG CATCATAAAA ATCAACAATT GTATCATCAA AGTGTATCAA AATATTTTAA 60

TATCCCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646:

AGTGACACTT TCGTTCCACC ACATCGTAAA GAAGTACTTC AAGCACGTGA AGATGACATC 60

AAAGAAAAAG TTG 73

(2) INFORMATION FOR SEQ ID NO: 1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647:

CTGTGATTGG TGTGTGATT GTCTTGCTTC CTGGTTGTCC TTCTTGTTTC GCTCGCTCTT 60

CGCCGGGTTG T 71

(2) INFORMATION FOR SEQ ID NO: 1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648:

AACTATAGAA AAATTCGGAA TTATACCAGA AATGGAATAT GAAATGGAAG AGGTTAAACA 60

10

AAACGAGCAA TATATTAGAG AGCAAGAAGA AGCTGGAACA ATAGAGGCGA TAACA 115

(2) INFORMATION FOR SEQ ID NO: 1649:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649:

TGTTGTCATG ATCTGAAAAG TCAAAGTCAA TAGAACATTG GCTTTGGCTT TTTATTTGG 59

25

(2) INFORMATION FOR SEQ ID NO: 1650:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650:

35

ACCGATAATA GTACACGGCA TAATGnAACA ACTTGGCATG CACCCTTTTT ACGTTTCCTTT 60

ATCTCTGCAT GATTGTCATG TTCATCATGG TTTGGCTTGC ATTAATAGAG AGGGTTGACG 120

40

CAGAA 125

(2) INFORMATION FOR SEQ ID NO: 1651:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651:

TGATTAAACGC GAATGCCACT TTTACTACCA ATGTTCCCAA AGCTGCTTCT GACAAACGCC 60

55

ATTGTACTCT G 71

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652:

TCACTACATG CACCATAAAT ACAGTATGAA CGTATTGAAA TGGGCATTAC ATGATACAGA 60

(2) INFORMATION FOR SEQ ID NO: 1653:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653:

TTAATTGAAA CAATTGACAA ATGCAATTTG ACGCCAAACT TTGAACTTTG AATGGATTAT 60

CACATTATGA TTGTTTCATCC ATGGnCAATT AGCATGGACG TATTACATTC TGGATTATCA 120

AGC 123

(2) INFORMATION FOR SEQ ID NO: 1654:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654:

CTATGACGTC GCATGCACGC GTAACCTGGG CCCCTCGAGG GATCCTCTAG AGCGGCCGCC 60

CTTTTTTTTT TTTTTT 76

(2) INFORMATION FOR SEQ ID NO: 1655:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655:

TTTTAAATTT TCGTGAAATC GGAAATGTAC GATTAGTTAT TAAGCGTTAG AATGTGTGAT 120  
 ATGTGAACCT GGTATTGACG GCGCT 145

(2) INFORMATION FOR SEQ ID NO: 1656:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656:

TTTAGAATTC CAATACGCTA TTGCCAGCGA TTTAGCCACT TGTGGGTAAT GATATTGAAG 60  
 GTGTTAGTCA AGT 73

(2) INFORMATION FOR SEQ ID NO: 1657:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 93 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657:

CTTCTGAAAA GTAGTAATGT AACCTATTGG ATGCGAATGA ATCCCCAAAT TTAGTGGACG 60  
 TATGTGGCTT CATCTTCAGA ACCTGTATCT GGT 93

(2) INFORMATION FOR SEQ ID NO: 1658:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658:

AAGTTAACAT GCAAGTTGAC GATGTAATGA CTCAAAAAGA GTGGAAACAA AAACACGA 58

(2) INFORMATION FOR SEQ ID NO: 1659:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659:

TTAATCCCAC AAACAAATGT ATGAAATTGA GTCAGTGATA TTAAATATGG GCTTGAAAGT 60  
 5 GTCTA 65

(2) INFORMATION FOR SEQ ID NO: 1660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660:

TGCATTTTTG TAAGAACGCA AAGCATTGTA AATTAGTTTT TATAAATTAG GATATTATCA 60  
 20 TGTGTATTGA AAACAATGAA GTGTGCTATG A 91

(2) INFORMATION FOR SEQ ID NO: 1661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661:

ACATATCTGT CCACACAACA AGGACCATTT GTCTGAAGGG ACAGTGAGTG GGGAAATATGT 60

(2) INFORMATION FOR SEQ ID NO: 1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662:

TGGGGTTTTA ACCAGGGGAC CTAAAACCAG CCCCCATTTT CCAAGTTTGG ACCCCAAATT 60  
 CCCnAAATTT AAAAAAAATT TGTTTGGGGT CTAAGTTGGG CCGGTGCCTT CCTGCCTAAA 120  
 TTTAGCCCAT GTCTAACATA GTACTTTGGG AACGTAAAAG TTTAATTTA 169

(2) INFORMATION FOR SEQ ID NO: 1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663:

TGGCACAATT GCACCAATTA AATGAATAAC TTTATCATTT TTATATACAG GTACAACAAT 60  
 10 CGCTTCTTTT ACGAACTCAG ACTGGCGTAA TTGTGTTTCA ATTTCTTCTA ATTCCATTCT 120  
 GTAGCCATTC AATTTGATTT GGAAATCAAT ACGACCTTGA ATGAACCATT GACCATTTTC 180  
 AACTTCGCT TTATCACCAG TGTGATATGT ACGAATACCG TCATCGAAAT TAAATACTTC 240  
 15 AGCTGTTTTT TGGTCATTTT TTAAGTATCC TAAACTTACA CTTTGACCTT CGATAACAAG 300  
 TTCACCTTCA TCTGTAGTAG ATAATCTTGC GCCTGGTCTT TCAACGCCAA CAGGTAATGT 360  
 CGGATATTGA TCTAAGATTT CTTGTGTAAT TTGAATACTT GTAACGCTA CCGTAGCTTC 420  
 20 AGTTGGACCA TATGTGTTGT AAATCGTCGC ACTTGGGAAA CGGTTTACTA ACGCTTTTGC 480  
 TGCTCTGTGA GGTAGAATTT CACCACAGAA GAAGAATTCG TTAAGACTAC CATATTGTTC 540  
 25 TTCATTAAGC GTTGGAATA ATAAACACAT TTCCATAAAT GATGGTGTG ATACCCAAAT 600  
 GTTAATCGGT GTTGCTGTTA GCATTTTATT TAATAATTTA GGTTTATTAA TCATGTTTTT 660  
 ATCTACAAGA nTnAAnG 677

30 (2) INFORMATION FOR SEQ ID NO: 1664:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664:

40 GTTACAACAA TAGTGGTATA AAACGGGAGC AATTAGAGAT CAATATATGA TTATTAAGAG 60  
 CA 62

45 (2) INFORMATION FOR SEQ ID NO: 1665:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665:

55

GTTTACGCAA ATGATAGCTC GGTAAAACAT GAGCAACATG TTGAAGCCAA TTTGGAAATG 120  
 TGTTTATCGG AAACCACAAT CCACCTAATA CTGCTAAACC AATTGTTACG ATATTAGCTA 180  
 5 AAGCACTTGT TTTTGAATA TCATTTAACA AAGAACCATA ATATGCCAAA AGTTATTAAT 240  
 AGAGACGCAC CTAACCATAA AAATATTCCT GACTCTAACC ATTGAACTGC ACTCATTGCA 300  
 ACACCTTTAT AAAAATGTCC AACCATAAAA ATAATAATA TC 342

10 (2) INFORMATION FOR SEQ ID NO: 1666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666:

GTCCAAGAAT TCAAAAACGT TTTCAACTTC GGCCAAAGCC CAATTTnTCT TTGTGGTTTA 60  
 ACTTTTTAAT TTTGAACGTT TTAGGGCATA AAAAAAAAAA GG 102

25 (2) INFORMATION FOR SEQ ID NO: 1667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667:

35 TTGATAGTAG CCATAATCAT ACCACTTAAA TAATATGTTT GATCATCGGC ATAATTTTTA 60  
 TTTATTGTCT GTTCGCAATA TTTTGAGCAT TATCATAATT ACCACTAGTC ATATCATCTT 120  
 40 TG 122

(2) INFORMATION FOR SEQ ID NO: 1668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

45 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668:

AGAGATGAAA TTAAATCGC AATTGAAAAT TTCAAATCAC GATGAGAGTG GGACAGA 57

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669:

AACTACTGCC AATATTAATA GCATTGGTAC ATCTTAGAGG CATTGAATTC CTTACTCAGA 60  
 CTCATAATGC 70

(2) INFORMATION FOR SEQ ID NO: 1670:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670:

TTGTCTGATA TAATCCATTT CGATTGGACT CCACACGTTA CACCGATACC TTCTTTACCA 60  
 GCCCCGACCCG TAC 73

(2) INFORMATION FOR SEQ ID NO: 1671:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671:

GAAGAATTGT ACTGTAAAG TGA CTCTAAA CTATCGCGGA AATAACAGTG AAATCACCAA 60  
 TTAGACTAGC GAACTGAAG TCATTAAAAA CAGACATTTG TAGTGGTGCA CTTATCACCG 120  
 CAAATACAAG AGAGTTTCTC 140

(2) INFORMATION FOR SEQ ID NO: 1672:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AACAACGTTT ACTATTGGCA CAGAACGGTT GGTACTTAGT CTAATACCAT TGTCATCAA 59

(2) INFORMATION FOR SEQ ID NO: 1673:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673:

ATCTCTTTGA CTGAAGGAT TGGATTAAAA TCTTGGTGAT TTGGGCCGTG AAATATTTCC 60  
 AGAAAATTCC TCAGACGTAT TAGTATAATT GTAACGnTAC ATTCTAATAT ACCTTTCTTC 120  
 GATG 124

(2) INFORMATION FOR SEQ ID NO: 1674:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674:

CACCACCACC ACACACACAC ACACAAACAC ACAACCCCCC CACACACAAA CCACACCACC 60  
 AACACACCAA CACAnCACAA AAACCCACCA CACACACCAC ACACCAACC 109

(2) INFORMATION FOR SEQ ID NO: 1675:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675:

TnGTCAACTG ATTTATGAAA TGGCAGAGCA TATGGCGTCA AAGGTTCTTA ATCGTTAAGC 60  
 CAGACCACTG GAGGACCATT AGATGCAGCG TTGCTTTCAA G 101

(2) INFORMATION FOR SEQ ID NO: 1676:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676:

	TTTTTAAAAT TTGnAAATTT TAGACCTTAT TTCACGTGCG ATTTAATCGA TGTGTTAATA	60
5	AAACAATACT GGCATTCAAC ATGTAATCCG ATAATAAAAT AAGGTTGCAA TTATGTTATT	120
	GCATATTTTG TTTATTACTT AGAATAATAC GATGGTTAAG ATGAAATATA TGACAAAGAT	180
10	AAATAATGAC ATTAAATTCA AGATGTTTAC GCCTTTTAGA TCTTTTTTAA GCATTTTAAA	240
	TCCTGTCACT TCKACATTAC CGACTAAGAG TAATAAGACG ATAAATACCC ACCAATTsTC	300
	TTTTGGAAAA CTCATCGTCG TTAATGCTAA GACGAATAAT AACAACACAC CCATAATAAT	360
15	TCTCAAAATG CGAGTAAATA CAACTTCCAT TTTAAAAATA	400

(2) INFORMATION FOR SEQ ID NO: 1677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677:

	TCTTACTCAT GCATATGAGT GCAAGGGCCT GAGCATTTCAT CAGCAAGATT AGAGCGATT	60
	TTAC	64

(2) INFORMATION FOR SEQ ID NO: 1678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678:

	ACAGCTGATT TATTAAATGA TACTAAGTCC AAAGGCATGC GCATTATATC AGTTGGTACA	60
	TTTCA	65

(2) INFORMATION FOR SEQ ID NO: 1679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679:

5 AGCGCCACCA ACTGACGAAT TAGGTGGTAG TTGGACACTA TGGAAAAATT TAGCGCGACA 60  
 AAGTCCTGAA TTTGGTAATC CTGATAAGTT TTGCCAAAAT ATTCCTA<sub>n</sub>AA AAAGTTGGTT 120  
 TGTTTCAGCA ACTTCTACAA CAAACAATAA AGAGATTATC GATACAATAG AAAGTATTTG 180  
 10 TAAACGTGAC CCACTTGGCA GGCAAAACAG TTACAGGCGG TATTATTACA ATCAATGATT 240  
 CTGcATGGCA AATGAGTTTT ACAATCAATC GTGCAGCAAC AGTTTGAAAG ACCAACCTGG 300  
 AAAATGGAAA TATCTACATG GGGTTTGATG CCTTATGATT CnGGnGTAAA CGGCGGTTGA 360  
 15 TG 362

(2) INFORMATION FOR SEQ ID NO: 1680:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680:

AGATACTTCA GATTTAGCAT CATGAAGCAA CTTTAAAAGC AATCGCTGAC GCTGGTATTC 60  
 30 AGCCCGAGG 69

(2) INFORMATION FOR SEQ ID NO: 1681:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681:

TAACCATTTT TTTTGACGTT TTATGTTGTT TTAAGAAATA AATACCAGTT AATGTA 56

45 (2) INFORMATION FOR SEQ ID NO: 1682:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682:

## (2) INFORMATION FOR SEQ ID NO: 1683:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683:

CCCCAACACA ACAAACAACA CACCCACCAC CCAACCCAC CACACCCACC CACCACCCCA 60

ACCCACCACA ACACCACnCA CCAACACACA CCACACAACA ACCCCACAC 109

## (2) INFORMATION FOR SEQ ID NO: 1684:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684:

ATTATGTTTCG CGATAATTTA AGTAAAAGAA GCACAGATAT TGAATTTGAT AGGAGTAATT 60

GT 62

## (2) INFORMATION FOR SEQ ID NO: 1685:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685:

CATAAGGTAC TTAAATTAAG GCATATCTGC TGTCTAGCAG TCGCATAAAT CATTAGA 57

## (2) INFORMATION FOR SEQ ID NO: 1686:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686:



## (2) INFORMATION FOR SEQ ID NO: 1687:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687:

CTTTATAGTA TATTGCTTTT TGTTTTTCTT TTTCGTCATA TTTCACCTTTT AAATAGATAC 60

CTGCAACACT AATTAATATG ATTAACATAA TACTAGTTAA TATTAAATT 110

## (2) INFORMATION FOR SEQ ID NO: 1688:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688:

AATTACTAGT CTGCTTGTCC AAAGATTATT TATATTCTAG CTCAACATTA ATTTCTTTGA 60

TTTTGGTACC ATCTATCGTG TCACCCATGC GATGCGGTG TAGTTTTTTT GTAAGTTCTGA 120

AAGTATAAAA CTTATCATCT TCCATTTTAA CTACAATTTT ACCTTTTCTA TTATTAACAG 180

CACCATATAA TTTTCTTCT TCCATCAATT TTTT 214

## (2) INFORMATION FOR SEQ ID NO: 1689:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689:

GCTAGTTGTA ACGTGCTTTT TCACCACCAG ATAAATCATA ATATCTTTTA ACATCTCTG 59

## (2) INFORMATION FOR SEQ ID NO: 1690:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690:

CCAAACTTTA TAATATGAAA TGCTTGGTAA TTACAAAGAT AAAATCATAC TCACG 55

5 (2) INFORMATION FOR SEQ ID NO: 1691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691:

TAGACAGCAA TCCATTGCTA TAGGGGTGGA TATCTCATTT GCGTTTGGAG CTGTGCTTGT 60

TATG 64

20 (2) INFORMATION FOR SEQ ID NO: 1692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692:

TGCATGGGAT TGCAGCTAAG AGAATCATAA AAATATATTA CTTTAATAAG TGTAGTA 57

(2) INFORMATION FOR SEQ ID NO: 1693:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693:

45 CGATGTGTAC GTCTCACCTG ATTTGCGACG GTAAGCTAGT GCATATTCAG CACCGCTACT 60

CGCCCAGCCT AGAC 74

(2) INFORMATION FOR SEQ ID NO: 1694:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

AACTTTTCAG ATGTTGATAG CTATAGATTT AGGCGCTATT CACCA~~n~~GTCT ACATGCAATA 60  
 5 CGTACGTTAT AATGCACTGC AACGAATCGC GCGTTATGAG TTGGTAATTG TTGTTCAATA 120  
 TTGGGTGTAT AGTTTTCAAC GTGGTTACAA GCAACTACCT AA 162

(2) INFORMATION FOR SEQ ID NO: 1695:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695:

20 AATTATCTCT ACACCTTTTC TTTCACATAA TTGACGCAAT ATAATCCCTA TATCT 55

(2) INFORMATION FOR SEQ ID NO: 1696:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696:

30 ATGCAACGTT GGCATTGGGA AATGGTCTCG CCTAAATTAA CACGCAATAA AATGTG 56

(2) INFORMATION FOR SEQ ID NO: 1697:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697:

45 ACTGTGTAGA AGATGCTATT ATTGTAAAAC ATAGTTTTAA TTTTATTTTC TGATATA 57

(2) INFORMATION FOR SEQ ID NO: 1698:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear  
 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698:

AAAATTTTCC CCCGGAACC CGGTTTTTTA AACCCCCCGT TTAAAAAAA TTTTGGGGGG 60  
 5 CCCAAAATTT CCCAAAAAAA nAAAAAATTT TTTTTTCCC GGGGAAAAA 109

(2) INFORMATION FOR SEQ ID NO: 1699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699:

GTGTTAACGT GGATTATATC AAnGAGGCGG TCAGGTACAG TCCACACGCA CAGCGCACAG 60  
 20 AAGTATCACA TCCAGTAAAC AAGGCTAGTA CAGCATTGCA 100

(2) INFORMATION FOR SEQ ID NO: 1700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700:

AAGGTTAAAT GAATTAGGTT GATCAATGCT CTATACTCAT TGCTAAGTCA ACGCACCTTT 60  
 35 ACCACCTTTT CCCTAACTCAG TAAGGCATTC GACGTATTTT TTAGCCAAGn TTACATATCT 120  
 ACTCTGCAC 129

(2) INFORMATION FOR SEQ ID NO: 1701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701:

CAAGAGGAAC AACTCGGTAC TGCGCATCAG CAGAGATGGC GAAATCACAC TTAGAAGACA 60  
 AGG 63

(2) INFORMATION FOR SEQ ID NO: 1702:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702:

10 TATTTAATAA ATCTTCAATA CCTTGTTTCAT CAGTTTGTG ATAAATAAGA CCTCTCCATT 60  
 TTAAATCTTC AATTAATACA TTCGTCATTA TTATTTCTC CTATTTATAA TTATTTATTG 120  
 AATACTTGTT AAAATACTTT AAAGkTTTTT GAACGTAAAA AAAACCCTTA CAACAAATAT 180  
 15 GTAAGGGCGC GATTGCACGT TACCACCAAA CTTAAACATA ATCATAAGAT AATGTTCACT 240  
 CTATTAATGA TACGTTTCATT AATAAACGTA GGACATGTTA GTTATAAAGG TGTATTCATA 300  
 TTATTAAAAA CACTAGTTCA CAGCGACCAC TAGCTCTCTG ATGATTTCAA ATAATATTAC 360  
 20 TTGTCCTTTT ATCCTATTCT GTATGCATTT TCCCTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 1703:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703:

TCAATATTGA TATCGAAACG CTTTGCAGAT TGATATAAAT TATCAGAATC AAGTAATTCA 60  
 35 TTTATTTTCT TTGGTGAAAG TACTTGAAA ATACTATACT GATGAAACT TAAAAATGAA 120  
 ATGAAGTATG GAAGTTGTTG CTTTGGGTAA GcNAAATTTT TAATACATAC TGATTAACT 180  
 40 GTTTGTTTAT TGnGAATTGC AACGCATC 208

(2) INFORMATION FOR SEQ ID NO: 1704:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704:

AAGCCGATGT AATTATTTAT GCAACACCTG TTCTAATGCA CAAAGAAATA TCTTAGCGAG 60  
 CTTATAG 67  
 55

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705:

CCAAGTTGCA TGTTATTTTA AGCTGACTTT CCACCAACTT CTGAGTTTGT GGCC

54

(2) INFORMATION FOR SEQ ID NO: 1706:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706:

CAACTACACG AAAGGGTAGT GCTTCAAGAT AATAACGTCC AATTATTAGG AACTGTGGCG

60

A

61

(2) INFORMATION FOR SEQ ID NO: 1707:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707:

ACCATTCCAA ATGAACCTAA ACCACTTGAT ACGTTGACGA CAACAGGTTG TTCA

54

(2) INFORMATION FOR SEQ ID NO: 1708:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708:

AAATTTGAAT AACTGTACAC ATTTTTTTGA TCATAGTCTA TATACTTTGT GAATTAATT

59

(2) INFORMATION FOR SEQ ID NO: 1709:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709:

10 GCACAATAGC CAATTAGATG GGGCCGGTGC GGTAACATTT TGCTTCATTC CTGCATTAT 59

(2) INFORMATION FOR SEQ ID NO: 1710:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710:

TTACAATTCA ATCAAGTTCT TCATTATCAG ACGAAGAAAT CCACCGTATG GTAAA 55

25 (2) INFORMATION FOR SEQ ID NO: 1711:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711:

35

TTTCTGCTTA TTGTCATTCG ATATCGAATT ATTAGAAAGT GCAGATTTTCG CATCAG 56

(2) INFORMATION FOR SEQ ID NO: 1712:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712:

TAAACCTTTA GGATTGCTGG CAATAGTAGT GCAGTTGGCT GGACTTGTCA TGCCC 55

50

(2) INFORMATION FOR SEQ ID NO: 1713:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713:

5 CAAGAGGATT CGTGCAnTGA ATTCATGGAG ATATTTAGAT CTTTCACTGG AGAGAAAATA 60  
 AAAAGAAGAA AAGAGTAACC TTTAGATTGC TGGATnTGTG CAGTGGCTGC TTGCGTGCCT 120  
 TTAGGTGGCA TAAGGAGGCT ATACGCAGAC AACCACCGTC CCGGGGTTTT ATTGTACACT 180  
 10 GTGTAGGACG CAGACTTTAT GTGGTTG 207

(2) INFORMATION FOR SEQ ID NO: 1714:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714:

TGGTTATCGA CTGCTCGTAT ATTTTGACTG TTTTGACTGT TGTTCGGTA GCAATACTAT 60  
 25 CTCCTAAGCC TTTCAATTGGC ATTG 84

(2) INFORMATION FOR SEQ ID NO: 1715:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715:

GTTTGAATTG ACTGACTTCG TTTTACCGCG TGTTTAATAT TGTTATACAT ATAT 54

40 (2) INFORMATION FOR SEQ ID NO: 1716:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716:

50 GAAGCCTGTC AGTGGATCAA ATTATTGAAG ATAACCTGGG TGGCATT TTTT GGAAAGTCCA 60  
 AATGCTGGGA ATGGTCA 77

55



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717:

GGGCCCTTTT TTCCCAAAA AAAAAAACCC CCCCAACCCC AATTTTGGnC CCCCTTCCCC 60  
 TTTAAAAATT TAAAAATTGG GCCAAAAGGC CCCCCCAAAA AAAACCCCCA ATTGGAATTG 120  
 GAAAACCATT GGAACCAATT CCATTGAACC AGGA 154

## (2) INFORMATION FOR SEQ ID NO: 1718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718:

ATTGTCTACA CTGCCACTTT ATTTTCATTA ACCATTTCAC AAATGTGTTC ATCATTCAAC 60  
 ATGAACATCA ATTGTTCAAT TACATCGACA CCTGATGCCT AAnCACGCAC CTTTTCACA 120

## (2) INFORMATION FOR SEQ ID NO: 1719:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719:

TTCATTTGTT TGTAAGAGTG GCATTTCTAT GTCTTAAAG TGACGAAACT TCAC 54

## (2) INFORMATION FOR SEQ ID NO: 1720:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720:

## (2) INFORMATION FOR SEQ ID NO: 1721:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721:

TTTGGATTAT AAATTGACAT GTAAGTACGA GGCAGCTGTA CCCGATATAT AATTGCTAAG 60  
 AGTTAGGGCT G 71

## (2) INFORMATION FOR SEQ ID NO: 1722:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722:

TTTTATCTTT ATTACTAAAA CCAACTGCAC CAAAGTTTGC AGTCATTACC ACACGTTTAA 60  
 CACCCGCATG TTCTGCAGCT CTTAAAATAC GTTGTATACC TTCAATTGCA GGCTTCGCCA 120  
 TCACTTCTGC ATCGTCTGTT TTACCGAAAA ACACCGGAGA TGCTACACTC AAGACATACT 180  
 TGCAATCTTT CATTGCTTCA TCCCAATGTh CATCTTGTGA TAAATCCGCT TCGACAAACA 240  
 TTAAATCGCT CTGTGGAAAT GCCCATGTCT TGCATTGTTT nAATTACTTT ATCAGCTTTA 300  
 CTTAAATCAA GnATCGTCGT TTGTA 325

## (2) INFORMATION FOR SEQ ID NO: 1723:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723:

CAGTATTGCA GTCACGACAA TGTGATGACT AAATTATCCA AAGTATGAAT TCCATGCGGC 60  
 ATTAATCCTA G 71

## (2) INFORMATION FOR SEQ ID NO: 1724:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724:

10 TTGCAACGAT ATTAGGCTAT CTAGTCGGCA TATTGTAAA ACAAGATCCA ATT 53

(2) INFORMATION FOR SEQ ID NO: 1725:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725:

ATCTATTCAT CTTCGTACAC GGACAGGAAA TGAGTCCAGT AGATGCACAT TGGGAATTAA 60

25

TCGAAGCTAG C 71

(2) INFORMATION FOR SEQ ID NO: 1726:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726:

CATCTTGCAG GTCTACATTA TAAAATGTGA AGTTTCTAC GATAACAATT GGGAAACTCA 60

40

GGGGCATCTC C 71

(2) INFORMATION FOR SEQ ID NO: 1727:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727:

TTCTTTTTTA AAAATTCCCC ATTCCTTTTT AAATTTCTTT CCCGCTGGAT TAAATGGATT 60

55

TTAAAAATTC CACCCCAACT TAAATTTAAA TGGCTTGTGG AAAATTAACG GGATTGGCAT 120

TCCAGCTTAA ATGGTTTTTT TGGAGGCTTC CACGTAAAA ATGGCGGGTG GCTTT

235

(2) INFORMATION FOR SEQ ID NO: 1728:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728:

TAGAGTGGCT ATAAAGCTAA GTTCAATTGA CCAATTTACA ACAGGTATT GAGGACAATA

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61

(2) INFORMATION FOR SEQ ID NO: 1729:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729:

ATCACCAAGA AGTTCTAATG CTTGGTATAA ACGTTGAATA CGACGTTCCG TATT

54

(2) INFORMATION FOR SEQ ID NO: 1730:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730:

CGTCCCGAAG CGTTGGAGGC GGGAAATCC AGAGTAATTG GCACAGATTA TGACCATAT

59

(2) INFORMATION FOR SEQ ID NO: 1731:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731:

## (2) INFORMATION FOR SEQ ID NO: 1732:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732:

TATGTGGTGT TCAATGCAGT GGTCAATTATG GTGCATCTTA CCAGATTCGG CATTCTTATT 60

ATAACTATAC TTGTAATAAA TGGCGACATG CAGACACGnC AATAC 105

## (2) INFORMATION FOR SEQ ID NO: 1733:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733:

TTTACGTTCC ATAGCAAAGT GATACAAACG TCAGCATCAA TGTAAGGCAT AGATCATAGT 60

## (2) INFORMATION FOR SEQ ID NO: 1734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734:

TTCCATCATA CATTGCGGTT TTACTTTTCT TCTGGTATGA TCAAATATTC ACATAA 56

## (2) INFORMATION FOR SEQ ID NO: 1735:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735:

AAATGGGGAT GAAACAGTTA GTGTACAGGT GAAAGCTTAA CAGCAGCTAC AATTGCA 57

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736:

GATTTGCAAT TAAACTTAAA TGTAATTTTT CGGAATGTGT ATTTGGTTTA CTAAAGTAA 60  
A 61

(2) INFORMATION FOR SEQ ID NO: 1737:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 57 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737:

AAAGAAGCTA AAGAAAAAGT TGATAAAACA GCAAAAGTGA TTATTAGCTA CAGCATT 57

(2) INFORMATION FOR SEQ ID NO: 1738:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738:

CAATAATATC GCTAAAACCG CCATTTGTAC CAAATGAATT TGATAATGCT GCAG 54

(2) INFORMATION FOR SEQ ID NO: 1739:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739:

TAGAGCCCAA CCGGCAACCC ATCCATGGAA ATTCACCAAA ATAATACATT GACCCCAAG 59

(2) INFORMATION FOR SEQ ID NO: 1740:

(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740:

10 CCTTTTGGn AATTTAAGGG GGTTCACAAC CAAATTCACC CAAATTTTTT TGGGTAAAA 60  
AAACCCGGCC CAAAAATTTA AGGGAATTTG GAAAAAGGTT TGGTTCCTT TTTTCCCAA 120  
GGCCCAAAT TTGGA 136

15

(2) INFORMATION FOR SEQ ID NO: 1741:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741:

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CATTCAACCA ACGACTGACA ACAGAACATT TAAGAGTCTA GGACATTGAT TGA 53

(2) INFORMATION FOR SEQ ID NO: 1742:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742:

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GCTCGTCTGA TTCAGTCACA AAATTGTCTT GTTATACTTG TCACCTATCA TC 52

(2) INFORMATION FOR SEQ ID NO: 1743:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743:

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TGTTATTTAA AGAGGCTCAA GCTTTCATAG AAAACATGTA TAGAGAGTGT CAT 53

(2) INFORMATION FOR SEQ ID NO: 1744:

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- (A) LENGTH: 94 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744:

10 TCTGAGTTAA AGACGTCTCA CTAAAGCTT TAGCAATTCC AACAATCAGA TATCTTCACA 60  
CGTGTTATAT GTGTCCATTA ATATATCCTG TGGC 94

(2) INFORMATION FOR SEQ ID NO: 1745:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745:

25 GGAAAAAAnn TTTTAAAAA AAGGAAAAG GGAATTGGGG TTCCCGGCC CTTTTTAAAG 60  
CCCCCAAATT AAGGAAATTT TAAATTTTGG GGAAGGGGAT TTTCCACCGG TTAATAAACC 120  
GCCGATTTTG AGGGGGTTGA ATTAATTGGC CCAAATTTAA AAACCTGGAT GCTGGGTCCA 180  
30 ATTTTTTACC GGGACCAATT GGTCTGTCAT GA 212

(2) INFORMATION FOR SEQ ID NO: 1746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746:

TATCTTCCGA TGAAGAACAA GATGCACAAG AAGTACGCCA ATGATTTAAG AAAGTGGT 58

45 (2) INFORMATION FOR SEQ ID NO: 1747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747:

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AAAATTAAGn CCTTTTTTAA CCTTCCCTT CCCCAATTGG GGCCT

105

(2) INFORMATION FOR SEQ ID NO: 1748:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748:

AGTGCCTATT ACTTTGATTG ATGTCCAAGT TTCCTATCAC ACAACTTAAT TT

52

(2) INFORMATION FOR SEQ ID NO: 1749:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749:

AAAGCATCAT CCGAACTCCA ATGATTATAC TCCCTAGATA TTATTATGTG ATGCTTTGAG

60

CATTAATTAG AGATGGGACG ATTCCATGAA AGATA

95

(2) INFORMATION FOR SEQ ID NO: 1750:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750:

TTGACACATC TACTCACATT AAAAGTAGAT GAAGCGTTGA GATTAACATT TCCACATTTA

60

CAA

63

(2) INFORMATION FOR SEQ ID NO: 1751:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TCGATATTTG AGACACGCTG CTGTAATAAA ACATCCTATA AAGTATATAC CAAGATCTAC 60  
CAATATAAAC AGCGGCTATA TGATATAAAT GCTCAGACAC ACCCnCTGCG ATCCAT 116

(2) INFORMATION FOR SEQ ID NO: 1752:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752:

TATGATTAAAG CTTAGTGCAG ATTTGATTTA TThAACAAACG CTTCACTACA TTAAAAATAG 60  
GGCACTCGCA CATATAGTTG TATCAATAGC CTTTATCAAT TTTTGGGAA GGTT 114

(2) INFORMATION FOR SEQ ID NO: 1753:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753:

AACTTCAAAT GTGCCAAGTG TTGAATCACA TCAAAATCAT TTTTATTTAA CG 52

(2) INFORMATION FOR SEQ ID NO: 1754:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754:

ACTAATCCCT TCGTGTTTC CAATCAATTG CATTATTAGT GGCCATTGT TTGATATAAC 60  
TGACAAGCTT TAACC 75

(2) INFORMATION FOR SEQ ID NO: 1755:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755:

GTGAACAAGG GTAGATGTAA ATAGTTGATG CATGTGTACA CATCATAACA AAA 53

(2) INFORMATION FOR SEQ ID NO: 1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756:

TTATTTGGGC AGGCAAATAC CCTTAATATA TTCAAATCAT GTTAATATCA TTGCTATTGC 60

TAAACC 66

(2) INFORMATION FOR SEQ ID NO: 1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757:

ATTAATCGGA GCACTTGGGT TCGCAATTTA TGCTGAAATG GATCATTCTA CATCATC 57

(2) INFORMATION FOR SEQ ID NO: 1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758:

CGAACAATAA CTCTAAGTAT CCAACAAATG CTGCAAGTGT ACCTACTGTG ATTGATCCAG 60

AAATAGCAAG ATATGCACCA ACACCGATGA CAATAATTGG TCCAATATCT GTAACGTAT 120

TAATTGCGGC AAAGGAATAg GCATTCCATC TTGTATGTTT CAACGCACGT GTTAGGAAAT 180

TAGTATTCTT TTTATCAAAG TTTTTCGCTT CATGTCTTC AATCGCAAAA CTTTAAACGA 240

CTGAAATACC TTGAACACGT TCATGCAAGA ATCCTTGAAC CTCAGCTAAT GCTTGAGATC 300

TTTCAnGTGT CAATTTTCTT AATCTTCCAA AGAAAACGTA CACCGTTAAA ATGTAAAATG 360

## (2) INFORMATION FOR SEQ ID NO: 1759:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759:

RATTATGTCA TGCTAGGTCA CTTGCATCAT CCATTTAGTA TAGAAGACGA CAAAATTAAA 60  
 TTATAGTGGG CTCCTTGATT GGCAGTATTC ATTTTCGGGA AGCGGGGTCC AGGCTTAAAG 120  
 GGTATTAGAC GTGGTTACC 139

## (2) INFORMATION FOR SEQ ID NO: 1760:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760:

TCGCCCCTCC AGGCTATTAT TTCATCTATA TCATTGTCAT CAGTTAAATT CAGCCTCGAC 60  
 ATTTCCATTT CAATAGACTG TTCATTCAAT TCTAAGTCAT TATTGTAAGT TTCTAGTTGA 120  
 TTTTCATAAT GATTAGATT ATTTTGCTCA ATTAAC TTTC TTTGAGACAA TTGCATTAAC 180  
 TTATCTTCAA TCTCCTTTGA GAGTTCTTGA TGCTGATTCA CATCTTGAAC ATACTTCTTA 240  
 TAATCCACCT CAAAATTAGT GATATTAnTA TATnTCGAGA GTGTTTCAAA TTCAGTGATG 300  
 AGATCTCGAC ATAAT 315

## (2) INFORMATION FOR SEQ ID NO: 1761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761:

TAAATCCTCG AGATTCTTAA TAGGGTAGAT ATCTAACGTT TTCGCAAAGC TCTTTTTGAT 60  
 TTGTTCTTCT TTTGAATCTC CAATGATCTT ATTATCACCA TCACAAGATG TAACAAAGAT 120

CCATCCTCAT CATTTCATCAT CTTTCATCTAC CTTTCGCgGCT GGAAATTCAA aGAaTCTATT 240  
 ACTGACAAAT CGCTTTTTTCC ACCTTTTGGAA AAGTCAATTT CCAACTTTTT ATAACCCACA 300  
 5 GAACTTCCTT TCAAATTACC ATCAATATGC ATTTTAAATA CCGGTGCTTT ATCAGTAGGA 360  
 ATATTATAAC GACTTCTTAA TTGCTTAACA TTTTCATCT 399

(2) INFORMATION FOR SEQ ID NO: 1762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762:

20 GTATAGAAGA CGACAAAATT AAATATAGTG GTCCTTATT GCAGTATTCA TTTTCGGAAG 60  
 CGGGTCAAGC TAAAGGGTAT AGACGTGTAC AATTAATGAT GGCATTATTA ACGATGTATT 120  
 TATTCCTCTT AAGCCACTTA GACAATTGGn AATTATCTCA GGCGAATATA ATGATGTTAT 180  
 25 TAATGAAAAA GTTCATGTGA AAAATAAAGA TAATTATnTA CATT 224

(2) INFORMATION FOR SEQ ID NO: 1763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763:

AGCAACCAAC GCCAGATAAA GCAGAAGATA ACGCATTTCC CCCCATCACC ATAT 54

(2) INFORMATION FOR SEQ ID NO: 1764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764:

ATTCCCTTAT CGCATTCTGT AAAATGATCT TCATCAGAAA TTGCTTCGAT ACGTTTATG 59

(2) INFORMATION FOR SEQ ID NO: 1765:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765:

10 GATTCAATTC ATCTGTATAG ACGATATATC CTGATATGAA TTGGAAATGG AATA 54

(2) INFORMATION FOR SEQ ID NO: 1766:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 85 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766:

ATCGCATAGA AGCATTAGAC TCAAACATATT TTCGGTTATG AGAATAACTC TGACATCCAT 60

25

ATGGATACTT AGTTTCCAAG TTAGA 85

(2) INFORMATION FOR SEQ ID NO: 1767:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767:

CAGTACTGCT GAATGATGCT ATTGATTTTC TCATGAGACA TGGCGATAAC ATCG 54

(2) INFORMATION FOR SEQ ID NO: 1768:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768:

50 GNCACACTACTA ATCGTATCAG GATCACTAAT TAAGGCATCC AGCATCAGAT ACGAGCGCAC 60

GTCAGACTAA TCTACTGTCA TGATAAAGCA GCTGCTAACC TTGTAAGTTC GTGAAA 116

(2) INFORMATION FOR SEQ ID NO: 1769:

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- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769:

10 GTTCTATCCA ATATGGAAAT GAGGACATTA TCGTGAAAG CTATGGACGA TGGACGATGG 60  
 TACACGCATG TTGTGTAAGC AG 82

(2) INFORMATION FOR SEQ ID NO: 1770:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770:

25 TATCTGTATT GTAGTAATCC GCTTCTCCCA TCTATATAGG GATCTTTCGT AGATATTCAC 60  
 TTTATGCCTA GGATCCAAGA TGTGTAAGCA GCACTTTGCA TTATCTAATG CAAAGGGnAC 120  
 ATCGCGCTGT AAGCCCTGTT CTGATAATCA TA 152

(2) INFORMATION FOR SEQ ID NO: 1771:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771:

40 TGGAGGCGAA GTAAATGAAA AGTATTACGT TTGAAGAACA TTATGTCATT G 51

(2) INFORMATION FOR SEQ ID NO: 1772:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 232 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772:

nGAAACAAAT ATCTGATGAG ATATGCAATG ATGACTATAA GTAACATTAA AATGAAGCCC 60

55

CGTACACCAA TTATATCTTT GTGGnTGTTA TATTAAATCT ATATTATGTT CATTTAACAG 180

CATATGTTAA AAATTGACAG TTAACACATG TAGCTATTTG ATGTGAATGT GC 232

(2) INFORMATION FOR SEQ ID NO: 1773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773:

TAATGTCCCC CAGAATGTAG GCAAATGCAG AACCTGGTTT TAGGGTCAAC TGTTTnTTCT 60

CCAAGCAGAA ACAAAGTTCT TGTGTCAGTG CACTTTTGGT CCACCATT 108

(2) INFORMATION FOR SEQ ID NO: 1774:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774:

CGCAATTGAA GGATACACTA TTTTAAGAGC TGCAAACATG CGGGTGTAAC GTGTGGTATA 60

CTGCAACTTT GGThATTGGT TTAGTATAAG ATAAAATCAT CACAATGAAT C 111

(2) INFORMATION FOR SEQ ID NO: 1775:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775:

CAGGTTATCA GCTAATAGAT ATGTTGAAGA GGCAGTTGCA GGCCAAATGA AACTGCAGAT 60

GTAGTTCAGT ACC 73

(2) INFORMATION FOR SEQ ID NO: 1776:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776:

5 TAGACACAGT GCAAAATCTG GTACAGCTTA TGGGAATTAGA CGGGTAAAGC AAATTACTGA 60  
GTACCCA 67

(2) INFORMATION FOR SEQ ID NO: 1777:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777:

GTATGCCAGT GTCATTGCTG AAAACATCAA CCATTCCCTG CACCAAAATT TTTTGGTAGA 60  
20 GTTTGATGCT GGCCATCCTC CAAGGGACTA AGGGTAATTT TGTtTAAAAA GAGCCAAAGG 120  
CCCAATG 127

(2) INFORMATION FOR SEQ ID NO: 1778:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 236 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778:

35 GAACCCAAAA ATTAGCAACA GTGGCTACAA TAGTTGGGCA CTGAAAGCCA GCCAAGTGGG 60  
ATTTTITAGCC CTTGATTIGA AAGCGGGGTC CCCAGGATTA AAAAATTtTAA ATTAGCCTAA 120  
TAAGCCCAAA ATTCCCATTT GGAAAAGGAA ACCTCCTTAA ATTGGGTTGG AAAAAAGnTT 180  
40 AAAAAAAAAA AGGCCCAGnC CTTGGAATTT TTTGGAATTG GAAAAAGGAA TTAAAA 236

(2) INFORMATION FOR SEQ ID NO: 1779:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779:

## (2) INFORMATION FOR SEQ ID NO: 1780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780:

GACGACTCGC TTCTATTTTA AAATCCGGCG TACTTgGTTA TATAAATATC ATAATGGTTA 60  
 AAATTAAAAA GCAATGTCAG TTCACACTAT TACTGACATT CTTTtagTTA TGTGTATATT 120  
 ATTCAATCAC AAGCTTTTGG TCTATAAATC GAGTGATTGG CTTTGTTTGT ATATAACCAT 180  
 CTGCTACATA TTCATCGTTC ATTGTAATTA ATGGATAAAA TAGTTCATCn n 231

## (2) INFORMATION FOR SEQ ID NO: 1781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781:

GTCTCCCTGC CCCACATTTA ACATTGTAAT TTTGTGATGT GAATTTGTTG GAAACGTTAT 60  
 TAATAATGTC AGAATAATTA TAGTCCAAAA CGTAACCAAT ATATATTTAC GTTTAGCCAA 120  
 TAACCAAAAT ATGTAATAAA CAGAAATTAT AAATACTATA AATATCCAAT CATTAAACTT 180  
 GGGAACAGAA AAATGTGATT GCTTGATTG 209

## (2) INFORMATION FOR SEQ ID NO: 1782:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782:

GTTAAACTTA GTTAGATAAAA ATGCAAATCA CATTATTGTA GATAGTCTCT TTTC 54

## (2) INFORMATION FOR SEQ ID NO: 1783:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783:

TCTGGAATGT CTCCTTGTCT CTCTATATAG CTATAGTCCG TCGCAAGCGG ACGTAATGTT 60

10 CATTTTCATA ATGATTATAG TATGAAAGCG CTTTCTTGTA TATGTGACAT GTGCGTGTnG 120

(2) INFORMATION FOR SEQ ID NO: 1784:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784:

CTACCATTTA CATAAAGACC GTCTAATTCT TCAGTTTCAA TGGCATTTTG GAGCAAT 57

(2) INFORMATION FOR SEQ ID NO: 1785:

25

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785:

35 TCATAACCAT TACCAAGTAT CCAAGCAGCT TTAAACAAT ATGGCATAAA CATT 54

(2) INFORMATION FOR SEQ ID NO: 1786:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786:

GGATGGGTGA TTTTAGCAGG TTTGGCTATG AGTACCGTAT TTGCATTAGG ACCGATTTCa 60

TTTAACAAAA TCATAATTTT GGGC 84

50

(2) INFORMATION FOR SEQ ID NO: 1787:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787:

CCGGTTTACC CTTAAAATTA TTTTGTGGG GGTTCATTA AACCTTCAA TTCCCAATTA 60

10 ACCCCnACCC CCCTGGGTTT TCCTTAAAA CAAAAGGCC CTTTTTTTC CCAACCCAAC 120

CTTGGGGGAA TTGG 134

(2) INFORMATION FOR SEQ ID NO: 1788:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788:

TATATCAACT AAAAAGCGCA TCTGCAACCG ACGGTTGAAA ATTTGGACAG GAGACAGATA 60

25 ATGTAATATA 70

(2) INFORMATION FOR SEQ ID NO: 1789:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789:

AATATCCAAT TATACAAGCA GGTATGGCAG GAAGTACGAC ACCGAAATTA 50

40 (2) INFORMATION FOR SEQ ID NO: 1790:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790:

50 TGATTACTA GCTGAATCCG ACATGCTTGA TGATACACTA TGTGAATTCA 50

(2) INFORMATION FOR SEQ ID NO: 1791:

55

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791:

10 CCGGACGCTT TACTTCCAAC TTTAGGTGGT CAACACAGGT TTAAACATGG CGATGTCA 58

(2) INFORMATION FOR SEQ ID NO: 1792:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792:

CATCATCCTC TAATTTAGTC CAAACTCCTG GATGATATCC AAATGAAGTT CCAATTGA 58

(2) INFORMATION FOR SEQ ID NO: 1793:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793:

35 CACAAGTTTT AGAAGGAAAC CAATAACAAA TGACGAGATT AATTGCCACA AACATTAACG 60

AC 62

(2) INFORMATION FOR SEQ ID NO: 1794:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794:

50 AAGGCCCGGG GGGTTTAAAA AAAAAGGTTT AAAAAAGGnT TTGGCCCTTT AAACCCAAAG 60

GGAAATTTTA ACCCCAAAAA AAAAAACCC CTTTGGGAAA GGG 103

(2) INFORMATION FOR SEQ ID NO: 1795:

55

(A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795:

10 TATCGATCGA TCATGTCGAA TCGATCTGTC GATCGATCGT ATCGATCGAA TCGCGTCGAA 60  
 TCGAATnCGT CGAATCGATG CTATCGATCG AATGCTATCT GAGTCGAATC ACGTCGATCT 120  
 G 121

15

(2) INFORMATION FOR SEQ ID NO: 1796:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796:

25 AATTCATGTT AAAATCCTCC TGATATTAGA TGGCCCATTT TTATTTTTTTT CGTTTCCATA 60  
 TA 62

30

(2) INFORMATION FOR SEQ ID NO: 1797:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797:

40 CATACTCGAC AATTAGATG GTGAaTACTT ATCATTTAAG TCCTTTGACA CCTCATCTAA 60  
 AATTCTAGGA CTTTAAACAA TTTCTTTATA CGTATTTACA AGTTGAATAT TACTTTGAAC 120  
 CTCTTGCGCC ATAAACTGAG GATTGTCACC CTTAGTTTGA TTCACTAAAA TTTGAGTATT 180  
 45 AGCTTGATAT TTAGGTGATA AGACGAAAAA TGTAACAATA GCGCTAATAA TTAAAAATAA 240  
 TAGCGGTAAA ATAATTAAAA TCTTCAAGTT TTTTGTAAAT ACTTCTTTAA TTTTGTAA 300  
 TTCTAATGTA CTTTCCATTA TTTACCTCCC TTAAAAATTT TCATTAAAAT TGGTATTATA 360  
 50 TATATAGTAT TTACATATTA CATATCGTTT AAACAAT 397

(2) INFORMATION FOR SEQ ID NO: 1798:

55

(A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798:

10 CGGGTAACAG CGAATGGTGT GTCACCGTAT ATAAC TTTAC TATTTAATAT TTGGCCTGTT 60  
 GCTTTC 66

(2) INFORMATION FOR SEQ ID NO: 1799:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799:

25 GTTGCTAAGT TTGTATTACA ATTTAAATGA TTTT TAGCTT GAGTAAGTTT ATTTAAAGAT 60  
 GCAGTAATTT CGCTAGG 77

(2) INFORMATION FOR SEQ ID NO: 1800:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 172 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800:

40 TAATGCTATT TAATTTTCTA CTCCTAAGC TTCCACCCAT AACGAGTAAn ACTTTTTTTAT 60  
 TTTCATTAAA GCCTGTTAAT TGATAACCAT TATGTGCATT ACCATTTTTT AAATCTTCTC 120  
 GAATTGTTGC TCCAATAAAA TCAGCTTTCT CTTTAGGTAA GTAGTTTAGC GT 172

45

(2) INFORMATION FOR SEQ ID NO: 1801:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801:

55

AGTAAAAATTT GTCATCACGA TCAGCAAAAG CTTTGTGATTC TGACGTATCT TCCATAAATG 120

ATCTAAAAAT TGGTAGTTCG 140

(2) INFORMATION FOR SEQ ID NO: 1802:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802:

ATCCCCCGTA CAGACTTCAG CTTACGTAAA CATGCTGAAC ACTCTAGTGA AGATTTCAAA 60

(2) INFORMATION FOR SEQ ID NO: 1803:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803:

CAATTTAAAT GCATCTTTCC CATTAAATTC ATTTGTGTC GCTTTAGCTG TGTTAATTAA 60

(2) INFORMATION FOR SEQ ID NO: 1804:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804:

ACTTGATCGA AAAGGTTTCA TACCGGTAAA CGATAAAGTT GAAACAAATG 50

(2) INFORMATION FOR SEQ ID NO: 1805:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805:



## (2) INFORMATION FOR SEQ ID NO: 1806:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806:

AAGAACTGTC TATGAATATT GGATGACGCT TTGATGAGAA CATTAGTAAG CCATTTGTTC 60  
 AAGGAGTACA 70

## (2) INFORMATION FOR SEQ ID NO: 1807:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807:

TAGCATTTCT AATGGAATCC AATCTTACCG AATGACAATT GGAATATAAC TGGTGATAAT 60  
 GTTGAATGGT CCTGTGA 77

## (2) INFORMATION FOR SEQ ID NO: 1808:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808:

CCCGGCCCAA AACCCCTTTT TTGGGTAAAA AATTTTTTTT AAAAAGGGAA AAATTTCCCC 60  
 TTTTTTGGTT CCCAAATTTT AAATTAGAAA GGGCCCCCCC TTCCCCCCCCA AATnTTTCCC 120  
 A 121

## (2) INFORMATION FOR SEQ ID NO: 1809:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809:

5 AAGTTTGGTG AAGGAACCAC GTGCATGATG GTGTTCAAAC AATGCGTTAC GATGTTGACG 60

(2) INFORMATION FOR SEQ ID NO: 1810:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810:

TGGTTGAGAA AACACAGCGT TAAAGTTGAG GTATTTCAAA AGACAAGTTG GAACATTA 58

(2) INFORMATION FOR SEQ ID NO: 1811:

20 (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811:

30 CTAAATAGC AAGTGGTTTT ATAACAACIT TGAGTTATCT CAATATAGTT ATCGC 55

(2) INFORMATION FOR SEQ ID NO: 1812:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812:

TAAGTCTTCA ATTTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT 50

45 (2) INFORMATION FOR SEQ ID NO: 1813:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813:

## (2) INFORMATION FOR SEQ ID NO: 1814:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814:

```

TGGTCATGCG GGAAATACTA GGACATGAAA ATTATGCTAA AGGCATCAAA GTAAGTGAAG      60
ATAATGGCGT AGTGGATATA GATATGTACA TTATTGTAAG TTACGGTGTG AAAATATCTG      120
AAGTTGCCAA TAATGTACAA TCAACAGTGA AATATACTTT GGAAAAATCA CTTAATGTAT      180
CAGTAAATTC AATCAATATA TATGTACAAG GTGTACGTGT GAATAATACA GGCAAGAAAG      240
CTTAGGAGGA CAACTTGAAA TGATTAGCAA AATTAATGGT AAATTATTTG CCGATATGAT      300
TATACAAGGG GCACAAAATT TATCTAACAA TGCAGATTTG GTAGATTCTT TGaATGtGtA      360
TCCAGTGCCA GATGGtGATA CAGGAACAAA TATGAATCTT ACTATGACTT CAGGTCGCGA      420
AGAAGTAGAG AATAATTTGT CGAAAAATAT CGGCGAATTA GGTAAAACAT TCTCGAAAGG      480
TTTACTAATG GGTGCAAGAG GTAACnCTGG TGTCATCTTG nCACAATTAT TCAGAGGATT      540
TTGTAAAAAT ATTGAAAGTG AATCTGAAAT TAATTCAAAA TTGTTAGCTG AAAGTTTnCA      600
AGCTGGTGTG GAAACGGCAT ATAAAGCTGT TATGAAACCA GTTGAAGGTA CAATACTTAC      660
AGTTGCAAAA GATGCTGCGC AAGCTGCAAT AGAAAAAGCA AATAATACTG AAGATTGTAT      720
AGAATTAATG GAGTACATTA TTGTAAAAGC CAATGAATCA CTTGAAAACA CACCAACTT      780
ATTAGCTGTA CTTAAAGAAG TTGGTGTGTG TGATAGTGGC GGTAAAGGTT TGTATATGCGT      840
TTACGAAGGA TTCTTAnAAG CGCTTAAAGG TGAnAAAGTT GAAGCCAAAG TTGCAAAGAT      900
AGATAAAGAT GAATTTGTAC ATGATGAACA TGATTTCCAT GGTGTAATTA ATACTGAAGA      960
TATTAAATTA TGGCTATnGT ACTGAGATGA TGGTTCGTTT TG      1002

```

## (2) INFORMATION FOR SEQ ID NO: 1815:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815:

GACAACGCTA TTATTTT TAG TTTTTC AATT CTATTATGTC ATAATTATGT CACTCAAAAA 120  
 CTGTTTTCCA ACATTGATTT ATTGTTGGAA AATCTCGAAA ATCTAGTCTA TTTCTCCAAC 180  
 5 AATCGAAGAr TTATGCCCTT TTTTCTCCCT TTaAATAAGT CATAATACGA GGCATACATG 240  
 CAACATTTAC AATAAAATAT GTTCCTACAT CGTATTATAC GAATGCTCAC ACTTATAGTT 300  
 10 GTTTAGTAAA CCCAGATGTA TTGCTAACAT ACCCATnAnC nCTATATAGT T 351

## (2) INFORMATION FOR SEQ ID NO: 1816:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816:

ATATCGTATC CCATGCGGGA AGGGCTTTAT TTATACTGTG CACGATGAAT GCGCACAACG 60  
 25 GG 62

## (2) INFORMATION FOR SEQ ID NO: 1817:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817:

AAAGGGGGGA AATTTTTTTT TTTTGGGTTT GGGGGGAAAA TTTTTTTTGG GTTTGGGAAA 60  
 40 TTAAATTAA 70

## (2) INFORMATION FOR SEQ ID NO: 1818:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818:

CAAGTTCGGA ATGCGAACGC GTCTTAATCT ATATACAAGT GATGCACTCC A 51

## (2) INFORMATION FOR SEQ ID NO: 1819:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819:

10 TCGCCATACT ATCGACAGCT GCTAAAATTG CGCTCTTCTT GTGTCGCAAT CG 52

(2) INFORMATION FOR SEQ ID NO: 1820:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820:

CAAATTGGGG AAATTACTAG AAATGAAGAT ATTTATAAAG ATGACTGGAC GTCAACTT 58

25 (2) INFORMATION FOR SEQ ID NO: 1821:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821:

35

ACTGCTTCAG CACCTGTATT CATTGGGGAA AGCTTTATCG TTGACCGGCC AGTTTACA 58

(2) INFORMATION FOR SEQ ID NO: 1822:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822:

ACCTGTTGCT CGTGTCAATA ATAGGTGACT ATAAATCTCT GTTCAATATA CTTTTCGTTT 60

50

TTCCAATCTT AAAGGTCGAT GTTCGTGAGT AATCTTATCT CTGGnCCAAT TTTAATGTCA 120

TGATATGTTT ATAGTATCAC CCCTTTGTTG TGTAATAATA ATCAGGTGGG TGGTTAGAAC 180

55

GGTGTGAATA 190

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823:

AGCnTTAGCn TATGGTTTAG ACACAACTGn TAAAGATGCn AAGTTCTTGT

50

(2) INFORMATION FOR SEQ ID NO: 1824:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 102 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824:

AAAAATTGGA AAAAAGGGGC CCAAAGGTTA ACCCAAATTG GAAAnAAACC CAAATTTTTT

60

GGAAATTAAC CAAAAAATTG GCCCCCAATT GGAACCCAAA AT

102

(2) INFORMATION FOR SEQ ID NO: 1825:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 57 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825:

ACGTACCAAT GTCATAATCA GTCATTTTAC CACTCTTAAT AATCTGCTTC CGGGCAA

57

(2) INFORMATION FOR SEQ ID NO: 1826:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826:

ACCATCTTGT ACAAAGTGA TGTCATATGC ACCATCTTGT GTTTTGAGCT GCATTTAATT

60

G

61

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827:

ACCGTTTCGC CAAGCCGACC TAATTTCTCA GCAATATTTC TTTCTACGCC ACCAAT

56

(2) INFORMATION FOR SEQ ID NO: 1828:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 62 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828:

ACTTATAGGG CGCACTTATT TTTCGCTTCC ATAGCGAAAC TAGTGTCCT TATACGTATG

60

TG

62

(2) INFORMATION FOR SEQ ID NO: 1829:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829:

GCTACACACG ATTTACCTTT CTTGTACAGT TTTGCGACCA TCATTGTGAT GATA

54

(2) INFORMATION FOR SEQ ID NO: 1830:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 67 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830:

GTAATGACCA TCGCTGATTT ATGACATTGT TAGATCTCAT GTGCCATTTA GTCTGCTGAA

60

TCTTGGG

67

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831:

ATAACTCTTC G<sub>n</sub>CAA<sub>n</sub>CTCC TCAACAA<sub>n</sub>CT TCTTGTGTTC CATCTTCTGG

50

(2) INFORMATION FOR SEQ ID NO: 1832:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832:

AAACG<sub>n</sub>AGA ATATTTAATG GAGCCAAGAA TGGTTTACAG ACGGAGAAAT GGGATATGTT

60

GAAGCGAGGC GTACGCGGAA AGCGTACTAG GCTAGAACAC T

101

(2) INFORMATION FOR SEQ ID NO: 1833:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833:

TCGTCATCAT GTCTGTGTTA CCAACGTTTG ACGATTTA<sub>n</sub>T TCATGC<sub>n</sub>GAA

50

(2) INFORMATION FOR SEQ ID NO: 1834:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834:

ATAAGTTAAT TGATTTATTG ATAAAGAGAA GCCAGATTTA AATATTATTA AACGT

55

(2) INFORMATION FOR SEQ ID NO: 1835:



- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835:

10 AAACAAGAAC CCCCATATGG TTAAGCTGCG CGTTTCAACA TACGGGGGGT TTTCATAT 58

(2) INFORMATION FOR SEQ ID NO: 1836:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836:

TACGTTTTAT AAAAACAAGA ACTAAAGTAT GCAGTGTGAA TTGTTCACTT TCnTGGCGTT 60

25 GGAATTGATT AAAACGAGAT ATGGTGTGTG GGAAGTTGTT TGTGTTTGCA TATTTTAAAC 120

CGATT 125

(2) INFORMATION FOR SEQ ID NO: 1837:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837:

40 AATCTACAAT CCTGAATCAC TCGTTAAGAT TAAAAGTATC GACAATGAGT ATCTGAACAT 60

GAGCTCATCT GCCGTTTTTA ATGChAAAAA CCGGCGGCGG GATATTTTTG ACCACGGC 118

(2) INFORMATION FOR SEQ ID NO: 1838:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838:

55 ATTTGGGGTT TTGGGACCCT TACCCAAAAA TTGGGGTTTG GTTATTAAAA AAAAGCCATT 60

GTCCCAGTTT TTGGGATTGC C

141

(2) INFORMATION FOR SEQ ID NO: 1839:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839:

TCTGGGGACT AAGTATGTCT CAGGCTTTAT GCTGTTATGT TTGAAAATGA AAGG

54

(2) INFORMATION FOR SEQ ID NO: 1840:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840:

ATTAAAAAAC CTTTTTAAAC CGGGAACCCA AGGAAAAATT CCGGGTTTTTA ATTAAACCT

60

TTTGTTAATT GGTTCCAAAC CAACCTTTTG GGTAAATTTT AACCAGGAAT TTTGGAAAAC

120

nGTTTTATTT GGA

133

(2) INFORMATION FOR SEQ ID NO: 1841:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841:

AAAGTATGGA TTGATCGTGG AGAAGTTCTT CCTACTAAGA AACTAGTCG

50

(2) INFORMATION FOR SEQ ID NO: 1842:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5 GCGTTTTCCT GGGATATGTT TGATGAATGG ATGTTGTAAC ATGTTAATAA ATCGTTGGTA 60

(2) INFORMATION FOR SEQ ID NO: 1843:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843:

15 CTGAGATGAA TATTGTGTTT CGCCATACAT ACTGGGTAAT ATCCCAACCA TTGCTGTAAA 60

(2) INFORMATION FOR SEQ ID NO: 1844:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844:

25 CATTACCTGT AAAAGGAAGC TAAAGACGAT GAGTATTTAT AGAAACCAAT TGCCGACCAT 60

30 TTGCAGCCAT TAGGAGGGTA GGAGGGCAAT CGCGnCCAAA GGTATTAAAC CGTCAATTAC 120

CTTGA 125

(2) INFORMATION FOR SEQ ID NO: 1845:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845:

45 ATCCACCTGG GTTTGTTCTT AATTTAACCT GnTAATTAAT TGGGTTGGGT CCGGCAAAAG 60

TCCGGACCTG CAAATCGGAT TTTATCGTTA AATCTTGAAT TCTATTGCCC ATATTAAATC 120

GCAAAT 126

(2) INFORMATION FOR SEQ ID NO: 1846:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846:

5 TTTTGGGAAT AAACCAATTA ATCATGGGCA AAAAATAAGC AATCCAAGTA CTTACTA 57

(2) INFORMATION FOR SEQ ID NO: 1847:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847:

TGATAAATAT TTCATCTAAA GAGAGGGAGT CATTATGACA CTACTTACTG 50

20 (2) INFORMATION FOR SEQ ID NO: 1848:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848:

30 ATCTAGGCAA TGAATGGACG GACTTAATAT TGATGTGCAA CAAGAAGAGG AGAAGCGAAT 60

CAATA 65

(2) INFORMATION FOR SEQ ID NO: 1849:

35 (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849:

45 CGTGTGAAGT CATTACTTTT AATCCCATGA TGATGGTGAT GGATGAGACG ATATCTCTCT 60

GTCTTTAACA GTTAAGTCCA ATTCTTCCAA CGAAACTTTT CCATAGGTTG TTTTATAAGT 120

TGGAATACTT GCACAAATCA TACCTAATTG CTTATCAATT TTCTCAAGAC TGTCATCAGT 180

50 TATAAGATCA ATTTTATTAA TAATAATCAT GTCACCTAGT TTCAACTGAT CTTCCATCAG 240

GCGA 244

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850:

TTTAAAGGTT CCCGGAAGG TTTGAAACCA AACCTTTGCC CCGGCCCCC GGGAAAAAAA 60  
 AAAnTTGGTT TAACCCCCCG GGGGGGGGGC CCTTAAAAAA ACCCAA 106

## (2) INFORMATION FOR SEQ ID NO: 1851:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851:

TTTTTTAAGG CCCTTGGGGG GCCAATTTTC CCCCCCCCC AACCTTCCAA AGGTTGGGGG 60  
 GCCTTTTTTT TTAAATTGGG GGGA 84

## (2) INFORMATION FOR SEQ ID NO: 1852:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852:

TCATGATTAA AATTCAACAA TTACAACATC ACTTTGGATC ACATAAGAGT AA 52

## (2) INFORMATION FOR SEQ ID NO: 1853:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853:

ATAAAACATT TCAAGATGCG CTTGTAATTG TATGTGATAC TGCCAATGCT CCACGA 56

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854:

AAAAGATCAT GCGCATAATG ACATGGTGAT GATATGAGTA TGATGGTGGG TACA

54

(2) INFORMATION FOR SEQ ID NO: 1855:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855:

ACAACAAATG GTAATGCATA AACATACAGC CAATAGCTAC AATTGCACGA CG

52

(2) INFORMATION FOR SEQ ID NO: 1856:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856:

ACGGCTGCAC TCATCATGGT CTGTGGCGTG ATTGTTAATG TTTTAGTTGC CCGCTTC

57

(2) INFORMATION FOR SEQ ID NO: 1857:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857:

GCAGATAACT TCCTTGATCC TAACAAAGCA AGTTCTCTAT TATCTTCAGG GTTTTACCA

60

GACTTCGCTA CAGTTATTAC TATGGATAGA AAAGCATCCA AACAACAAAC AAATATAGAT

120

GTAATAnACG AACGAGTTCTG TGATGACTAC CAATTGCACT GGACTTCAAC AAATTGGAAA

180

## (2) INFORMATION FOR SEQ ID NO: 1858:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858:

CGCTGCACTT CCTGAACGCA GTGAGACCAG AACGTGGTGT CACTTTCGGT CTATTCCGGT 60  
TAAGTGTTGG TCTCGGA 77

## (2) INFORMATION FOR SEQ ID NO: 1859:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859:

TTTGCGTTC GTGATTTTCT CTAGACGTAG TAACTTTCCC ACTCTTTGCG TCC 53

## (2) INFORMATION FOR SEQ ID NO: 1860:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860:

TTTCTCACTC GCGCATTTC ATTTGTTTTG ATTTACCCGT CTCTTCTATT TGTCTTAAT 59

## (2) INFORMATION FOR SEQ ID NO: 1861:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861:

AATGAATGTA TGCACATTAA CATCATCAAT TAATCCTTTT AATAAATTGA GTTGTAATTT 60

## (2) INFORMATION FOR SEQ ID NO: 1862:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862:

ATTAACTG AGCAAATGTG CATAAGACAT CATGAATTAG CACCAATTTA CAGG 54

## (2) INFORMATION FOR SEQ ID NO: 1863:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863:

TTTAACCATC ATTCTATGTC AAAGTTTGA AATGATGGTT ATTTTTTATT GCTTAAATTT 60

ATTATTGCTA CTACTATACC AATGAAAGT 89

## (2) INFORMATION FOR SEQ ID NO: 1864:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864:

AAAGCTGGTA CGCCTGCAGG TACCGGtCCG GAATTCCCGG GTCGACCCAC GCGTCCGGAA 60

CCAAAATTGC ATCTGATGGT CTCAAGGGTC GTGTGTTTGA AGTGAGTCTT GCTGATTTGC 120

AGAATGATGA AGTTGCATTT AGAAAATTCA AGCTGATTAC TGAAGATGTT CAGGGTAAAA 180

ACTGCCTGTA CTAACCTCCA TGGCATGGAT CTTACCCGTG ACAAATGTG TTCCATGGTC 240

AAAAAATGGC AGACAATGAT TGAAGCTCAC GTTGATGTCA AGACTACCGA TGGTTACTTG 300

CTTCGTCTGT TCTGTGTTGG TTTTACTGAA AAAACGGCAA CAATCCAGAT ACGGGAnGAC 360

CTCTTnTGCT GCAGCACCAA CAGGTnCCGC CAAATCCGGA 400

## (2) INFORMATION FOR SEQ ID NO: 1865:



- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865:

10 AAATGGCGTA TCTTTATGTA TCAACTAAGT AATCACCAAT TTCTTTCGGA T 51

(2) INFORMATION FOR SEQ ID NO: 1866:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866:

GTGTTGCGGA TAATCCGTCG ACATTAGCGT CTGAAGGTAT CATGAGGCAA CTGCGCAA 58

(2) INFORMATION FOR SEQ ID NO: 1867:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867:

35 ACAGCAACTG ACCCAGTTTA CTACCGTCAC TCAAATCACA CAGGTGGTAT CAAATCAATC 60

(2) INFORMATION FOR SEQ ID NO: 1868:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868:

CAATCTCTTA CCATTTATCT CAGCTGGTGA AAACGGTCCA TTACACTTAG AATAAA 56

(2) INFORMATION FOR SEQ ID NO: 1869:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869:

5 GCTATAGACT AGAGGTACAG CAAATTCATG TGTACAGTGA TTAGAAGGCG ATGAGCAAAA 60  
GTAAT 65

(2) INFORMATION FOR SEQ ID NO: 1870:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870:

20 GCTACTGGCG GGGGATAGTA ACACCCAATG TTACACGTAT ATACGTACGG CTTCTTGATA 60  
AAAAGATGAA GCCnTTACAA GTAGAGAGCG TAAGAACGTG ATCATCTAAA TGGTAAGGGT 120  
AGACTATCCC ATGCCATTGT GGGCGGTTGC ATAGGTACCA CGGCACATAG CGG 173

25 (2) INFORMATION FOR SEQ ID NO: 1871:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871:

35 GCTGTGGGAT TGTCTTTTGG CATGGGGTTA GGGAGAGCGT TTCTAAGGGG CGTTTGAAAG 60  
CCATTGATCC GTAAAAGGAC CATTGTTGGA AGCnGCCTTA AGAA 104

(2) INFORMATION FOR SEQ ID NO: 1872:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872:

50 CCATTATCTC AAGAGGTTCT AGTAAGGGGA TGGCATTTC TTCTTATGAA TTTGACCAGA 60  
ATAA 64

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873:

GACAACCTAT TGTTCCTTA CCATACTGTT GTCCGGTTTG ACAAACGGC GTTCCACAAT 60  
 CCATACATCG TGCACCTTGG ATAGAGGCAT CTTCTTTAGT AAATCGTTGT TGATATGCTT 120  
 TATGATGCTT CAAACGGTCT ACCAGTGATA ATTACCTAA GTACTGTTTG TCATACTTCA 180  
 TAAATCCTTT AAATTCACCC ATCGTATCTC CCCCTTTCCT TAATACACAA CGGCTGGTTT 240  
 ATGTTTAGCA TCGATTGTTT TGA CTGTnCA TCGTAAATG CAGCTAACAT CGCTTCATCT 300  
 TCCATTGTCA TGTGAAGATT TTGTGGCAAA nGGAATTTTT TGCATCAATG AATnGGTGAA 360  
 CCTTTGGGGG TGACCTT 377

## (2) INFORMATION FOR SEQ ID NO: 1874:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874:

ATTATCTGAA TACGCAGCAG TTGCAGCACT TGATGGATCA GCAGTATTTA AAAGAGGTTA 60  
 ACACATTACC CAATAGTG 78

## (2) INFORMATION FOR SEQ ID NO: 1875:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875:

CTAAAGAAG TTAAAGAGTG TGATGGTAGA ATTATATTAT TTATTGATGA AATgCCATAT 60  
 GCTTGTAGGT GsTGGTAAAA CAGATGGTGC CATGGATGCa GGCAACATGC TAAACCAAT 120  
 GTTAGCACGA GGAGAGTTAC ATTGTATTGG TGCAACAAC TTAATGAAT ATCGAGAATA 180

TGTTGAAGAT ACAATT

256

## (2) INFORMATION FOR SEQ ID NO: 1876:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876:

15	AGCGCGAAAT TGAGCAAGCG GAACATGCGA CTGATGAAGA AAAACAAGTT GCTTTAAATC	60
	AATTAGCGAA TAATGAAAAA CGTGCATTAC AAAACATCGA TCAAGCAATA GCATAAATG	120
	ATGTAAACGT GTTGAAACAA ATGGCATTGC TACTATAAAA GGTGTACAAC CTCATATTGT	180
20	AATTAAGCCT GAAGCACAAAC AAGCAATAAA AGCAAGTGCA GAAATCAAG TAGAATCAAT	240
	AAAAGATACA CCACATGCAA CAGTTGATGA ATTAGATGAA GCGAAT	286

## (2) INFORMATION FOR SEQ ID NO: 1877:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877:

35	ACTTCCAAAC ATGATAAAGA CAGACTACTT CACAGGTTTA AGGGAAGCAA CCACATTAGC	60
	GGGATTCACC CTAT	74

## (2) INFORMATION FOR SEQ ID NO: 1878:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878:

50	TTTCATTAAAG TTCAAAAAAT CTCAATAACT TTAAGGATTG GTCCGCATAT TA	52
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## (2) INFORMATION FOR SEQ ID NO: 1879:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879:

ATACCCCTGA GATTAATTAC TTGTCCTTTT TTTAGAACAA CATCTCCTGG CTTTGTTTCG 60

10

(2) INFORMATION FOR SEQ ID NO: 1880:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880:

20

AATATCATTA ATAATATCAT TGATGCAAGT CCTATTGTGC ACAACTGGGG TGATTGCCTT 60

(2) INFORMATION FOR SEQ ID NO: 1881:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881:

ACAATGGCAC ATGGACTTAT GCCTGGGGTG TCCTGTTTCGT CGCAGCATCA AAATGA 56

35

(2) INFORMATION FOR SEQ ID NO: 1882:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882:

TGCAAAGCAT TGGCACATGG CCAGTCAGTT TTACAACGTC GTGACTGGGA AAACCCGAGA 60

nGCGACGTTG TAAAACGACG GCCAGTGCCA AGCTTGCATG CCTGCAGTCG ACTCTAGAGG 120

50

A 121

(2) INFORMATION FOR SEQ ID NO: 1883:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883:

ACATTTAATG TATAACCACT TTCAACATTG CCGATTTAGT GGCAGCAGTT GCAGGA 56

10

(2) INFORMATION FOR SEQ ID NO: 1884:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884:

20

TGCATCCATT TGATTGAATT TTATGTTTTG ACCAAAGCCG GTTGCAATGT AC 52

(2) INFORMATION FOR SEQ ID NO: 1885:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885:

TGAAAAGTGG TGAATGGTG TTAAAAGTTG GTGGGTAATT TTAGAGAAGA G 51

35

(2) INFORMATION FOR SEQ ID NO: 1886:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886:

TACACGAACC ATACTACCA GGTTCGTC TCATGAGGCG ATATTTTTTG TCATTTTATA 60

TACATTTATC CAAATTCATC TTTTAAATGT TGAGT 95

50

(2) INFORMATION FOR SEQ ID NO: 1887:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887:

GCTACCAAAG GCGTTTTACC TATTGCTAGT CACTGCAAGT GGCTTAGCTA TGCAGATCAA 60  
 5 CTGGT 65

(2) INFORMATION FOR SEQ ID NO: 1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888:

GTGGGACCAA CTGGCCGGTG ACGGTGGTAA AGGTGCTTCA GTCGTATTGA AGTGGGATGA 60

(2) INFORMATION FOR SEQ ID NO: 1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889:

TGTTGGAGAA ACAGTTAACG AGGTTTAATG TTAAAAAAGC AACGTATCAT GGGTATA 57

(2) INFORMATION FOR SEQ ID NO: 1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890:

TGGGATCTGC TTGCAAATAC ACAAACCTTT CTGGATTTTA TTACAATTGC AATATAATCA 60  
 45 AACA 64

(2) INFORMATION FOR SEQ ID NO: 1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891:

GGCATCCACT CAGATAAAAT AAAGATGTCA AAAAGGCCAA GATGGTGCTA AAAAAACAA 59

(2) INFORMATION FOR SEQ ID NO: 1892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892:

GGTATCTCAA CGATCCTTTA GGTAAATTCG GAAATTTCTA CACGTGAGTT AGCA 54

(2) INFORMATION FOR SEQ ID NO: 1893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893:

TTGTCTTGGC AATGGCAGAG CAACAGAAGT TTAAAGTGCT TGCTGATCAT AT 52

(2) INFORMATION FOR SEQ ID NO: 1894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894:

TAAACCTATA CCCTGTAAAA AGAAAAATCG TGGATCGAAA GAACATGTAT GTGGCATTTA 60

TGATTGATGC TCAAGCAGA 79

(2) INFORMATION FOR SEQ ID NO: 1895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895:

TTATAAAGGA GAGAAATCCT TAATTATGAA TAAAGCATCA TTTGATAAAA AAGTTAAAAA 60  
 5 GCAATTATGG TTTTGAACA AGAAGGAGAA ACAAGCATTG GATCAACGAT TGTCTTCTAT 120  
 ATCTGATGAT GACAGCGTTA ACTTAAATAA GCCTGTTACC TTTGCTAATG CTTACTTAAG 180  
 ACAAATGTA TTTCGAAATA AAGAAACAAA AAGTTATAGT ATGTTTGTTA CATTAGTAGT 240  
 10 GATGATGTTT GCTTATGTTG CTTTATTAGG TTTGTTTATA TTTGGGCTAA TTACAAGTCT 300  
 ATCTGGCGTA CAATTTTTCG TTAGTCCTAA GGTAGATTTA TCTACnACTG TTGTTATTTT 360  
 15 AACAAThATT GGAGCGA 377

## (2) INFORMATION FOR SEQ ID NO: 1896:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896:

TTAGGATCCG TCTTTGCCGC AGCGTGGGTG TTCCGCGAGC GCTTCTTAGA GGTTTTGC 58

## (2) INFORMATION FOR SEQ ID NO: 1897:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897:

40 ATCGCTCAAA CCGAAATTGA AAATGCATCT ATTACTTCAT TAAGCCGTTT ACCAGACGTT 60  
 ATATTAGCAT TGAAAAGTGG AAAGGTTGAA GGTGCTGTAG TTGAAAACC TGAGCAGAA 120  
 GCATATTTAA AACAAAATCC TAAATTAGGA ATTTCCAATG TGAAATTTAA TGAAGAAGAA 180  
 45 AAAGATACAG TGATAGCAGT GCCAAAAGAT TCACCAAAT TATTGTCACA AATTAATAAA 240  
 ACGATTAAGG AGGTTAAAGA TAAAGGATTA ATCGATAAAT ATATGACTAA TGCTGCAAAT 300  
 50 GCGATGAATG ATGACAGTGG TTTTATTTCT AAGTATGGTA GTTTTTTCTT GAAAGGAATT 360  
 AAGATTACAA TATTAATTTT ACTTATCGGT GTTGCAATTAG GTTCTATTTT AGGTGCATTC 420  
 GTTGC GTTAA TGAAATTAAG TAAAA 445

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898:

ACCTTTTCAA TGTTGCTTTG ATATAAATTC ACAAAGTTGA CTTTThAATT CTTCAATAGA 60  
 TTCTCTACTG CGATAGCTGA ATTGCCATCT TTTCTACTAC T 101

(2) INFORMATION FOR SEQ ID NO: 1899:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 75 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899:

TGCCCTGGAT GCCTTTAACT TGATTCATGA CCTGTGGTTT TATTTCAATT TAGATGAGCT 60  
 ACCTTCAAGA CCTTC 75

(2) INFORMATION FOR SEQ ID NO: 1900:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900:

AGCAATACGG AACTGATGAA CGGAATTGTA ATACGAGAAT ATGAAGCATC AACG 54

(2) INFORMATION FOR SEQ ID NO: 1901:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901:

AGTACCTGAG TATCGCAGAC CGGCTTCAGG TCGTAGAATT TCTATACGTG GAGCTAGAAG 60

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902:

GTCTAACTAC AGCATGCCGG CTTATTGTTG CACTTTCTCA ATATTTCAT A

51

(2) INFORMATION FOR SEQ ID NO: 1903:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903:

GGATTnAAAC GTGCATTAAC GCGTGTnTTA AATAGTTATG GTTTAAGTAG

50

(2) INFORMATION FOR SEQ ID NO: 1904:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904:

ATCGTATTTA TTTCAGCGAG TAGCGGTAGC CTTCAATACA CAAAGATTTT ACC

53

(2) INFORMATION FOR SEQ ID NO: 1905:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905:

ATAAGACGCT AGATCTGGTC AATTTATTTT CGATTTTTTTC AACACTATTC

50

(2) INFORMATION FOR SEQ ID NO: 1906:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906:

TTCATCTGAA TCGTCGGCTT TCGCGATTAC TTCTTCGTCA GGGTTGCTAT C 51

10

(2) INFORMATION FOR SEQ ID NO: 1907:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907:

20

CAATTGCTAA TAATCCTTTT AAGTCATTAA TGATTGATC TTCCGTAATG TTGAA 55

(2) INFORMATION FOR SEQ ID NO: 1908:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908:

TTGCCAAACA GACATGACTT AAATTTCAAT ATCTTCTTTG ACTGCATCGA TAT 53

35

(2) INFORMATION FOR SEQ ID NO: 1909:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909:

TGAATTTCTA TACAATTATG GGGAAGGGTA TTGGTGAATT GGAATGGGCT CCTAAGTTTA 60

CAAGCCCCCA TTCGATGGCC GTTAAAGTTT TTAA 94

50

(2) INFORMATION FOR SEQ ID NO: 1910:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910:

5 AACATGATCG TGGGGGGATG TTATGTTTGT TCATATATTT AGGAAGTCGT TTGTAGTTAT 60  
TGTTTG 66

(2) INFORMATION FOR SEQ ID NO: 1911:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911:

20 ATCTTCGCTC CACTTACTGC AATAAGGATT TCGGCAATC CTAAACCGTT TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 1912:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912:

AACAATCGTA ACGATAACAAC GCAATCTTCG AAAAATAATG CAAGTGCAGA TTTCCGAAA 59

(2) INFORMATION FOR SEQ ID NO: 1913:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913:

45 ACACCACACA CACACACACA ACACCCACACA CAACACACAC AACACACAA A 51

(2) INFORMATION FOR SEQ ID NO: 1914:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914:

TGTTACGACT TGGTCGACCT GGCAAGCGCT TCGCGCACGT TCTGCAGCnT CTCACCTTATT 60

GGTATCGCGA TGCGACGTTA AGAAATTTTCG GAGTTCTGGT CACCTTATGT T 111

(2) INFORMATION FOR SEQ ID NO: 1915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915:

TGGTCCGCTC TCAATCGCAT CTTTCAGGTTT TACTTGGCAA AAGAGCGCGG TGCTCA 56

(2) INFORMATION FOR SEQ ID NO: 1916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916:

GCCGACAGTA AAATAAAGGT ACTTGATATA ACATATAACG GAAAGCAACA GTTACTGTCA 60

CA 62

(2) INFORMATION FOR SEQ ID NO: 1917:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917:

ATGATATTTA TTTGATTGAA GAGATGTTGC TTAAACAAGA AGACGTACAA TTGATAnAAC 60

GTAAAGATTA TATTCAGCAC CCTAAAGAAA ATGGTTACCG CAG 103

(2) INFORMATION FOR SEQ ID NO: 1918:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918:

5 CAGTGTAGCG TGTGTCATGC CGTTTTACCA CAATTGAAGA CTGAGCTCTA TCCCTGTGCC 60

(2) INFORMATION FOR SEQ ID NO: 1919:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919:

TCAAATTAAC TTCCAACAAA AACAAATGCA AGGTGAAGAA ATTGCTGAAG AAGATTTACA 60

20 AAAAGCGCAA GAACAAGCGC AAGCAATTGA AAAAGATGAA AACATCTCTn CATTAAT 117

(2) INFORMATION FOR SEQ ID NO: 1920:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920:

TGCCTAATGA AACATTTAAA AATATTTTTTA AATATATCTA TCAACACATC GTTCTATTAA 60

TTGGGATTGT TAGTTTTCTC AAAGGATTTT TAGGATTTTT CATGGAAAAA AATGGAAGTA 120

35 ATTTATATTT TGTTCATTC CCGTTTTCAG TAGTCGTGG ATTCTTTATT GTCTTTTAT 180

TTATATGGTT TAGTTTTAAA ACAATACAAC TGCAGTGTTC TAACAATTCA AATTGGATAT 240

GGATATTCAC CTATTTAGCA ATCATTCTAC TAATTGTAGG ATTTTCTAT GTATTCTTTA 300

40 TTCCACAATC ATTACTTGCC TTTGGACCAT ATATTCAGGT AAGCAATTGG GTATTTATTA 360

TATTTTCATT TATAGTTATG CCTATnGGAT TACGCATTGA 400

(2) INFORMATION FOR SEQ ID NO: 1921:

45 (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TCACAGTCAT CATTThATT TCGATTTTCA ATAATTGTAT TTTTAATTa TCTTGATATT 60  
 CATTAAAGATT TATACAAGCT ATCTTTAACA TTGCCTTATC TTTGATATAT TTCTTGCAAT 120  
 5 CG 122

## (2) INFORMATION FOR SEQ ID NO: 1922:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922:

AGAAGATACC ATACACATTT aATTAGTTAC AGCATAAATC AATTtATACC CTTAATTATT 60  
 20 ACATTGTTTA TATTTTAAAT TCGGGGGAGT AATTTTAAGT AATATCTTGT TGCTGCTAAT 120  
 TCTATTGTTA ATAAATTGAT ATTAGATGTA GAAATTGAGT GTGAAAGTTA ATAATAGATG 180  
 ATTTAGCTAG TAACATAATT AATTCATATA TAGTCAAAAA GTTCTGTTAG ATACTGTTCT 240  
 25 TGATGAATAT TCTTTGATGT TAGGTGTTAG CTATTCTAGA TGAGTTTCTT AGATGTGGAT 300  
 GCCTGTCTTG ATGAAGTTAT CTATGATGTT AATATAATAC TTGATGTTGA TTCTTAGATG 360  
 TTAGTGCGAT TTCAAGATGC TGATTCTTTG TTGTTGCACT ATCTTGGTGA 410

## (2) INFORMATION FOR SEQ ID NO: 1923:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923:

TTTCTATGGT TTATCAGGTG ATTTTACGGA AAACAGTGAA GATTATGGCG TATACCGCTT 60  
 TAAACGTGGA TTTAATGTAC AAATCGAAGA ATTAATAGGG GATTtCTATA AACCAATTCA 120  
 45 TAAAGTGAAA TATTGGTTGT TCACAACATT GGATAAATTA CGTAAAAAAT TAAAGAAATA 180  
 GATGTAAATG ATGTTAGGGC TTATAGThAT TGATACTATA GGCTCTTTTT TATATGTTTT 240  
 TTAATAAAGC CTCGAATAAT GATATATTAA ATGACAAGTT TAACAAGTGA TTGCAATAAA 300  
 50 TATAAAThTG AATTGCACAA CCGATTtGnA AATGATTGAG TTGAGGAA 348

## (2) INFORMATION FOR SEQ ID NO: 1924:



- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924:

10 AGGGCAGATT TAAGCTAACT TGGAAATGTTT TCGAGTTTTT GAGTTAGTTC TCTATCCATT 60  
 TTTTCAGTTA CATGAGTATA TATGCGAATG GTTGnTTGTT CATCTACATG TCCTACCCTT 120  
 TTCATAATTG CTTTTAAAGA AACATTCATT TCTACTAATA AAGTTATGTG TGTATGTCTA 180  
 15 AATGTGTGCG TGGTAACTTT CTTATTCATA TTAAAGCTT TTGTACGTTT TCTTAACGCA 240  
 CACCGGCCAT TTC 253

## (2) INFORMATION FOR SEQ ID NO: 1925:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925:

30 GGTATAGGTG CAAGTCCTAT CTCCGCTCC ATGGTTTAAT GATAATGCGG GA 52

## (2) INFORMATION FOR SEQ ID NO: 1926:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926:

TGGTCACTGT TCCTGATGCT TACGTTAGAA TGTAAGATTC CCGATTTATC AGTTATATAC 60  
 TGTTTGCTTC ACTTTGGAGA TCTG 84

45

## (2) INFORMATION FOR SEQ ID NO: 1927:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

55

CTTTCTAAAT AATTCTAGTA TAGTTTTTAT TCAAATACGC TAGGCTCAGA GCTATT

56

(2) INFORMATION FOR SEQ ID NO: 1928:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928:

GCAAATTGTC ATTAGACGGA GTATTATTTA GAATTTTCGG TGATATCCAC CGGCACAAGA 60  
 TCGATGTTGG ACAATATCTA ATATACTGAT ACGCATTTAA ATAGAAGAAG GGAATTAGAG 120  
 TTTGGTTnTG AATGCAAA 138

(2) INFORMATION FOR SEQ ID NO: 1929:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929:

ACATCTTTAT ATGCTTCAAC ATCAAATACA CCACATATTG GTAAACAACA AA 52

(2) INFORMATION FOR SEQ ID NO: 1930:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930:

TTTAATGTTTC ACAACACCGG AATAATAATA ACTAAAGCGC CGCTAATAAA T 51

(2) INFORMATION FOR SEQ ID NO: 1931:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ACGAAAAATA AATAATCATT TCACCTTTAT AGCCAGTATT TTTAATTAAT ATATTTTCAT 60  
 CTATTAGCGC TTCTAAAAAT CTATTGACT TTTGAACATA CTCTTTAGCT ATATTATTAA 120  
 5 CAACAGTATA GGATTCTCA TAATTAGTT GATTAAATTC TGAGTCGTTT ATTAATTCAA 180  
 CTAATCCTTT TATTACTTTT TGTACAACAT TAATATTTT ATCAAAATCA AATTTATCTT 240  
 CCTTAGATAA ATTAATAnnn AAAGTCTTAA GAACATTTGT AAATAGCTCT GCAACACTTA 300  
 10 TAGTTTGGnC AAATTCCTTA AATTTATTTA CACAGTACTC ACACATTAGT TTTAAAAATA 360  
 ATGGATTGTT GAATTCTGGA TTTAATATAG GTAACCTAGG 400

(2) INFORMATION FOR SEQ ID NO: 1932:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932:

25 ACTTGCGGAA nGACGCAACG TTTATGTACG TTGGAAGAAA AATTCAGGAC TTACGTTCAA 60  
 AACTACCATA GCAATATGCA TTGAAAGATG ACAGTATGCG 100

(2) INFORMATION FOR SEQ ID NO: 1933:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933:

40 CGCTCTGCTT TAAGCGTTGG GACTTTGTCA ACGGTAGTGG ATGGGAAGTG GTTCTGCTTT 60  
 G 61

(2) INFORMATION FOR SEQ ID NO: 1934:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934:

## (2) INFORMATION FOR SEQ ID NO: 1935:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935:

ATGTATTACG GTTTAATTAA GCCACATACC AACAGATTG CATTATGGT ATCTCA 56

## (2) INFORMATION FOR SEQ ID NO: 1936:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936:

TCGCACCAGA AACAGGGAT TGTTAAAATT GCGTAAATCC TTAAATTTAT TTGTAAATAT 60

A 61

## (2) INFORMATION FOR SEQ ID NO: 1937:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937:

ATGAATAATC ATATTTCTAA TCAAAGTAAT AGCATTTATA TTGTGTTTAA A 51

## (2) INFORMATION FOR SEQ ID NO: 1938:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938:

TTGCTGAAGA TAGAGGCTTC ATGAAGGTGG AGAAGTTAGC TGATTTCTGG AACAGG 56

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939:

ATCTCAATGT ATTCCTCTAG TGTAAGTTCT TCATAAATAA CCGGTGATTC C 51

(2) INFORMATION FOR SEQ ID NO: 1940:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940:

CTCAGGTCGA CTCTAGAGGA TCCCCTGTTA AATAAACTT CTTAAGCACA TACTTATTTTC 60  
 ACTATGCCTT TTACGTTCCC CTTATACTTT TCTCACATCT TTCTCTTAGA CTACTCCCTT 120  
 ATACGCCCCG CTCAATATCT TTAATCATTT CATCTACAGT TATTTTCGCA CTCGTTAAGA 180  
 CAATAGGAAC GCCTGGCACC TGGATGCGTA CTTGCACCTG CAAAATATAW ATCTTTATAA 240  
 TCTCGCGATA CATTyTGTGG ACGATAATAA TTACTTTGCG CTAAAGTTGG GCATTAAACC 300  
 GAATGCCGAA CCAAATTC 318

(2) INFORMATION FOR SEQ ID NO: 1941:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941:

CCGGGAAAAT TTTTGGAATT AAGTGGAAAA AAAATCCCCT TAAAATTCCC CTGGCCA 57

(2) INFORMATION FOR SEQ ID NO: 1942:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942:

5 TGTTCCTCTT TTGAATCTGT TTTATTCGTT TGTTCTCTCT TTTTCTGTTC ATCTTTCATA 60  
 TTTCACATC CCCCAATAAA AATGATTAAA AGTAATACAC TCATGTACAA AGCAATTTTT 120  
 TTTATATACT CCATCATTTT ACATCTCTCT GTTTTAATTT TATAAACATT TGAATATTTT 180  
 10 ATACAACTTA TTAAAATAGT GATTATTCAA CTTTTATGTT ATCAAACAAA ACTAACTTAT 240  
 TCAATTTAAT ACATGTAATT CATTTTAACT TTATTATTAA ATGTTCTAAC GTnATTTTTT 300  
 ATATTAGTAA TTATATTTAT TTATCTCGC TTGGATTAAA GTAGATACTA TCTGTGAAGT 360  
 15 AnATATTTTC TGCCTTGn 378

## (2) INFORMATION FOR SEQ ID NO: 1943:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943:

AAGAAGAAGT CAAAATTCAG CTAAGTAAAA GCTCGAGTTA TAAAAAAGTC TAAATTGATT 60  
 30 CAACAGGAGT AGAAAAGGAA ATTAGTCTTG CATATTTTAG AAAATGAATA AAAACAGTTA 120  
 CTATATGCAA CTCAAGAATT AAATATTATT TAAGCCACAT ACCTATTAGA GTACAAAATA 180  
 TACAAGTTGT ACTTATATCT AGGTATGTGA CTTTGTATTT TAAGCGTAAA GTAAAAGTTT 240  
 35 TTATGTTTGT ATTAGTTCTA AATTATTTTG CACTTGGATG ACACGTATTT TTGAGTTTAA 300  
 GTGGTGACTC AAGTTCAATA AAATAAATAT CAGATAGGAT AATTTGAnAA TnATATGAAA 360  
 40 GGGTTATCTC CAAAATnATC TCCATATTAT AAGG 394

## (2) INFORMATION FOR SEQ ID NO: 1944:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944:

50 TATTCGTGAT GACGATTGTC GGTGACATGA AGTTCTATTT GCTGGCACTG AT 52

## (2) INFORMATION FOR SEQ ID NO: 1945:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945:

10 CGTTTAAAAA ATGATATCAA TCTTTATTGT GGATTGCAAC ATCCGTGTGC TCCATAAAAC 60  
 GTGTGGCGAG ACTTGGGAAA GG 82

(2) INFORMATION FOR SEQ ID NO: 1946:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946:

25 GTATTATTGA TGAAGAAACA GCTCTCCAGT TGTAGATGCA TGCTACGTTC ACGTTACCAC 60  
 TGTATCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1947:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947:

40 TATCACCAGC ACCAAGGnTA ATGACATGCT GATCTTTTGC AGTTATGGTh 50

(2) INFORMATION FOR SEQ ID NO: 1948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948:

50 ATTGTATGAA TCTTTGGGGA ATGAACTTTn AACGAACGGA CATCTTGCAA TGACGCATCA 60  
 55 AAATGGTTTT AACACATGTA ATCGGCTCTC GGTACTATTC GTGTGATGTA CACATGG 117

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949:

TTTGATGATT TCGGGATGGA TTGGTATTGT GGTGAATGAA TTTTITAGCT CATCATCAAA 60  
 TTAG 64

(2) INFORMATION FOR SEQ ID NO: 1950:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950:

CTCTAGTGGC CATTCAATTT TGTCGCTGAA TGATGTTGGT ACATCCATTG CTGCTGT 57

(2) INFORMATION FOR SEQ ID NO: 1951:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951:

CTGTCCTTCT GAAACTTGGG TATTTAATTA GGAATAGTTA AAAAAATCAT TCACAGAAAC 60  
 ATTTAATA 68

(2) INFORMATION FOR SEQ ID NO: 1952:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952:

TTAAATTAAC CTTAAGGTTG GnATTTTTTAA CCCCCAAATT TTTGGGGTGG TTAAAAATTCC 60



## (2) INFORMATION FOR SEQ ID NO: 1953:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953:

GACATTTACA CCTGCTTCAA TCTGGTCCAG TGCAGCATCT AATTCTTCGA 50

## (2) INFORMATION FOR SEQ ID NO: 1954:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954:

ATTTGGCCAA CTGTTTCAGCA CGGTATTGGT TCAATGCAAC ACTTTATCAT TGCTTCAGGG 60

CTATATCGGT GGTATGGGnt GTATCACTTC TTAGAACGTG GTATTAA 107

## (2) INFORMATION FOR SEQ ID NO: 1955:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955:

GAAGTGAATA TGAAGCTGCT AAAGACTCCG GAATGCTACC TCAGACAACT GATG 54

## (2) INFORMATION FOR SEQ ID NO: 1956:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956:

ATGATTATTT TAGTTCATT TGTTGAGTCG ACTGCTAAAG TTCCATTAA ATGTTGTACA 60

ATAAGCAGTA ATTTATGATT GTTTACAGTT TTTAATTTAC CATGAACTTT TGAAGCATTT 180  
 GCATGTTTAA TAACATTATT TATCGCTTCA CGCGTAATCA TAACTAACAT AGATTGTTTA 240  
 5 GTAGGACTTA ATACTTGCGC TAATTCTTTA TTTTCAAATG TAAAATCAAT ATCAGCATCn 300  
 nTnAAAACTT TACGTATACT ATCAATCTCT TCAATAAATG ATGGTAATTT TACATCATCA 360  
 ATAAT 365

(2) INFORMATION FOR SEQ ID NO: 1957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957:

AAATAATGTC ACAAAGTTA AAGATACTAA TATTTTTCCA TATACTGGTG TAGTTGCTTT 60  
 TAAAAGTGCA ACTGGATTG TAGTTGGAAA GAATACTATT TTAACAAATA AACATGTGTC 120  
 25 GAAAAATTAC AAAGTGGGCG ATCGTATTAC TGCACATCCA AATAGTGATA AAGGTAATGG 180  
 TGGTATTTAT TCGATTAAAA AGATTATTAA TTATCCAGGT AAAGAAGATG TATCAGTCAT 240  
 30 TCAAGTTGAA GAGCGTGCAA TAGAACGTGG ACCAAAAGGC TTTAATTTTA ATGATAATGT 300  
 AACGCCATTC AAATATGCGG CAGGGGCTAA AGCTGGTGAG CGAATT 346

(2) INFORMATION FOR SEQ ID NO: 1958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958:

TTTTCCAGTT AATTTTTCCA GTTCACTAAA TACTTTATTG ACTGTACCAG ACCCAATAAT 60  
 45 AATTTGGTAT TGTCCCCCAG TAGAAAACGT CCCTTTAACT ACATCCATAT TGTTTAGCGC 120  
 CTCTTCATTT ACTAACTTT CATCATTTAA AACTAATCGT AGTCTCGTTG CACAATGCGC 180  
 50 CATTGCATCT AAATTCTCTT CTCCGCCTAT CGCGTTCAAA ATTTCTTCTG CGGATTGCTT 240  
 ATAATTCATA TATTTAGCCT CCTAATTAGA ACCGGTTCCA TTTATTCCAC TTTATTGTAA 300  
 CCGGTTCCAA AAATATTTGC AACACTCTAT TATCATTTTA TATAAACACC TACACCATT 360

## (2) INFORMATION FOR SEQ ID NO: 1959:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959:

GATTGCATAT AATAGTAAAA ACATTACATC TTGAACAGTA CTCGTTTTGT 50

## (2) INFORMATION FOR SEQ ID NO: 1960:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960:

AATTGAACC AGACACTGAT ACAAGTCACA CCCAGAACT TTAAAGGACG TAAATGT 57

## (2) INFORMATION FOR SEQ ID NO: 1961:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961:

AACGCTATAT TAGCGATATA CAATGATGCC ATTATCAATA nTACAnCTGn 50

## (2) INFORMATION FOR SEQ ID NO: 1962:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962:

TACAACGTCA GTTGGCAGAC ACCAGAAGAA GGATTCATAA GTATATTCAG GAACTTGTTA 60

## (2) INFORMATION FOR SEQ ID NO: 1963:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963:

10 AATTTTTCCTTTTAA TTTCCCAAAA AAAAnCCCCC AAnAAAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 1964:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964:

CAACAAGTAG ATGCATCAGA GAGTAGTGT CAAACGTTAA TAGATGTGGC ATG 53

25 (2) INFORMATION FOR SEQ ID NO: 1965:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965:

35

AGCAAAGGCA TAACTGCTAA TGACCATGTA AATGAGACGA GTCGATCGTG GCCA 54

(2) INFORMATION FOR SEQ ID NO: 1966:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966:

CTCAAATAAC TGGCTCAACT CAACCGGTCT ATAACACCAT AACACCGCAT GCCACTCTAG 60

50

CATACTCAAT CGCTCTGGTA CCAGCnCTCA AATAACTGGC TCACGCCAAC TGTCTATAAC 120

ACTAACACGC ATGCACTCTA GCCTACTCAG AGCTCTGGTA CAGCACTCAA TAGCTGACTG 180

55

TCACAGTCCA CACACACTCA ATACTGGCTG ACACAGTTCA CACACnGCTT ACTCGCTCTC 240

## (2) INFORMATION FOR SEQ ID NO: 1967:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967:

CAGTTTAAAC TCGATGTTGT GTACTACTGT GCCAGCTGGA ATGTTTTATA ATGGTGATG ) 59

## (2) INFORMATION FOR SEQ ID NO: 1968:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968:

GTTACATGGC ATCACGCCAA ACCTGTCTAT AACACCATAA CACGGCATTG CC 52

## (2) INFORMATION FOR SEQ ID NO: 1969:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969:

ACAATTTTAA TTATATAACT CCAGGGGCTA CAGTAATACG ATTTCTCCAG ACTCCAAA 58

## (2) INFORMATION FOR SEQ ID NO: 1970:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970:

TGACGTATAA TGGATGAAAG TCTATTAAGT TTAAGAAGCT AATACTGTGA AATCTTTCT 59

## (2) INFORMATION FOR SEQ ID NO: 1971:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971:

10 TATCATGTTA TCTTCAATCG TTCACCAACA GTCATTTGCT GCATCAGTAA CG 52

(2) INFORMATION FOR SEQ ID NO: 1972:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972:

TTGCTGGTGC CATAGACTAC ACTTGTTTGA TATCAGAAAT GGGATCTGTT CCATTACC 58

25 (2) INFORMATION FOR SEQ ID NO: 1973:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973:

35 AGTTAAACCG AGTCCAACCC AAACCTCCAA TCCACCTAAT GGTTAAAATT CCAAACCATT 60

ACCAGGGAGG GACCAAAAAA CGGAATGGGG CCTATTGGTA GGGTACCTAT CCCATTTAAA 120

40 AATCCATCCA AAAGCCCAa TTATCGGACC ATTTTCGCCA AAAATAATTT AAGCGGAAAT 180

TGAATACCTT AAAATTCTCn GGGCCCCACT 209

(2) INFORMATION FOR SEQ ID NO: 1974:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974:

55 ATCTGAGTAT TTATAACATA AATCACTAAT ATCGTTATTA CATAGGGATA GGGTAAAAGT 60

## (2) INFORMATION FOR SEQ ID NO: 1975:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975:

TTCTGTCATC CGAGTCTGAA TCGCTGTCGA ATCACGTCGA GTCGATCGCT ATCAGGTCGA 60  
 GTCGCGTCGA ATCGnTCGCT ATCGAGTCGA TCGCGTCGAA TCGAATCACG TCGAGTCG 118

## (2) INFORMATION FOR SEQ ID NO: 1976:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976:

TTGCAACnTT TGATCTAGAT ACTACCTTAG TTGGATTGTA CTACTTGATT CTACTTCACC 60  
 TTTAGTTGGT TTTGTAGCAG GCGTTTTGTC TTTACCTGAC TCACTAGATG CGTCATTTTC 120  
 TTTTTCACA CTGGTAATT GTTTATTGTC ATCTTTTGG CTGTCTTGTT TTTGTGATTC 180  
 TTTTTCACA GGTGATGGTG TTGGTTTGCT AGGCGTACTG GAGTAGCTTC CTTCTTAGCT 240  
 GAGTTATCTT GTTGTTCTTT TTTGTTAGAT TTATCGGTAT TGGCTTTTGT AAATGCTTCT 300  
 nTATCAACGA TTCTGACATG GTATTGTCCA TCATAATCAA TCGTTTTTAC GTGAACITTA 360  
 ACGATAGCAT CATATAGAGT TTACCTTCAA CATATGGGAA 400

## (2) INFORMATION FOR SEQ ID NO: 1977:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977:

TAGACAAAGA CAGTAACAGT AAAGTACGCT TCAGAACTGA TGGCTCACTG CGAGTATAAA 60  
 AACTTGTAGT GTCC 74

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 72 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978:

ACTCAAAAAC TCGGAAAACA TTCCAATTGA GCTTAAATCT GACCCTTTTT TTGACCCTTA 60  
TATTTTTTAC AA 72

(2) INFORMATION FOR SEQ ID NO: 1979:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 69 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979:

ATGTCATTGG CTTTGAACCTT TATCTTCAAG CACCCAATCG TTTTAACTTT TCAAAATTTG 60  
GCACCATAA 69

(2) INFORMATION FOR SEQ ID NO: 1980:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 109 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980:

CAGAGAGTTG TCGCTCATTG AACGCCACnT GATGAGTTTT CGCTTACGAA GTGCCACGCG 60  
GTATGGATAA TTTTCACCTG TTGCTGAGTC TTTGATAAGC CTCGACTGT 109

(2) INFORMATION FOR SEQ ID NO: 1981:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981:



## (2) INFORMATION FOR SEQ ID NO: 1982:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982:

GAATCTGTTC AAGTTAGAAT TATCCCGGCA TAATGATAAA GGCGAGTAAA TGG 53

## (2) INFORMATION FOR SEQ ID NO: 1983:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983:

GnCTTTTGAA TAAAGAAAAA TTCATCAATA GAAAAACCGT CTTTATCGTC TATTTTTTTTA 60  
 ACTAGTAAGT TCGGCGTTCT TAGAGACTCA AATATTGATT TTACGTTTTT CTTTGTTACA 120  
 CCACTAACAC TAAATATTCT TCCATCTAAA TCTACTAATT CTGGTACCGC AAAGACATCT 180  
 AAACCATGTG TTTTTTCTTT GTATTTATTT TCATCTTTTC CCAATAAAAA CACTTGGAAC 240  
 TTTTGATTn GT 252

## (2) INFORMATION FOR SEQ ID NO: 1984:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984:

CGTGTTAATC AACTAATTCT TAGTTTTAAC TGTCGTAATA ATCAACTGAA CACTTTCAAT 60  
 CTA 63

## (2) INFORMATION FOR SEQ ID NO: 1985:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985:

5 TCCTAAAATG ACCGCTAATG CCTATGGATT GTTATCACCG ACCGCAGGGA CAGCACGACC 60  
TAC 63

(2) INFORMATION FOR SEQ ID NO: 1986:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986:

GGCATATAAA AATTAGAGAA ATTATTTCAA ATGAACAGAT AGAGGCACAA GATGAATTAG 60  
20 TTAAACGATT AAACGATTAT GntTTTAAATG TCACTCAAGC AACTGTTTCT CG 112

(2) INFORMATION FOR SEQ ID NO: 1987:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987:

TTTATCAATT TGTAACGAAC ATGAATTACA TGTTTCAGGA AAATATATTT CATCCCATTT 60  
35 TTAAAAAGTA TAAGATTTTA TGAAAAATTA AACCAATTna GTATAA 106

(2) INFORMATION FOR SEQ ID NO: 1988:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988:

AATGGCGTAG TTACAGCATT TATGATTGTG TTAATCTTTT CTTCTGATAA ACATAATCTG 60  
50 TTTGACCAAA AGTATTTAAG TGTTCAATTA ATTAGTTTTA TTATTTACGT CGTATGGCAA 120  
GTTTTATTGA TAATGTTTTA TTATCATTCA AAACCAAAAA ATAATTCATT TTCAAAATTT 180

TGGTTAGGTG GACATCAGAT TCACTTCCAT GAAAGTAAAT TAATTGAATT TGTTGGTTTC 300  
 TTAGGAATTT CTTATGTTAC ATTCAAAAGT GTGCAGTTAA TTATGGAAAT TCGTGATGGT 360  
 5 TCTATCAAAG AAATTAAAGT ATGGAAATTA ATTCAATTTA 400

(2) INFORMATION FOR SEQ ID NO: 1989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989:

TTCAGCTTAC AATAATGAGC AGGTTGGGGT GGGCTCCAAC GCAGAGAATT TCGATAAGAA 60  
 20 ATTCCACAAA TAATACAAGT TGGCCCACTC CCATTCTGTA ATAAATATAG GAGGTCATTG 120  
 TTATGCAAAT AGAACTTACT GATGCAGCAG TAACTTGGTT TAAAAATGAA CTTGAGTTGC 180  
 CTGAAAATAA TAAAGTGCTC GTGTTTTTTG TAAGATATGG TGGCGAATTC CAACTCAAGC 240  
 25 AAGGATTTAG TCCTGCTTTT ACAGTTGAAC CAAAGGAAGA TGTTGATATT GGCTATGAAC 300  
 AACAAATATGA CGATTTAAAT GTTGTCTAG CGGAAAAAGA TTTGTGTTAC TTTGAAGATG 360  
 ACCACATTAT TGTAATGTA GTTGTACGA AGATGAATTT 400

(2) INFORMATION FOR SEQ ID NO: 1990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990:

CAATTTATTA TGTAACATAAT TATAGCATTG ATGAACAAGG CGCTCAACGT AATANTACAA 60  
 TTAATGGATT GTTTCACAAG ATGGTAAAGC TAGGATGTCT TTTTATTAAG A 111

(2) INFORMATION FOR SEQ ID NO: 1991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TAAACAAATT CATCAATTGT TAGTGGCATA TCCTAATGTA ATTAGAGAGG AGTT

54

(2) INFORMATION FOR SEQ ID NO: 1992:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992:

GAACGATAGA TTGATGAAAA GTTTAAAAAA GTACGTATAT GTTTATTAAAG TTTGAGTTT

59

(2) INFORMATION FOR SEQ ID NO: 1993:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993:

CGAGACCAAA ATATTCGAAC GAATAATTTC AGTGTTTTC TCCTTTATTA TAGATTCAAG  
CTATGGATAA TAG

60

73

(2) INFORMATION FOR SEQ ID NO: 1994:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994:

ATCCATACAA ATGTAACAAG CACAATTGCn GCCATACTTn GCATGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 1995:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995:

## (2) INFORMATION FOR SEQ ID NO: 1996:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996:

TCAnTTAAaA TTAATGTnCG TTGGGGCTCT AATAAAATTT GTTTACAACG

50

## (2) INFORMATION FOR SEQ ID NO: 1997:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997:

TCATGATTTG AAATGACTTT CAATGACTTG GGTGGGACAC TTGTTGCACA GCTGGATGTG

60

C

61

## (2) INFORMATION FOR SEQ ID NO: 1998:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998:

CATGCATTGA TGnTCTCAA GAACATGATG AAACAGGTCA nCACATGnCA

50

## (2) INFORMATION FOR SEQ ID NO: 1999:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999:

GGTTCGCTAC TGATTGGGTA TACATCTGAT TTAGCAATCT TGCGCACTTG TT

52

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000:

ATGTGGTTAG ATATCTGCAC ACTTGAACGT TATTGTGGGA TATACTTGGC CAT

53

(2) INFORMATION FOR SEQ ID NO: 2001:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001:

ATCTCAGTAA GGGTAAGCGT CAAAGTCTGC ACGGATGCTA ATGTTTACCA GGTT

54

(2) INFORMATION FOR SEQ ID NO: 2002:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002:

CTAAAGATTG TAATGCTTGA ACAATTGGTT CAGTGAATTT TTGGAAATTG TGGAAACTGT 60  
 TACCATCATC ATCTGTTATA AACTAAAGT TTAAATTGCC AGTATCATGA TAAACAGCGC 120  
 CACCACCAGA AATTCTTCTT ACTACATCGA TGTGTGAGC ATCGATATAT GTCTGATTTA 180  
 CTTCTCTAT CGTATTTTGA TTCTTTCCAA CAATGATAGA TGGTCTATTT ATGTAAAATA 240  
 AAAAGTAACT TTCTTCTGCT GGTAAATTTT TAAAACATA TTCTTCCATT GCTAAGTTTA 300  
 AAGTTGGATC TGTAATATTA TTATTACTAA TGAATTTTCA TACAATCTCT CCCTTATATC 360  
 TATATATATn CTCTACTTAT TTATGCCTTA ACTTTGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 2003:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003:

CCGAAATAGG ACGGGCAGTT GGATTATTC GAAATGGGTG GCGTTAATAT ATACAGT 57

(2) INFORMATION FOR SEQ ID NO: 2004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004:

NAGTAGTTGA AGGCGACCGC GGTCCACAAG CTGCAAACGT TGTAACTA TAATCTTAG 60

ATTTGAATCA TTGATTTTAA CTAACACCTT ACCAAGAAGT AAGGTGTTTT TA 112

(2) INFORMATION FOR SEQ ID NO: 2005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005:

AAATCTTGAC ATAGGCACAG GAATGTATAT TGATCTCGAT CACTTAAGTC 50

(2) INFORMATION FOR SEQ ID NO: 2006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006:

AAGGTGGGTT TAAATTTCCC AAAAAAAAAA GCCTTTTAAC CTTTGGGGG GTCCCCTTTC 60

CTTGGAATTG GAAAGGGGCC AAAATTGGAA TAAGGGGnTT GGAAAAACCC AAGCC 115

(2) INFORMATION FOR SEQ ID NO: 2007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007:

TGAAGAAATA GCAAATGAAC TCAATATTTTC TATTGAACGT CAATATTTCA ACCAATTATA 60

5 TCGCTTCAAT AATCAAGATT TAAAGCATCT TGAACAAGAN TTTGA 105

(2) INFORMATION FOR SEQ ID NO: 2008:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008:

ATTGGCTACT AAAGTTAAGG ACATGATGGA TTGGATTAGT GGTATGCGCT TTGAAAAGAT 60

20 CAATTAT 67

(2) INFORMATION FOR SEQ ID NO: 2009:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009:

TATAAATTAG CGTCCTTCAT ATCACAACGA TGATGCTCTG TCGGAAGATC TGATTTATTT 60

35 CAATGTGCGC ACG 73

(2) INFORMATION FOR SEQ ID NO: 2010:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010:

CTTTGTTTAT GTTTCGTTTA ATTTGTAACC CTCTCTTTGG ATACCGAGGT T 51

(2) INFORMATION FOR SEQ ID NO: 2011:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 88 base pairs

55



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011:

TAACGACCAA GCTTAAAGAG ATACGCTCTT ATGCGATTGG ATAGGTCGTT AAAGTTAACT 60

10 ACAATACCTC ATAAGTAGAT TTAGAATC 88

(2) INFORMATION FOR SEQ ID NO: 2012:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012:

GTCAACCCTT GCCAAGCTTA TATCAGGATA CTGGGATGTG ACTTCCGGTG AATTAC 56

(2) INFORMATION FOR SEQ ID NO: 2013:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013:

35 AGCTTATAGT ACTTGTGACT TCATAATGGA TGAAGTTGAA GTACCAAAAG AATTAACACA 60

ATTACACGAA TAATTTAAAT AGAGAGTGTG ATAGTAGGTG GAATTATTAA ATAGTTATAA 120

TTTTGTTT TA TTCGTATTAA CTCAAATGAT ATTAATGTTT ACAATACCAG CTATAATTAG 180

40 TGGTATTAAG TACAGTAAAC TTGATTATTT TTTCATCATA GTAATTTCTGA CATTATCGTT 240

ATTTCTATTT AAAATGTTTG ATAGCGCGTC CTTAATCATA TTAAC TTCAT TTATTATTAT 300

AATGnATTTT GTCAAAATCA AATGGnATTC nATTTTGTTG ATTATGGCTT CGCAGATTAT 360

45 CCATACTGGT GCCAACTACA TGGATATAGT TATATATGCA 400

(2) INFORMATION FOR SEQ ID NO: 2014:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014:

TCTTTTCGAGG ACAGTAGAGG GTCCACCCTA TTGGACGTGG TACTGTACTA CTTTTAAA 58

(2) INFORMATION FOR SEQ ID NO: 2015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015:

TCTACCTGCA GGCATTCAAG CTGGCACTT GCCGTCTTTT TACAACGTCG TGA CT 55

(2) INFORMATION FOR SEQ ID NO: 2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016:

TACTCTTAAG CTAACAACGG CGGTTATGAG TCCTTTGACA AGGTATCGGA GGAAAGACCG 60  
TAAAGC 66

(2) INFORMATION FOR SEQ ID NO: 2017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017:

CCAATAAGCA CACTGCCATT ATTGAGGACG GTACATnTAC GGTTAGACCC AATTGTTTCAT 60  
GGCGGTGGGC ACATAGTGTT TGGCTTTGAG GAGGTTACCA TTGCC 105

(2) INFORMATION FOR SEQ ID NO: 2018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018:

CCTTCCAATA GTAATTGATT GATGTATGAG TATATTAGGT GTGAAATCAA GAGGATTG 58

(2) INFORMATION FOR SEQ ID NO: 2019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019:

TTTCCTCGTA GGTGGTTCTT CTTCATCTTC GTTGTTTTGT CCGAAGTTTG GA 52

(2) INFORMATION FOR SEQ ID NO: 2020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020:

ATAGTTTAGG TGAGGATGTT GnGGTACGAC AGGAAGAAAG ACGGCAAACA 50

(2) INFORMATION FOR SEQ ID NO: 2021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021:

TTGTCACAAT AATTTCTTCA GGATCATAGG AAAAATGATA ACGATTTTGT AAGTATTGAC 60

TAATTGCTTC GCGAGTTTCT AATAACCCTT TATTGTGAGA GTATGATGTC TTGTCATTGT 120

TAATAGCATC AATATATGCC TTTTTCACAA CATCAGGCAT CGGGAAGTCT GGTGGCCAA 180

TAGTTAAATT AACACAATCA TCCAAATTAT TCATACGATT TGAAAATTGG CGATACTTGG 240

GTGGCTCCTA AAATAATTAG GAAATGAGGA nTThAAGGAA GGTTCCTT TnGTGGACAC 300

(2) INFORMATION FOR SEQ ID NO: 2022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022:

TCATCCAAAT TATTCATACG ATTTGAAAAT TGGCGAATAC TTGGTGCTCT TAAATATTTA 60  
10 GAATTAGAAT TTAAAGAAAG TTTCATTTGT GACACCTCAA ATATAAATCA AATATTGTCT 120  
AAAAATTTAG AAATTAATAA TATCATAACA TACTTTTAAA GCAAAAAAGG GTAAATTACT 180  
TAAGCTTTAT TTGAAAAACG AAAAATGTCT AAATACACTG TAGTAACTAC TTTTCAAAAT 240  
15 GAATAAAGTG GTTACAGTTA ATGTACTTAG ACAGTATAAA ATTATGAATC TTAAACTGT 300  
GATGGTCTTT GTAAATTAAT TATTGGATTT GTCCATTTAC AAACAAAGTT TGTAGATAAT 360  
ACATATACGA TGATTACAGA TATACTTATT AAATAAAGAT 400  
20

(2) INFORMATION FOR SEQ ID NO: 2023:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023:

TThAAATATA CCAATCACGT TCATCCACAG TGATCCTAGA CCAATCCAGA 50

(2) INFORMATION FOR SEQ ID NO: 2024:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024:

45 TTTTAAATGG TTAAAAAATT CCCTAATAAA ATTTTGGAAC ACCTAAATTC CAAGGGGTTA 60  
AATTCC 66

(2) INFORMATION FOR SEQ ID NO: 2025:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025:

GTAAGAGCAA TGGCGCAAAA TGCCTGTAAT GATATTGTGA ACGTAATTGA ATCAGTAGAG 60  
 5 GACC 64

(2) INFORMATION FOR SEQ ID NO: 2026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026:

CTGTCGCTGC GTGACTTAAT TCTTTTGGCC CGTTGGCATA TGAGGAAATG TCA 53

(2) INFORMATION FOR SEQ ID NO: 2027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027:

CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028:

CAACTAGACA TAGTATTGCT GCATTAAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 60  
 45 AACGGAATCG TCA 73

(2) INFORMATION FOR SEQ ID NO: 2029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029:

AATAATAATT CTGGAATAGT GTTTAATACT TATTnTCCGT TTAAGATTTC AACTTAATAT 60  
 5 GGGTTTACAGC GCGTAGCTCG TCTAATTCAT CATCACGTGT AGAGTGCTCT GCCTTATCAG 120  
 ATCAGTT 127

(2) INFORMATION FOR SEQ ID NO: 2030:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030:

20 GCAAGTGAAT TGAAGTGACA TGTGGCTGGT GCTTCATGGT AATGATAAAC CAACACCATG 60  
 G 61

(2) INFORMATION FOR SEQ ID NO: 2031:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031:

35 ATAAATATCT ATTTAGATAT AAGTATTGAT AAGTTGCTTG AATTTATAAA GTGAAGGAGT 60  
 AGGTGTCATT AGTATAGT 78

(2) INFORMATION FOR SEQ ID NO: 2032:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032:

50 GAATAGTGTT TATAAAATGT TGACACTGTA GTGGCATATT GTAAATTAAA TATTATTATG 60  
 TGATCATTTT GTTTAAATAT TAGTTATAAG AAGTGAAATA nTCATTTTAA AAGGAGACTT 120  
 AAAACTTGAA ACGATCAACG AATCAAGAAA AATTTCTTGA TACTACTAATT AGACTTAATA 180

## (2) INFORMATION FOR SEQ ID NO: 2033:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033:

TTTTGTCATC TGTATAGGTA TGC GCGCCGG TGTCTTTATT CACTTTGAAC TGTGCGT 57

## (2) INFORMATION FOR SEQ ID NO: 2034:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034:

AAGGCATTGG ATATAAGACT TGATGTTGCA TGGCAATCAC ACTGCCTAAT CCTTGCATAT 60

AA 62

## (2) INFORMATION FOR SEQ ID NO: 2035:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035:

ATGGCAAATA CTATACATCG TCCAATTGAT TGAAAAATAT GGTATTATAA GA 52

## (2) INFORMATION FOR SEQ ID NO: 2036:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 86 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036:

AAGGTGTTTT TATATGCTTA TTACAAATAC TTAACGCGAT GAGTTTCTCA ACCAAATTGA 60

## (2) INFORMATION FOR SEQ ID NO: 2037:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037:

TACCCACCCC CAAACCCAAG GTTTTAAAAA ACCCCTTCCA AAAGCCCGGA AAAACCAAAA 60  
 GGAATTATTT T 71

## (2) INFORMATION FOR SEQ ID NO: 2038:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038:

GAATCCCGGA AGTACAATTT GGTACGTGAA GAAAATGGTA GTGGAATTAC 50

## (2) INFORMATION FOR SEQ ID NO: 2039:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039:

CAGTATCTCT TGGTATTTTA ATTGGTGCTT TATTAAACGT AATTTTACCT TTATATATCG 60  
 ATGGAGCGAA GAGTATTTTC GTATACGTTT ATAGTGCCTC TATTTTACCA GGTATGATTC 120  
 CTTGGTTTAT GATTTTATTC AGTCATTTAC GTTTTAGAAA ATTACACCCCT GAAGAATTGG 180  
 AAGGTCACCC ATTCAAAATG CCTGGTGGCG CAGTAACTAA CTATTTAACA ATCTTATTCT 240  
 TAATATTAGT ATTGGTTGGT ATGGTATTTA ATGTTGAAAC TAGAATATCA GTGCTTATTG 300  
 GTGTCATCTT CTTAACGATT GTAACGATTT ATTATTTTAT TAGATATAAT AAAAnTAATG 360  
 TAAAGCAnAA TAGTATGTTA TAAngAGCGn TACTTATGAC 400

## (2) INFORMATION FOR SEQ ID NO: 2040:



- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040:

10 AAGCTGATTT TTCTAAATGT TGAAAATCAT AAAC TGCTTA ATAATAAATA ACGAGATCTA 60  
 AGTAATAGTG CTCCATTAA 79

(2) INFORMATION FOR SEQ ID NO: 2041:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041:

25 AATTGAACGG ATCGTTCCCA ACCGTTATCA ACCCAGACCG GTGTTTGAAC CCAA 54

(2) INFORMATION FOR SEQ ID NO: 2042:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042:

AATGGGATTG GTTCAAAC TG AAATGGGCTG TTAGTCCCTG TAAACCAAG 50

(2) INFORMATION FOR SEQ ID NO: 2043:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043:

50 ATTGGnATAA TCAAAGCATT GAATCATACA TAGTCACATT GATTGTTTCC TCAGAGTTTC 60  
 AACACTCTAT AACTCAITTT AGTAATTTGC TGATTGCGCA CTTTCATGTG 109

(2) INFORMATION FOR SEQ ID NO: 2044:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044:

10 TTTTATGGAG GTGATGAAGT GGGTGAAGCT GAAAGGAAGC AAAAGCTTGG

50

(2) INFORMATION FOR SEQ ID NO: 2045:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045:

TTGGCCCCCT TCCAACCCCTT GGAAATTTTA AAAGGCCAnT TTTGGGGTAA AACCCCTTGGT

60

25

TCCAAGGACC CCCAAAAGTT TTTTAACCTT CCAATTATTA T

101

(2) INFORMATION FOR SEQ ID NO: 2046:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2046:

ACCCCTTTCCA AAAAGCCCAT TTTGAATTCC CCAAAGGGAG CCAAATTTAA GATGGCCGCn

60

40

AAAAAGGACC GGGGGGTCCA TGTTTAAATT TAAGCCGGAC

100

(2) INFORMATION FOR SEQ ID NO: 2047:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047:

GTTAGTTATG AGCAACGTAT TAATGAAATT ATTGAGCAGT AATTnACCAG

50

(2) INFORMATION FOR SEQ ID NO: 2048:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048:

10 TACGTATTTT CAAATGACGT TGGTGGACGT CACACTCCAT TCTTCTCAAA CTATCG 56

(2) INFORMATION FOR SEQ ID NO: 2049:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2049:

TTTTCCCCC CCCCCCAAA TTGGGGGTTA AAATTTTAAA AAAAGGGGTT AAAGGGAAAC 60

25

CCCAATTCCG GTTAACCTTT TG 82

(2) INFORMATION FOR SEQ ID NO: 2050:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050:

TCAGATGGAT GGCAGTTATT TGGTATTCCA TGGGTATAAA GATAGCATAT T 51

(2) INFORMATION FOR SEQ ID NO: 2051:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051:

50 TGAACGGGAG AAAGATGTTG TTGCATGGTG TCTCGGAAAC GTTTGTGTCC ACGTA 55

(2) INFORMATION FOR SEQ ID NO: 2052:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 74 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052:

ATACCTGGAT GCAAAGGCAA AGTCGCAATT TTCCCTGTTC TAATGTGTCT AACTTCTCTT 60

10

CTAAAGTTCA GGTT 74

(2) INFORMATION FOR SEQ ID NO: 2053:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053:

AATCTTGTCT GATGTAATGT TCAGGTCCCT TGACCCTCAT ATGCATGAGG T 51

25

(2) INFORMATION FOR SEQ ID NO: 2054:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054:

35

CATCGACTTA TAGCTTAATT ATTATAAAAA ATTTCTCCAG ATTAACTTT CT 52

(2) INFORMATION FOR SEQ ID NO: 2055:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055:

ACTGACACAT TATATTAGTG AATTATTAAA AAATGATGAG AAAATTAAAA TCATCATGAA 60

50

TGAATTCGGT ACTTTTGATA TTGATAGCAA TAGTATTICA AATGAAATTG AAGTCCATTC 120

ATTGATTAAT GGTGTGTTTT GTTGCGATCT TAAACAAGAA CTTGTCTATG AACTAAAAGC 180

CATTGCTTTA AAAGGGGACG TTAATCATGT CATCATAGAA GCGACAGGCA TTGCGCATCC 240

55

TTATTTATGG TGTATTAGAT GCGACTCGAT TTTTAGAACG TCATCAATAT ACCGAAAAAT 360  
 ACAGTTTCGC TGGATGGGGA GGATCCAGTT GGAAACTAAn 400

(2) INFORMATION FOR SEQ ID NO: 2056:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056:

TCAAACTTT GAAGTTGTGC TTGCTTTGCA CCATTTTAA AATGTTTCAGC TGAGAGTATA 60  
 TCTTCCGCTG TAAAATTTAC TTCTCCTGGA CTAAAGATT CAATTAACAA CCAAGCCGAT 120  
 AACGTATCAT TTAGCAATTG ACTCATGAAA TCCACCTTG TTCCCTATTT GTTTTTTACT 180  
 TAATGCTATT TTAACAAATA ATTTAATCAT ATTAGTGTTT TTTCAAAAAT ATTCATATAT 240  
 TATCATTACC ATATTTATTC AACAAATGTT TGTAAGATCC TCACTAATAA AATTAATCGA 300  
 TATGACCATA ATTCATTATC CAATAAATGA CTATAAAAAT TTCTnCTATG CCTTCATTTG 360  
 CAACTAAATT TGGACATCAA AAAAGAGCAC TCCTGAATGA 400

(2) INFORMATION FOR SEQ ID NO: 2057:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057:

TTGTTGTTGT GATTTACAT TTTCAAAATT TTGTTGCATG TTGTTAACTT CATAAATTAG 60  
 TGATTCGACT ACATCATTCA TGAGGACGCC TCCTACATTT TTTAATTTAT CACAATATAC 120  
 TGTATTCGTC ATGTTTTAAC ACTCTATATA ATTTGATTTA ACTATTTTTT CAAATGTGTT 180  
 ATCTGTTAAA TCAAGTAAAT CTAAAACTT CCTATATAAA TACAAAATTT TATCGTGTAT 240  
 GTTGTATAC GATGAAAATA CTTTAAATCT AATAAAATCA TTTAAATCAA ATACACCTCT 300  
 GCTGATTAAAC AACACATACT TGTACTTGCC TCAAAAATAA AAATTACTAA TCATGATTTG 360  
 ACTTTTATAA CAAAATTCAA AAATATTGTA ATGAGTATTC 400

(2) INFORMATION FOR SEQ ID NO: 2058:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058:

10 TCTTTTTACT CGCAATTTTA GGAAAAATGG TTGGATCAAT TGATAAAACC GGAAAATTAT 60  
 TAACAATAAT CAATAAAATA TCAAGCATAA TAATTATTAT TGTGCTCTG ATGATATTAC 120  
 AAAAAGACTTAT TCAATTATTA TTCTAAAGCG TTATGTAGTT GTATTTTAAA AGCGTTATAC 180  
 15 AAAAGACATA CTTGTGTCTA TGTATAACGC TTTATTTTATT ATAAATTTGG ATCAATTAAC 240  
 TCAACAAATT TAAATGTTCC ATTGTCATAT TCAAATTTCA GGATATTACA ATTACCGATA 300  
 20 TTATGCTTTA ATGCTTCATC TAGTTTAAGG CAATATCTTA AAAATACCnC CCTTAnTGGT 360  
 CCATGACTCA CGACTAATGC ATTATTCTTT GGTtTGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 2059:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059:

AAAACAACAC AATCAAAAAT ATTGGATACA ACTGAAAAGT TATCAAAGCT A 51

35

(2) INFORMATION FOR SEQ ID NO: 2060:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060:

TTATCATGTT TAGTAGATTT TAAGAAGCTA GAACATTGTA GATATGATGA 50

(2) INFORMATION FOR SEQ ID NO: 2061:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061:

AACGTCGTnA TATCAnCTTG CCAAACAAAG ATATTGTCAC CTTTTATCGG

50

(2) INFORMATION FOR SEQ ID NO: 2062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062:

ACCATGGTGn ATATGGTCAT GATGATCGTT TGTGCCGGGA GCTTGAGCTG

50

(2) INFORMATION FOR SEQ ID NO: 2063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063:

TTTCCCTTGG TTTTGAATT TAACCAAATT TGGGAGGGAT TTGGGACCAC CCCCAGGATT

60

TTAAAAAAA AAAATCCCAG G

81

(2) INFORMATION FOR SEQ ID NO: 2064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064:

TTTTGGGGAC CTTAACTGGG TGGGTCTGGA ACTGTTTCCC TTCAAACAC A

51

(2) INFORMATION FOR SEQ ID NO: 2065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

ATGATGTATT CAAAAGGTAT CTATAAATA GCTTTAGTTG GAAAAGATGA GA

52

(2) INFORMATION FOR SEQ ID NO: 2066:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066:

TTTCATCACT GGCATCTTGT AATTTCTTGG TCTCATATCT GGAATTAATA GGT

53

(2) INFORMATION FOR SEQ ID NO: 2067:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067:

AACCATTAAG AAATTGGATA CACAGAGCAA ATATGGTTAT GATTAGGAAC CATGGCATT

60

ACC

63

(2) INFORMATION FOR SEQ ID NO: 2068:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2068:

AAAGGCAGCG ATGTTACTCA TACCGAACCT GGTTATATAT GAGCGATGAT GCAATGTA

58

(2) INFORMATION FOR SEQ ID NO: 2069:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069:



AACAGGA

67

## (2) INFORMATION FOR SEQ ID NO: 2070:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 86 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070:

CATTTAACCC ATCTTCTTTT TTAAATCTT CTATACTACG GTTTAAAAAC TCTACAATAA 60  
 CTGCCATTTC ATCATCATCA AAGACT 86

## (2) INFORMATION FOR SEQ ID NO: 2071:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071:

GTTTCTTCAA AATATGTGTA TTACCTTTTT GTATGGTTAA ATCTTTTAAT TCTATCATTC 60  
 TTGTCTTACC TCTTTTGGTG TATCCTCTTT TTCAACATAT GTGATCGATA TGACATATTG 120  
 CCCTTTATGC TTTATTTTGA CATACGTTCT ACTAGGTGAA AATCCATTAA ATGTTAATTT 180  
 ATAATCAAGC TTTTCCCCTC TTCACTATA AGCCGTAATA TTAACATATT GTTGCGTACC 240  
 TTTTGCACT TTGGCATAAC TATACTCCGT TTTAAGAAA GGATTAAAAAC GATCAAGTAT 300  
 AGGATGATGT ATGANTGTAA AAGCAATAGT AATGGATAAT ATTAATCCTA ATAATATTGC 360  
 AATGATAAAT TTCATAGTTA A 381

## (2) INFORMATION FOR SEQ ID NO: 2072:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072:

ATCCCCGAAT TGCTTCGCAA ATGTATCATC TTCGAGGCTA CGTTACTTAA AT 52

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073:

CCAAAAACAG CATCACTGTG ATTATGGTTT TCATCTTCTA TAACTAAGAA TACATGTTTT 60  
 TTTGTAAAAA TTTTTTTGAT CA 82

- (2) INFORMATION FOR SEQ ID NO: 2074:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074:

TTTATCGCAA TGAGGGAAGA TAAAGGATCC CGAAAGCGCC GTATGGGTTG GCAAACATTG 60  
 GGGACCAAGA CCGTTCCCCA TA 82

- (2) INFORMATION FOR SEQ ID NO: 2075:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075:

CTTGTTTGCT CTTTATTTAT TTAATTGAGA CCTAGAAATA AGTTATTAAG CACAATCATT 60  
 CACTTT 66

- (2) INFORMATION FOR SEQ ID NO: 2076:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076:

## (2) INFORMATION FOR SEQ ID NO: 2077:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077:

TACGTTCTAT CATAGAGCCT GGAGATGAAA TTATAATACC GGGACCAATT TATGCAGGCT 60  
 ACATACCACT CATCGAAGTA CTAGGTGGTA AACCAATTTA TATTGATACA ACAGCAACAC 120  
 AATTTAaAAT TACACCTGAT GCATTAGAAA GTCATATTTT TCCAAAGACA AGAGCTGTCT 180  
 TGTAAATTA TCCGACTAAT CCAACTGGCG TAGTTTTAAA AAGAAAtGAA GTTyTArATA 240  
 TCGTAAATGT ATTAAAAAAA TATCCGTTAT TTATTATTAG CGATGAGATT TATGCTGAAA 300  
 ATACATTTAG TGGTAAACAT GTATCC 326

## (2) INFORMATION FOR SEQ ID NO: 2078:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078:

ACCCCTTAAT TTAATTGATG TTTTGTATT TTTAAATGA ATAGTTGAAG AAAAAT 56

## (2) INFORMATION FOR SEQ ID NO: 2079:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079:

CACGTACTGC CATGTATGCA CAAGCCGGCA TTCATAAAGC CTTCCATGGC AGTCGTTATC 60

A 61

## (2) INFORMATION FOR SEQ ID NO: 2080:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080:

TGGGACAGGG CGTACCATT CAAAATGATA GTTCTGAGCT GCTAATTAAT ATGCCTTCGA 60

10 AAAAGATGAG TTAAATTGA GATGATGAGA CTGA 94

(2) INFORMATION FOR SEQ ID NO: 2081:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081:

AAGACGACAT GCAAGACATT GCCTTATCTA ATGACAATGT TAAAGCGAGT 50

25 (2) INFORMATION FOR SEQ ID NO: 2082:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082:

35 TTGTTGCGCT AAAAATAAAG TGGCATTGAC GTGACCGCAA GTTGACGTAC 50

(2) INFORMATION FOR SEQ ID NO: 2083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083:

CTTCCCAACA TTGCGCACTG AATGGCGATG GCGCTGATGC GTATTTCTCC TACGCTCTnG 60

50 CGTATTCAAC CGCTATGGGC ATCTCATACA TCTGTGCGATG CGCTATTAAG CAGCCCGAAC 120

CGCACACCGT GAG 133

(2) INFORMATION FOR SEQ ID NO: 2084:

55

- (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084:

GGTAGGGGCA CTATTTTGTA TG TAGAGGTT TTGTCGGGCA GTGTGAAATC AACGACT

(2) INFORMATION FOR SEQ ID NO: 2085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085:

CCCCCCCCAA AAACCGCCCC CCCCAATTG GCCTTTTTC AAGGGGGTG TTTTAA

(2) INFORMATION FOR SEQ ID NO: 2086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086:

AATAGCGAGA GCCCGACCAT CGCCTCCAGA TTGCGACTGA ATGGCAATGC GCTGATGCGT

ATTTCTCCTA CCATCGTGGT ATTCAACGAT ATGGGCACTC TCATACAATn GCTC

(2) INFORMATION FOR SEQ ID NO: 2087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087:

AAGGGGGAAA AGGAACCCAA GGCCCCCTTC CCAAGGAAAT TGGGGGGTTG GAAAAAACCA

AAAATTTTTT AAAAACCCGG

(2) INFORMATION FOR SEQ ID NO: 2088:

- (A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088:

10 GGGGTAAGTG GTTGAGACAG GAACTTTACA AGAGGTGTTT CGTCATCCTA GAACGACGCT 60  
TGCTCA 66

(2) INFORMATION FOR SEQ ID NO: 2089:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089:

25 ATCAATGTAT TACGTATCGA AGGTGAATTA TATCATACTG CTAAATATGA CGGTTTCACA 60  
TC 62

(2) INFORMATION FOR SEQ ID NO: 2090:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090:

40 GAATTCGCTA TCCTGAAATC CTGAGTCGCT GTCCTGAAAT CTGAAATCGC 50

(2) INFORMATION FOR SEQ ID NO: 2091:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091:

50 CGGGGTTCCC CCGTTCAATT CCCTTTGAGT TTTCAACCTT GCGGGTCGTA ATTCCCCAGG 60  
CCGGAATTGC TTAA 74

55

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 70 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092:

ATTGTTGGGT ACGGTGGTGG GTTAATAATC CAAACACGTT AAACACCCG TTTTAGATAT 60  
ACCTATACAA 70

(2) INFORMATION FOR SEQ ID NO: 2093:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 88 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093:

GTTTTGGGTC TTGGGTATTA GTTTAATCTC CATCATGGTT AATTGGTATG GTATTGGTAT 60  
TAGTAATCAT GTATGATGGG CTGGGCGG 88

(2) INFORMATION FOR SEQ ID NO: 2094:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 52 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094:

TGGCCATTGA GGCGCATTAC GTACTACGGC TTGTCGTAGG GACAATTATT AT 52

(2) INFORMATION FOR SEQ ID NO: 2095:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 85 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095:

AGTTGATGCA ATGAGTGATG CAAGGCGACT GAAAAGTTGG TATGAATGAC AAAACTTTAA 60

## (2) INFORMATION FOR SEQ ID NO: 2096:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096:

ACTTAAATC TAATACGGTA TTTTCAAAA CGAATAAAAG TTACCTCTTG TCT 53

## (2) INFORMATION FOR SEQ ID NO: 2097:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097:

AACTTAATAT TGCTACGATA TGAACGGCAT nAACATACTT AGCGnTGnTC 50

## (2) INFORMATION FOR SEQ ID NO: 2098:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098:

CAAAATAAGA AATTAATTAA GAAAATGCCA AGATGCCAGA TGCCATCGGC GGAAAGGAAA 60  
 TTGCACGTAC GG 72

## (2) INFORMATION FOR SEQ ID NO: 2099:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099:

CCACCCAAAC CCAAAAAATA AAGCCCAAAA AATTGCCAAG GAAGGAAAAG GAAAATTGTT 60



## (2) INFORMATION FOR SEQ ID NO: 2100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100:

CACCAATTTTCTCTGGnGCT GGATCTCGAC CTAAGTCCTG TAATAATTGA CGTTGAACAC 60  
 GAATTAATTTT ATTAATTGTT TCTACCATAT GCACAGGGAT ACGAATCGTA CGTGCTTGGT 120  
 CAGCAATTGC ACGAGTGATT GCTTGTCTAA TCCACCATGT TGCATATGTT GAAAACCTTAA 180  
 ATCCTTTGTT AAAGTCAAAT TTTTCAAC 208

## (2) INFORMATION FOR SEQ ID NO: 2101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101:

TAATGAAATT AAGTAAAATA AAAATTATTT CATGGATTGC TTCTATCTAT ATCGAAATAT 60  
 TAAGAGGAAC ACCAATGTTA GTTCAAGTAT TTATCGTATT CTTTGGTATA ACTGCTGCAT 120  
 TAGGACTAGA CATTTAGCT CTTGTTTGTG GAACAATTGC ATTAGTTATT AATTCCTCAG 180  
 CTTACATTGC TGAAATTATT CGTGCAGGTA TAAATGCTGT TGATAAAGGC CAAATGGAAG 240  
 CCGCACGTAG TCTAGGTTTG AATTATAGAC AAACGATGAA AAGTGTAATT ATGCCACAAG 300  
 CAATTAAAAA TATTTTACCA GCTTTAGGTA ATGAATTTGT CACTTTAATT AAAGAATCAT 360  
 CTATTGTGTC AACCAATTGGA GTTGCGGAAA TTATGTTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 2102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102:

## (2) INFORMATION FOR SEQ ID NO: 2103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103:

TTTAAGGAGA AAGGTCATTG GTATAATCTT GAGAAAGAGT GGCAAGAGTT CTTAAACTCT 60  
 GGGAAAGAGG TGAAAAATAT TAAATGGAA GTAAATATA GCGGTAATAG TCAAAGACCG 120  
 ACTATATTTA AAGTTGAATA TGAAATTAAT GGTGAAAGAA ATATTAGAAG AATATTAAAT 180  
 AAGTAGAGGT GCCAACATGA CATTTGAAGA GAAGCTTAGC AAAATATACA ATGAAATTGC 240  
 GAATGAGATT AGCAGTATGA TACCGGTAGA GTGGGAAAAA GTATATACAA TGGCTTATAT 300  
 AGATGATGGA GGAGGTGAAG TATTCTnTAA TTATACTAAA CCAGGnAGTG ATGACTTGAA 360  
 TTATTACACC AATATACCTA AGGGTATAAC ATTCCGGTG 400

## (2) INFORMATION FOR SEQ ID NO: 2104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104:

AACCATCATA AAATGTTATT AAACCGTCAT GGACCGCGTC ACCATTTAGT CCT 53

## (2) INFORMATION FOR SEQ ID NO: 2105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105:

AAGCACAAAT TAGCAGAGTG TTTAATTTA AATGAACAAG TACCTTTACA ATTTTTGGAT 60  
 AATGTAAAAG TTGGTAAAAA TAATATTTAT GnTGCTTTGG AAGAGTTTGC CAACAA 116

## (2) INFORMATION FOR SEQ ID NO: 2106:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106:

10 AATTTGCAAA AGAATCATGG ACAATTGAAA GCAAAAAGGA TCATCATTAA AATTGAACTG 60  
C 61

(2) INFORMATION FOR SEQ ID NO: 2107:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107:

25 GAACCAATGT TAAGCTAATT AATGGAATCC TAACAGCGTT AATCTATTTA AAAAAGTTAA 60

(2) INFORMATION FOR SEQ ID NO: 2108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108:

ATTTGAAAT GAATCTGTGG AACATTTTGC TAATCATGAG GATAAAATCA TATGATGTTG 60  
40 AAAGCGAGAA TGGGATTACG TTAAACGTGG GCGCTGCTAA TTTAAGCACC TTATTTAGTG 120  
GAAGAT 126

(2) INFORMATION FOR SEQ ID NO: 2109:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109:

55 ATAATGTTAA AAAAACGGCA ACTAATCTTT TCATACTAAC AATGATTATA TGTACAATAA 60

CGTTAATAAT GCTAGATAAT TTAAAAA TGAAAAACCG TGAATATCAA AAAGAAATAG 180  
 5 CAGAAAAAAA TAGACATATT AATACATTAA TTGCTGAACA AGAGCGACAT AGAATTGGTC 240  
 AAGACTTACA TGATACGTTA GGGCATGTGT TTGCAAGTTT ATCATTAAAA TCAGAATTAG 300  
 CTTATAAACT AATAGATGCT GATGTAGAA AAGTAAAAGC TGAATTATTA GCAATTAATA 360  
 10 AATTATCTCG TGAATCATTG nACAAAAGTC GAGAAATTAn 400

## (2) INFORMATION FOR SEQ ID NO: 2110:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110:

AAGATTTAAT ATCGGGGGTA ATGTTGATTT TCAAATATCG CGATGTGCTT GTACCACCAT 60  
 25 T 61

## (2) INFORMATION FOR SEQ ID NO: 2111:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111:

TATACTAAAT TATGGCAACT TGGCTCATAT AGGTCGAGTT ACCAGACATA TTCGG 55

## (2) INFORMATION FOR SEQ ID NO: 2112:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112:

50 CGAATAAGTT CTGGGCCTTT TGTGTTCAT TAGCTTGTTT CTGTTTGTAT TGTTCCTGCA 60  
 TTTGAACCTAC ACCAACCTTT TAAATTTATT CTAGTGACAG GATAACTAAA ATATATTTCT 120  
 55 TATGCAATAA TTTCTATTG ATAAGCATTT TCAGATTTTA GTTGTAATTT TTGCCCTAAT 180

AATTTATAAA GAATAAATTC GTCTCCTCTT TGACCTATAA TATATTGAnC ATTATAAGCC 300  
 ATGCGATTCA TTCCAGACAC AGCCATAAAC TCTTGTTTAT CTATCATTTT AAATACCATT 360  
 5 TTTAATTTGG CTTAATGGGA CATTCCGTAT TAAATCATTT 400

(2) INFORMATION FOR SEQ ID NO: 2113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113:

TGTTTTCAAA GCATGGTATA AATGCTTGT AACATAGGTT TTGCCTACAT CAGTATTCGT 60  
 20 ACTTGTAATA AAAATCCTCA TAAAAAT 87

(2) INFORMATION FOR SEQ ID NO: 2114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114:

TTTACAAGTT AAATATAnCA CTAAAAATTT TTAAGTCAAT AAGAATATAT 50

(2) INFORMATION FOR SEQ ID NO: 2115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115:

TGTGCATAAA ATCCTTTTAC TTTTGTGAAT TGATTGTTAT CTTTAACAAT TA 52

(2) INFORMATION FOR SEQ ID NO: 2116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116:

ATTTA<sub>n</sub>AAACC CAATTCCCCA TTATTTT<sub>n</sub>TA AAACGGATT<sub>C</sub> CATGGGTGGA CCATTGGAAA 60  
 TTTTAAAAAA ACCATGGCCC CATTC<sub>n</sub>AAAA AGTTAGGATG GCCAAAAAGC CTT 113

(2) INFORMATION FOR SEQ ID NO: 2117:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 93 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117:

GATTTATCAA CTATTTCCGT ATTTTGATTA TCTCCATACA ATTTCCAATC CTCTGGCTTA 60  
 TCAATAAATA ATGATAATGG CTTATCTTTC GAT 93

(2) INFORMATION FOR SEQ ID NO: 2118:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118:

TGATTACCTT GAnACATGAC TTTnCTGAn TGGTAAATAT TTACAGTTGT 50

(2) INFORMATION FOR SEQ ID NO: 2119:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 217 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119:

AGATATAAAA TATAAAAAAT TATTAAAAGC TATATCCAAT CAAGACTTTA AAGGGTTAGT 60  
 TCCAAATATC AATCAGAATG ATAATTATn<sub>C</sub> TGAAATATAT ATAATTAACA ATACTAAAAA 120  
 CTTAATATAT CATTTATATG ATGATAGAGG TCTATGGCTA GCTTTTAATA ATAATGAAGA 180  
 TTATGCAAGA TATnCTGAAA AATATAATGA TTTAATA 217

(2) INFORMATION FOR SEQ ID NO: 2120:

- (A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120:

10 AGACTTAGTA AAGTTAGATC ATCTAAAGAT GAGCGTAAAA TTTATATTTA TTAAATAAT 60  
GGATGATATA TCTAA 75

(2) INFORMATION FOR SEQ ID NO: 2121:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121:

25 CACCACCTAC ATTTACTATA TAAAATGTAG GAATGGTAGA TTGATTTAGA TAAACTGGAC 60  
GTATCACTTT AAGTGCTTTT TCAAAGA 87

(2) INFORMATION FOR SEQ ID NO: 2122:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122:

40 TGTCTTTAG CTAAAGCTTT AGCTTCTTCA TCACTTTTAA CTTCATAAAA ATCTACACCA 60  
GTAGCTTCTT 70

(2) INFORMATION FOR SEQ ID NO: 2123:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123:

55 TANATCTAAA AGGAGAAATG CTGAAGATGA GAGAGGTATT TTTGAAATGT 50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124:

TTAAAGGGTA ATTGTTTTAA AAAAAGATTA AACCGAGGAC TTTTAATTGT TAAAACCATC 60  
 CCT 63

(2) INFORMATION FOR SEQ ID NO: 2125:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125:

TGTAAACGAC TATTACATGA TCACAATCCA TTCAGCGCCA TTATATAAAG GTACTTAATA 60  
 TAGGACATCA TTCGCAGC 78

(2) INFORMATION FOR SEQ ID NO: 2126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126:

TTTGGTCGTG TGCAAGACAG AAGTCGACAT ACTCCAATGA AACATCATGT 50

(2) INFORMATION FOR SEQ ID NO: 2127:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127:

TTTGTGTCGA TCGCCTTTTT CACTTCTTCT GAATGCTCGA AATCATTCGT 50



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128:

TGTCCTGAAAT GATCATTAGG ATTGCTCCAG CTCAATGTCA GTnGnAATGA

(2) INFORMATION FOR SEQ ID NO: 2129:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129:

TCCAATTACC TACAAAGTGA GTGCTTTCTT GACCAAGTCA AAACGAACTT TTATATTTGT

CCAAC

(2) INFORMATION FOR SEQ ID NO: 2130:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130:

TTCCAAGGTG TCGCTGACTT TCAACACACT GAATATATAC CTGCCAGTCG GCTGGTCATG

C

(2) INFORMATION FOR SEQ ID NO: 2131:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 92 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131:

AGTTCCTCAG TCCAAATGCG GCATGTTGAC CCACCATAGG CGAGGGCATT TTCACCACGG

## (2) INFORMATION FOR SEQ ID NO: 2132:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132:

CCCCTCGAGT TTTTTTTTTT TTTTTTTTTT CTGGAGCAAA ATGAATTTT TTTATTGTAC 60  
 TTCAGGGCAA CAAGTCAACA GCTGCAGGAA AACAAAACCA GGTCCAATCT ATGATCTAAG 120  
 AGGAAGTCAG GAAAGGCTTG GAAGAGAGAT CCAAAGGCCA TCCTGGCAAG GGAATCCCA 180  
 CATGAGAATT CCTGGGAGAG AGCAGGCCCC AGGCAGCAAG GTCATCTTGC CTGCTTCTCT 240  
 GTAAGTTAAT CCTTCACAGG GAGCCAAGGC TTCTCTTGAC TGCTTGACA AGAGGGTAAG 300  
 GGCCCTGGTT GCAGGATTG CAGTGAAGT CATCCATGTC AATAGACCAG ATCATGGCTC 360  
 CTCCCAGGTT AAATTCCTTA AGAACTGAAC CTGnCTCCA 400

## (2) INFORMATION FOR SEQ ID NO: 2133:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133:

TTTCATCATAC AACATTACAC TTTGTATGAC TAAACCCAAA TTAACGATAT 50

## (2) INFORMATION FOR SEQ ID NO: 2134:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134:

GTGGCAAGCT TTTTAAAGT CTGACTGCCA TCGACGGATC TATGTTAACA GGTGGATCT 59

## (2) INFORMATION FOR SEQ ID NO: 2135:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135:

ATCAAAGTCA TCTnCATGGT CnATCACACC ACGCTTTATA TGGTAATTCT 50

10 (2) INFORMATION FOR SEQ ID NO: 2136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136:

20 CGGGATCTGA GGTCGCTATC TGCAATCTGC AATCGCTATC TGCAATCTGG AG 52

(2) INFORMATION FOR SEQ ID NO: 2137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137:

nCTCAACCAC CCACACAACA ACACAACAAG CAGCACCCAC ACACCACACA 50

35 (2) INFORMATION FOR SEQ ID NO: 2138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 87 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138:

45 TGTATTGTCA TTGTAGACGT GTGTAGCCAA ATCATAAGGG CATGTGATTT ACGCATCCAC 60

CTTCTCGGTT TGTACCGCAG TACTTAG 87

50 (2) INFORMATION FOR SEQ ID NO: 2139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139:

5 TTCACCGTTG CGCAACGTTT AAGTTTGAAG TCGTTTGGC ATGTTGAAAT AAGCACCAGT 60  
TACACCAAAA CGCCCAG 77

(2) INFORMATION FOR SEQ ID NO: 2140:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140:

20 ATCTTCTAAC ATTCACTTAG TAGCGTnATT TTTCGCTTAT AATGAAATGT TAAGCATATG 60  
CGGGATTTAT ATTTTAAAGA GACCTTTAGA TACCATATAT ACCTAGGTTA TTGAAAATAT 120  
GGATACCTTA TATAAGTGAT TTGCAATA 148

25 (2) INFORMATION FOR SEQ ID NO: 2141:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141:

35 GCTGGCACAT AGATGATCGT CAAGTCGATC TCGCCAGTCT GAAGTCAAGA 50

(2) INFORMATION FOR SEQ ID NO: 2142:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142:

50 TTGTTGTAAA TACTATCACT GTACATGGGT GCTATCAAAA TATTGTCAGT TCGTAAAATA 60

(2) INFORMATION FOR SEQ ID NO: 2143:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143:

GTAGTATATC TTATTAATTG TATCATGAAG CAATTTAAAT ATCATGACAA TTTAGTTTGA 60  
10 AAAACACACT TTGTGTTGAC GTTGTGTTTT ATGGGATATA GnATAGTAAG GAATGTAAAA 120  
TGAAGGAGTG AATGC 135

(2) INFORMATION FOR SEQ ID NO: 2144:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144:

25 TTTTAAGGTT TGAAGAAAAA AAGTTTTTAAA AATTCAAGGA AACATTAAAT TAATTTA 57

(2) INFORMATION FOR SEQ ID NO: 2145:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145:

TTTCGAAAGT TTGATAGTCC ACCTTACATT CTCCTACTAT TTTCTGATGT CCCAATACTT 60  
40 TATATTATTT AAAGTAATAT AAAAGCAATC TCTTTTGAAG ACATGTTAAC CTAAATATTT 120  
TTATATATAA TATATATATA AAATATAn 148

(2) INFORMATION FOR SEQ ID NO: 2146:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146:

55 GTTAATACAA TACGGTTAAC AGCACCTTTA CGnTAGTTGC TTTnCTGCAn 50

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147:

AATCCCCTCT TTTCTCTATT TCCTAAATCA TAGAACTTTT AACAGTAAAA TTCAATCATT 60  
AATACATG 68

(2) INFORMATION FOR SEQ ID NO: 2148:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 92 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148:

AGGTCCATTT GTAATTTATA ATGTTGACTA ATAACATCTA CAGAATTTAA CGTTCCCATA 60  
CCTCGCCACT GATTGTAAAT AAACAAACCA TA 92

(2) INFORMATION FOR SEQ ID NO: 2149:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 69 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149:

ACCATCCATT AAATCAGGAT CTTCACTAAT AAGTGCTAAA TTAGCAGCGC CACGTTTAAC 60  
GTAATCCAT 69

(2) INFORMATION FOR SEQ ID NO: 2150:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 384 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150:

TCAAAATATA TACGATCACC TTTCTGTAAA ATCACAATAT TTTTATTTGC CGCTTCTGGA 120  
 TGTGTGTTTAA AAAATTGTTG GCCAACTTCA CCTTTTAACG TGGCAAATTG ATAATTTCTT 180  
 5 GGTAGGTCAT GTTGAATTAA CCAAATGACA TAGTTATAAC AATATATACA GTTTCATCA 240  
 TAATATACGA TTGGCATAAT TTATTCGCTC CTTTAATAGT ACTTATAGTC ATTTTTCCTA 300  
 10 ATTTAAAAAC ATTTAAACAA GGTGTGCTACT TGATAAGTCC TCGCGACACG AAATTGCCAT 360  
 AAAATTTATT TTTCAGnTTn ATAT 384

## (2) INFORMATION FOR SEQ ID NO: 2151:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151:

TGTGTGTTTAT CACTATATTT TAAAAATAGT CTATAAGGCT TATCAGATGA AGTAGCTGCT 60  
 25 GCGTAACAC CACCACTAAA TGT 83

## (2) INFORMATION FOR SEQ ID NO: 2152:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152:

GTATTCGTAC ATTTTTCAGC AATTAACCAA GATGGTTACA AATCATTAGA AGAAGGTCAA 60  
 40 GCTGTTGAGT TTA 73

## (2) INFORMATION FOR SEQ ID NO: 2153:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153:

CCCCCTCCC CCCTCCCnC CCCCCCCCC CCCCCCCCC GCCCCCCCC 50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154:

TATTTTAGGC TTAGCATTGA TGATGTTGCT CATTTTCAAT AATATAGGAA TTATT 55

(2) INFORMATION FOR SEQ ID NO: 2155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155:

ATGCTTGCTG ATATAATGTA ATAGCGTCGT GATAACGTTG CTGGCTTATA ATATACATT 60

GCGAGATT 68

(2) INFORMATION FOR SEQ ID NO: 2156:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156:

TAATCTTTGT CGTCGAAATA CAACTAACT TTTGAGTTTA ATGATGAAGG TACGCATTGT 60

GTATCACT 68

(2) INFORMATION FOR SEQ ID NO: 2157:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157:

TCATTCATTT TCCTCTTTTC TTTTATTTAA AATGTTTCATG GTTGTTTCTC TTAATTCTGT 60



AGATGCTAAA TGGTCAAATT GAATAATTGT TTCTAGACTC ATTTCATAAA TTTCGAAAAA 180  
 TAATTCTTCG GGATTACGTT TTTGTATTTT TCCAAATGTT TCATAAAGCA AATCAATTTT 240  
 5 ATCAGCAACT GAAAGTATTT GGCCTTCTAA TGAATCATCT TTACCTTCTT GCAGTCGTTG 300  
 CTTATAACA TCTCTATATT GTAATGGAAT TTCTTCTTCA ATAAAGGTCT CTACCATTTT 360  
 10 TTCTTCAACT TGCGAAAATA ATTTTnnTAA TTCACTACTC 400

(2) INFORMATION FOR SEQ ID NO: 2158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158:

TATTTTTTTC TTCTAGGCAG TGTTAATACT GCTTCAATTT GTTTTTTACT AAATTGATAT 60  
 TTCTCTATGA TTGAATTAAT CAATTGATTG TCCATTTACT TAACCCACAC TTTTCTTAA 120  
 25 ATTTACTCAT TTATTTTAAC ATATTCTAA ATACTTCTAT TAAGATATGA TACTTAATGT 180  
 AATTTTCACT TCCAAAACAT TTAAAACGAA TGATTAGGnC ATACTATATT nT 232

(2) INFORMATION FOR SEQ ID NO: 2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159:

CCGTTTTTCC AAAAAGTTGA TCATAAACCC GCTCCTTTTT TCATCATAAC AAAATAAGAA 60

(2) INFORMATION FOR SEQ ID NO: 2160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160:

CGATTTACTG CACGACACAT TGCCACATCC TGGATGGGCA ATCTTTTCTC TTACCCGTCT 60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161:

ATTAGTTGAA GTTTTTGAGC AATTGAAAGA TATTCAGGGT CAAATAAAAA CGACAAAAAA 60  
 AGAATATCAA CAGACCAACA AAGAACTTTC TGCTGTAGAT AAAGAAATTA GAAATATAGA 120  
 AAAAGACCTC AATGATACAA AAAAAGCACA AAATGAATAC GAAGAGAAAT TGTATCAAGC 180  
 ATATCGATAT ACCGAAAAAA TGAAAACACG TATTGATAGT TTGGCAACGC AAGAGGAAGA 240  
 ATATACTTAT TTTTTCATG GCGTCAAACA TATTTTGAAA GCTAAAAATA AAGAATTAAA 300  
 GGGTATTTAT GGTGCAGTTG CGGAAATTAT TGATGTGCCA TCTAAATTAA CTCAGGCAAT 360  
 TGAAACAGCA TTAGGTGCTT CATTACnACA TGTCATTGnA 400

## (2) INFORMATION FOR SEQ ID NO: 2162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162:

GTGCGTACCA TTGTAATCTT CGTAAACTGG GTAATTATTT TGTCTTTCTT CATCATAAAG 60  
 TAATAA 66

## (2) INFORMATION FOR SEQ ID NO: 2163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163:

AGAATGGTAA CATGGTAATA ATAAAATATA AACAGAATAC TAGTTAATAC ACTTTATACT 60  
 AGAAAAAGAT AT 72

## (2) INFORMATION FOR SEQ ID NO: 2164:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164:

10 CGATAATCTG TTTTTTTAAA TCTGTTGCTG TTAGATTAG CACCGATTCTG TTAACTTCA 60  
 AATAATTTTT ATTACCTTTG GAAGAAAGTG GAACTATTGT AACTGTTTCT TTTCCTTTAT 120  
 TGTCTTTGTT ATCTAATATT ACACAAAAAT GATTACCAGA AAACCTCACTT CCAATATTAC 180  
 15 TCCCTAGTTT TACATATACC ACTGTTCTCT TACnATATGA TTTATAATAT CTTTnTTTAT 240  
 TGCTTGTAAC ATCGCTATGT ATAGCAATTG GAATAAACT CTAGCCAATG AGGCATGTnT 300  
 ATAACCTTCA TGTTTTTACT GTCGG 325

20

## (2) INFORMATION FOR SEQ ID NO: 2165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165:

30 TAAACCCCTT TTGGGTAAAA AAGTTTGGGA AAATTTCCCC GGGGGGAAAG GCCCCAAAA 60  
 AATTGTGCCC CTCnCGGGG GAAAATTAAA ATTTCCCCC TTTTAAAAGG GTTCCCCTT 120  
 35 T 121

## (2) INFORMATION FOR SEQ ID NO: 2166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166:

45 CGGACAGTTA AATGAACTGT TCAATGAGCC CAGGATGTTG TAAATGGTTC GG 52

## (2) INFORMATION FOR SEQ ID NO: 2167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167:

ATTACAGTAA AAAATGGATT AACATTACAA GCGTGTCTTG CTAGAGCAGC CAA 53

(2) INFORMATION FOR SEQ ID NO: 2168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168:

AAAGATTATT TATTTGCAGT CATTAATTGT GATTTAATAC GGTCAGCTTT GTTTGAATGT 60

ATTAAATTAC nTTGAGCAGC TTTGTCTACT AACTTAACTG CTAAGCTTAC TAAT 114

(2) INFORMATION FOR SEQ ID NO: 2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169:

AAGGAACCCC CCCCCCTTAA AATTTTTGGT GGTTTTAAAA AATTCCTTTG GATTTATTAC 60

CTTTATTCCCT ATnATTTTCC GTTTGGATTT TCCTGGATTA AATTTCCCCA TTAAGCCATT 120

TCCGCTTCCC TTATTTTATn ATTTTCCAAA ATTTCCAAAG GTTCCATTTG GGATTTTGGC 180

AATCCTTTTT TATTAAAATG GCCTAAAAAT TTTT 215

(2) INFORMATION FOR SEQ ID NO: 2170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170:

TATCGTTTTT AGAAATGGAT GTTCTCTCCA AAGATGATGG TATCTAACAT TATCTTATTG 60

GTATCATTAT GCAACnTTA CAAAACATTT ACGCAAGATG ATACATTATC CAAC 114

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 76 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171:

ATCACAGATG AGATAACAGA TCCACTGTAA CTTTACAATA AATAAATGGT ATCATAATTA 60  
ACACGTAAAT GGTTC 76

(2) INFORMATION FOR SEQ ID NO: 2172:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 64 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172:

ATTATCACAA AATGTTGACA CGCAAAAAGT TGGTCAGTTA TCAATATGGT ATATAAATCT 60  
GAGA 64

(2) INFORMATION FOR SEQ ID NO: 2173:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173:

AAAGGCCAAC CAACCAAGG CCAAAATTAA CCGGCCAATT CCAAGGGGTT AATTAAACCC 60  
G 61

(2) INFORMATION FOR SEQ ID NO: 2174:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 400 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174:

CACCCCGCAC TCTCCCATCT TTTACCTACT GGCCTCTTTG CATTGCCCTG GCACCTCCGT 120  
 CCTCAGCCTC CCAGGCTGTA TTCATTCATT CCCTTACTGA GCACGCACCA TACACCAAGC 180  
 5 ACCATTCAAG GTGAACCACT CAAATGAAGG CCTGGCTCAT TTTAATGGGG GACAATGAGC 240  
 ATTTTTGTGA CAATTCATG GAGTGATGAG TGCTGTGAAG AACTAAACAG GTCAGGTGTA 300  
 10 AGTGGCTCAT GCCTGTAATC TCAGCACTTT GGGAnGCCGA AGCAAGTGA TCATTTAAGC 360  
 CCAAGAGTCA AGACCAGCCT GGGGnnACAT AGTGAGAnTC 400

## (2) INFORMATION FOR SEQ ID NO: 2175:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175:

20  
 25 ATATCGTTTA AACCATCAAC AAGATTTTAT AGATGCAACT TTTACTGCGC TGAAATCAGA 60  
 TAGAGCACGT TTAAAAGAAG TGCCAGTTCA TGTTGAACTT ATAAGTTATA TTTCTAAATC 120  
 AAAATAAACT GCTATCTAAA ACGCAAAGTT GATCAAAATA TCGATTTTGT GTTTTTTATT 180  
 30 GAGAAATTAT ATAGGAGTGT CAATCGATGA TTTATTGTGA ACAGAGCGTT TAATATTAAG 240  
 AGACTGGCAT GAAGATGATC TGTTACCTTT TCAAAAAATG AATGCGAATT ATGACGTACG 300  
 TAAATATTTT CCAAGTTTAT TGAGTTAnCG nCGTTCAGAA TTAGATATGA GACCTATGGA 360  
 35 TCGGTTATn AAAGATTATG GCCATTGGGA TTATTGCCnG 400

## (2) INFORMATION FOR SEQ ID NO: 2176:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176:

45  
 50 TAAATCAAGG AAAGACATTT TAAGGTACGA AGGTTGATAA CAAAAACCA ACAGATTTAG 60  
 GGGTATCAGA G 71

## (2) INFORMATION FOR SEQ ID NO: 2177:

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177:

GTTGAATTAG GCAGCACGAT TATTGATGCT GAACTGTTAG AGTCAGATAA G 51

10

(2) INFORMATION FOR SEQ ID NO: 2178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178:

TTAATTAATG GTATTTACAT ATTCATAACC AAAGGATAAA ATAATTGTGA AATTATTCAC 60

A 61

25

(2) INFORMATION FOR SEQ ID NO: 2179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179:

CATTTTACCA TGCAGCAAAT AATACAGGTG GTGCCGTTAA CAAACGTGAN 50

(2) INFORMATION FOR SEQ ID NO: 2180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180:

GCCGAACGAA TCAAATACCA TACCTAATTG ACTGCAGGCA TGTCCATATA GTGCAGTTAA 60

50

CTGTCTACAA GGC 73

(2) INFORMATION FOR SEQ ID NO: 2181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181:

	TACTTTTGGC GATATTCGGT ATCGTTATTA CAGTTATTTT ATATGCAATT AAATTGCCGG	60
10	GTTCTATCTT TATCGGTATG ATCATCACAG CAATCGTTGG TATGTTCACT GGATTGATTC	120
	AAATGCCATC TGGTATTGTG GGTAAGATTC CAAGTATTGA ACCAACGTTT GGTGCTGCAT	180
	TTGAAGCGTT TAAAGACCCA AGTCAATTAT TAACGATACA GTTCTTAATT GTTATTTTAA	240
15	CGTTCTTATT TATTGATTC TTTGATACAG CTGGAACATT AGAAGCGGTT GCAnCnCanG	300
	C	301

(2) INFORMATION FOR SEQ ID NO: 2182:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182:

30	TTGATTCGCC TTGGCCAGAA TTACTTTTGT TTTGGGCGTC ATTGCAAGTT TCTA	54
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(2) INFORMATION FOR SEQ ID NO: 2183:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183:

	TTAGTnACAT TGGGACATTT AACTGATCCA CCAGTACTTT TGGCGATATT CGGTATCGTT	60
45	ATTACGTTAT TATTGCATAA TCGGTCCTACT ACGAGACACC GCACTGAGTC CGATATCA	118

(2) INFORMATION FOR SEQ ID NO: 2184:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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AGATAGTTAT ATAAAGATTT CATCTTCTGT ATTACATTGA TATTTT TAGG TCCCTGTATA 60  
TAAAAATCAT ATGCCTCATC AACAAACATCA CTTTTATTTT TGATTGCAAT TTGATGTAAT 120  
5 ATCTTTTGAC TAAAAACACG ATTAATCATA TTTCTATTAT CCATAGCTAC GCACCTCCTT 180  
CAACATACAT TTAATGCTTA TCCTGTTAAT ATTATAAnCn ATTTTAAATG CCTATAGACA 240  
10 TTATTCTAT ACACATACGA TTATnAAATT GTATTGAAAC CAAATGATGG TTGCCAAACA 300  
CAT 303

## (2) INFORMATION FOR SEQ ID NO: 2185:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 110 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185:

25 CCGGGGTTTT GGTAAACCC TCCCAAnATT TTTTTTAAGC CCAAACCTTG GAAAAACCCA 60  
GGCCACCCGT TGAATTTTT AAGCCTTGGA TTAATCCGGT TTGGTTAACC 110

## (2) INFORMATION FOR SEQ ID NO: 2186:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 86 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186:

40 CCTATATTGT CACCCAACCTT CATTACGGCA CCTTTACCGA AAGATTTCTC CATATTTTTTA 60  
ATTACTGTAT CTAAAGCTTT TTGACG 86

## (2) INFORMATION FOR SEQ ID NO: 2187:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187:

55 TTTGCTAGAA AACATACCAC ATTTGCCAAT TATATTATTT ATTCTGATGT TTATTTTCGG 60

TATTTAGAGG TGATAAAATT TGTCAACTAT TACAAAGACT AAAATAAAAA TCTTTATTAA 180  
 TTATTTTATT GGTATATTAG CCTTGGCGTT TGCTGCTTAT ATATTATTTA AATAAAGGTT 240  
 5 AGAGTGAAAC GTGTTTATGA ACTAGACGTT CTAGTATAGT TACTACAGCT TTAGTCAGAA 300  
 GGTATCATTG ATAAGATCAT ATTAAATCAA AGAGGCATTG ATATACACTA AAAAGAGGCA 360  
 AGATTACCTG CCTCTTTTTA GTnATTAAAT ATACGTGTTA 400

10 (2) INFORMATION FOR SEQ ID NO: 2188:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188:

TTTTATAAAA TATCAGACAT TTTTgntCAA CATACTCTC TTTCGATGTT TCTAATACTT 60  
 TATCATTAAC CATTACACCT TAAAGTTATG ATGTGGCATG TTTTCTTATA TTCATAACAT 120  
 25 CAATTTTATC A 131

(2) INFORMATION FOR SEQ ID NO: 2189:

- (i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 85 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189:

CGTAAATAT TTTGATTTAA AATGGAGGGT ATTAATATGA AAAGGTTTCAT GTAAATCTA 60  
 40 GGGGTATTCC AATATTATAA GGCAC 85

(2) INFORMATION FOR SEQ ID NO: 2190:

- (i) SEQUENCE CHARACTERISTICS:  
 45 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190:

CCCCGAGGAAT ACATGGCATT AAATACACGT TTAATATTTA TAAAGGTGAC TTAATTTTGT 60

ATAATTGTTT ATCAGTGATA AAATATTTGC AATAAGAAGA GAATGACTAA ATAATCTTAA 180

TTTTCAGAnA AGTAATTGTA ACCTTACTGG TCTTATGGTA ATAn 224

5 (2) INFORMATION FOR SEQ ID NO: 2191:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191:

AGCTTTTGTA GTTTCTTAA GCACACCGGC GATTTGATTA TTACATAAAG GATTCCCTTT 60

TTTTGTTGTG AATATGAACC CTCTGTCAAC ATAGCTCGAA TTCCATCTTT TCAACATTTT 120

20 GTTTTCCAGT ATTATCTTTT TAAAAATTC TACGGTTCTA GAATTGATGC TGATACTTCT 180

TTTTGAACTT ATAGTCTTTG TAGTGTCTTT GTATCCGAAT CCTTTCTCGT ATTTAATGCG 240

GTGAATTGTA CCTGTTATAT TGATAGTnTT GTTTAATAAA TCTATATCTT TTTCCTGCAG 300

25 TGCTTGTAAGT TCTCCTATGC GCATACCAGT TAAAGCCTGT ACTTCTAAGA TGCTGGCAAT 360

TAAAATGCGA TTTCGCTTTT GTAACCTATT ATCATTTAGT 400

(2) INFORMATION FOR SEQ ID NO: 2192:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192:

40 GACGACTGAG AGGCCGTTGA ATTTGACGTT GCCATATnTT CAAATTTAAC 50

(2) INFORMATION FOR SEQ ID NO: 2193:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193:

GTGTTTTTCA TATCAAAACA CCGTAGAATA AACAATGAAT GGAATTACTT TTGCAATGAT 60

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194:

CCAGTCACTG ACTACGTCTT CCTCGGTGCT GGCGGTGGAG CCATTCCCTT ATTACC

56

(2) INFORMATION FOR SEQ ID NO: 2195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195:

GTAGGGAAAG GAAAACTGC TTCCATTGGG AAATGTTAAA CCTTG TTCCT TGGTGATGCC

60

ATTGGATTT

69

(2) INFORMATION FOR SEQ ID NO: 2196:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196:

ATATGACACT ATATTTTATA AACATACATT TAATGATTCA TTATACAATT GCCAA

55

(2) INFORMATION FOR SEQ ID NO: 2197:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197:

GCCCTAGTTC AATCATATAA CCATCTTTAC GATACGATTG AATCTTTCCC CCCGGACGAT

60

TCGATGCTTC A

71

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198:

AGTAGCACAA CAGCCATGCG GAGACAGAGA ATCGTTAGAG ATTAATGGAG ATCA 54

(2) INFORMATION FOR SEQ ID NO: 2199:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199:

GGCGGTTTTA TATTTATCGT TGCAGTTATG CAAATTGTAC TTGGTAGAAG TATAGATTCT 60

CGTGATTCTGA AAAAAGTACT TTAAACGGGA TTGGGAATAG TAATCATATC TAGCTTTATT 120

TGTGCAGTGA CACATAACTT TATATTATTT GCTATATCAA GGTTATTTCA AGCAATTGGT 180

TGCGGAATTA TTCCTCTCGT GACTTTAACT TTATTAGCCA AACTAAGTAC AGATAATGGT 240

AGAGCTCAAG CTATGGCGAA CTATCAAATA TTTTATCAT GTGCACCAGC TTTGGCACCA 300

ATCTTAGGGA GTACTTTAGG TGGCAAGATG GGGATATATT GGTATTTTAG TTTTGTGGCT 360

CGTTATATCT ATCGGTATTA TTTTGGGATA nCTnTnTTAA 400

(2) INFORMATION FOR SEQ ID NO: 2200:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200:

GGATATGCCA TGGATGACGC ATTGCTATAT CGGCAATTGn GAAGCTGCTG 50

(2) INFORMATION FOR SEQ ID NO: 2201:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201:

ATCGAATATC ACTACTATCT CTnTtnAAGT ATCTACAATC TCTCCAATCT 50

## (2) INFORMATION FOR SEQ ID NO: 2202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202:

TCGACAATCC TAATGCAATT GCTTCATGTG GnTGTGGTAG TTCATATTAG AACTGCAAAA 60  
 GTTGCAGGTG ATCCTGAAAA TTGCTAATAA AATAACTTTT TAATGGTTAA CCCAATTTTT 120  
 GGGATACAAA TTGATATCAA TAACGATTAA GGACATATTT GATTATGTCC TATTTTGTCCG 180  
 TAAAGATATT TTGTTTTATT AAAAAGCTTA TTGAAAATTA AGAATCTGAC TATAAATAGT 240  
 ATTTTAAATG ATCGTGATAG CGGATACATT TTTAATCGAA ATCAGGCTAC GAAAAATTA 300  
 ATTAATTTTT TCACAATCTG ACTGAATCTT GCTTGAAAAT ATAACATAAA AGCTATAGAA 360  
 TTAGTATTGG ATTAAAAATG TCTTTTTTGT GAACATCACA 400

## (2) INFORMATION FOR SEQ ID NO: 2203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203:

GCGTTGTCCT TTTCGTGACA TGAAACAATG TGGAAAACAT AATTAAATnn AGGGAAAGTG 60  
 TGAATAGTTA AAAAATTAGT ATTGTGTTAT AAAAAATAAT TAATACTGTT AGGATTTTCAT 120  
 TAACTAACTT AACGTTGGTT CAAAAATAGT TAAAAAGAGG TTAATTCATA GCGCAGTATC 180  
 TCACCTATAT AATGATAGTA GATTGTTCGT ATTACGTAAT TGAATTAATC ATATAAAAAT 240  
 ATATTAAGAC AAATTTATAA ATAGATTGGG AGAnTAGTAC TGTGAAATTA AAAACGTTAG 300  
 CTAAAGCAAC ATTGGCATTG GGCTTATTAA CTACTGGTGT GATTACATCA GAAGGCCAAG 360  
 CAGTTCAAGC AAAAGAAAAG CAAGAGGGnG TACCACCATT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204:

GTTATTTTGT ATGGTTAGTC TTAAAATAn ATATAGATAT TAAATATTTA TTTTACGAAT 60  
 TGTTAAGTAA AGAAAAATA TTAATCAATC CGGGTTACAT TTATGGCAGT AAAGAAAAGA 120  
 GTATAAGGCT ATCTTT 136

(2) INFORMATION FOR SEQ ID NO: 2205:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205:

TTTTATTTTT TCGCAATGAA AAACAATCTT TCTGCATCTT CATTATGTTT ATCTATATTA 60  
 AAATCAGTAA ATGTTTCAAC ATGTTTAAAA CCAACTTGAG CTAACCAAGA CAAATATGTC 120  
 TTTTCATCAA ATGTTCTCTG AAAATGAGAC TCATCAAATC TTGAATATGT TTCATCTTCA 180  
 TGTCGAATGA AAAATGTCAT ATCATGATAA AACTTTAAAG GTAAATCTCC TTGCACAGCA 240  
 TCCCATGCTA AAAAAATGTC CCCTTTATCA TCAATATAAC TTTGATTATT AAACAAAGTC 300  
 ATCATTTTAT AACAGTATG TACATCAGAA ATAAATACAC CTGAATCAGT CAGATGATGA 360  
 TAAACATTGA TGAATGTTTC AATCACTGCA GTTTCATCTT 400

(2) INFORMATION FOR SEQ ID NO: 2206:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206:

TTGAATATCA TATAAAAACA TCAGGTTCAA AGTTGACTAC TCTTAATAAT ATAAAAATAA 60  
 GAATTAAAAA CATTAAACGA TACTGCTCTG AGAACTTGCT TTAAACAAA CTTGATACAA 120

GTCAACTCGG AGATATGAAA GGAGCnATTA AATATGCAGT TAAATTTTAC AATTATCCAA 240  
 ATGAATATTT GTTAACTAAT GTCAAAATTC CTAAAAGAAG AnAAACAATA GAGGATATCG 300  
 5 AAAAAGATGA ATCTAAAATG GTACCACTAT TTAGAAATGG AACCAAGTCC TACnGATACG 360  
 TGATCATATA CTAATGGAT 379

## (2) INFORMATION FOR SEQ ID NO: 2207:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207:

20 CATCTTGGGA CGTTTTAAAA AGTAACGTAG CGAAGACTAT TGGAACAACA ATGAGAACCA 60  
 ATGCTAGAAG GATCAAAAAG TATTTTAAAA ATTTATTCAT GATTGATGCT CCTATATTAA 120  
 ATTTnTGTTA AATCATA 137

## 25 (2) INFORMATION FOR SEQ ID NO: 2208:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208:

35 GCGCCGCTCT GTTCATTTTA CCTAAATCCA ACGTTTCAGG AATAGATGTT TTCAAACCAC 60  
 TTTGAAATGG AT 72

## 40 (2) INFORMATION FOR SEQ ID NO: 2209:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209:

50 ATGTAGCAAC TAAAGATGAT AGTGGATAGC GACACGGTCA ATAACTGCC TA 52

## (2) INFORMATION FOR SEQ ID NO: 2210:

55



(A) LENGTH: 206 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210:

10 TTTTTTATGT TCTTTTTTAA TAAGAGGGAA GTGAAGTTGT ATAAAAATGT ATTAAATATG 60  
 CACTTTTAT ACATTAAACGA TTCATATATG TCTATTATGT ACCAAATTTA TAATTTGTAT 120  
 AATTTTCGAA CTGGTTAAAT TCGAAAAATA TCACTAATAT ATnTAGATCG ATGTGTAACA 180  
 15 TTACGTTCTA nTAATTTAAT GTTGCA 206

(2) INFORMATION FOR SEQ ID NO: 2211:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211:

ACGATGTATT TTGATATCGT TACCAAAGTC TTTTAATAAC TCATTTTCAT CTAAATAAAT 60

30 (2) INFORMATION FOR SEQ ID NO: 2212:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212:

40 TGATAAGGTT TGTCCCATCG CTATTTGAAA TGATGCATTG TAAAAAACTA TCATTTGTTG 60  
 GTAATATCTT AGTTCGATGA CTTTCTTTCC AATCTTTCCG TGTCATAGAG ACAAGATTTT 120  
 45 TTGTAGCTAT CTTAGTTGCT TCTTGAATGT TCATTTGTTA TTCCTCCTTT TAAGATGTTT 180  
 GTnTTTCTTT AAATGCTAAA ATAATTGATT TCTTTTATC ATTCGTGAAT ACGAAATTTT 240  
 CGTATTCATT ACCTAAAAAA ATATCATCAT ATTTAACATT AAAAGCACTC ATATACTTAG 300  
 50 AAAGTAAACT AACnTTAATG GnTG TAGAGT C 331

(2) INFORMATION FOR SEQ ID NO: 2213:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213:

AGCATAAACC AAAAGATGCG GATATACTTG AACGCGTCAA AGATATACTT AATAAAAAAG 60

10

A 61

(2) INFORMATION FOR SEQ ID NO: 2214:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214:

TCTATTTGAG TTTACATTTG ATTAAATGAA TGACAATTAT ATGAACCTGA CTGGT 56

25

(2) INFORMATION FOR SEQ ID NO: 2215:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215:

35 ATACCACTAC TATACAGTTA AATTAATATA CGTTAAAACT TTAATCCGAT ACATTGGTTA 60

AAATGATGTT CCTCGCTGGT GGATCGAGAC ATACTTCGCT CTGACTTCTT TAGTCAGTTT 120

TTTTTCAGCT TTTTAGGTGT AATCACTGAC TTTGTTACAT CACGTCAAAT TTACAGTCGC 180

40

TATTATCTTA ACTTATCnAC GCTTATCACA CATCAATTCA GATATTATAT TGCATTGGCG 240

nCTATCACTT TGAACCTGCT GTGACTGGAA CTACTGGCTG TCAnGAGCGA GGGCTGATAA 300

TGAGCATAAA GCAACATATA AGTAATACGG CCGAATATGT AAATTCGGCA GCTTTAGGCA 360

45

ATGCTGCCCG GGCATGACTA GnACATTAC AAGAAGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 2216:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216:

TTTTTAAAAA AGGGGTAAAC CAAAGTTTGT GAACCCCAAA AAATTCGGA GTTAAAAAAA 60  
 5 CCCCCAAAAA TTAAATTAAC CGGTTATTCC GTTCCAGGAG CCAAATTTT ATGGTTCCAA 120  
 TTnCCAAAGT GGG 133

(2) INFORMATION FOR SEQ ID NO: 2217:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217:

TACTCGTACC ATTAACCACT CTGATTAACC ACAATACTAA GGTATTCAAT ACATCACTGA 60  
 20 CATC 64

(2) INFORMATION FOR SEQ ID NO: 2218:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218:

TATTCTATAG AATATGGATA ACGTTTAAAC TGATGTAGAG TATTCATCAT TGTAACACGT 60  
 35 CAATTTGATA TGTGAGATTA AC 82

(2) INFORMATION FOR SEQ ID NO: 2219:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219:

TTTGACGCAA TGATTTAGCT GTAAATATGC AATCTAAAGG AAAGTACCAC TTATGAGATG 60  
 50 TATTAAAAACG 70

(2) INFORMATION FOR SEQ ID NO: 2220:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220:

10 AAAAAATTACC CCAAAGAATT GAAAATTTGT TGTTTGGGTT ACCGGGTTTA AGATTAATCC 60  
GGTTGA 66

(2) INFORMATION FOR SEQ ID NO: 2221:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221:

GATCGCAACC AAAATAATGG TCTTCTGGA TTATTACTTT ACCAGCTGGC ATAC 54

25

(2) INFORMATION FOR SEQ ID NO: 2222:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222:

35 GTGTTGCTAC AGCTAnCATT TCATATTTAA CGnGTTGTGG TATTTCTAAA 50

(2) INFORMATION FOR SEQ ID NO: 2223:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223:

AATGGGGGnA CCCAGCnTGA GTTATGTCAT CATATCGGTA TGTGATACAT 50

50

(2) INFORMATION FOR SEQ ID NO: 2224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224:

GTAGATGCGC CCTCATATGG ACAAAGATAA AGTATCAGCA GATTGGACGC TTTA 54

10

(2) INFORMATION FOR SEQ ID NO: 2225:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225:

20 CGAGACTTCA CTTTGACTAA ACGCGTTAAG AATTTAGATT ATGCTTACGA TGAAGAAGAA 60

TTA 63

(2) INFORMATION FOR SEQ ID NO: 2226:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226:

35 TGGCCATTTT TAATGGGGGG AAACCTTAAA AAGGGGTTTT TAATTTTAAA CCAAG 55

(2) INFORMATION FOR SEQ ID NO: 2227:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 131 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227:

TCCATTTGGT TGCCTTCTTT AAATAAACCT TGGATTATGC CTTTCCTCCG GTTAATTAAT 60

GGGACCAGGG GCCAAAAATA CCCCCTTTTA AATATAnATT CCCAAAATCC ATAGTTAAAT 120

50

AATCCATTTG C 131

(2) INFORMATION FOR SEQ ID NO: 2228:

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- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228:

10 CCATCTGTGC TTCGTTAGGC GCTTTCGGCA TCACGGTGAT GGTITGCGAC AGATCCGCCA 60  
 TCCGGCTGAA TGGGAAGCCC GCGTTAnAAA GGCGCGTAGA TCCGGCATCG GGATGAAGTG 120  
 GTAATACTTC GAGAAGTCGA TGGTGGAGTC GTCACCAATC ACCACATGAT TCTGCACCGG 180  
 15 CTGGAAGGTA ATACAGTTAT CCACCGAACC GCCCGGCATC GGGTTCATAT ACTCAAAGTC 240  
 GAAGCGCACT GGnTTTGGTC GCGCCCAGTT TCAGCGCCGG AATAGAGACA TCTGTTTTGC 300  
 CATCCAGCAA ACCTTGTAAT ACCGGAnTCC GCAGCAGCAG GCGGTTTCGC 350

20

(2) INFORMATION FOR SEQ ID NO: 2229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229:

AACTAAAAAT ACTATATAAA AAAGGTTGTT ATAATTTAAT GGATATAAAT AAAAACGA 58

(2) INFORMATION FOR SEQ ID NO: 2230:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230:

45 GGGCGAAAGC TGGACGGAGC CAACGTCGCG TGAGTGGATG GAAGGTTCTT 50

(2) INFORMATION FOR SEQ ID NO: 2231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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AGCCATACGT GGTAAGCACA TGCTAAATTT GCCAGCCTGA AAATGTTTAG

50

## (2) INFORMATION FOR SEQ ID NO: 2232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232:

TGTATCATTT TGGCAAAATC ATAATCTTTA TCGTCGAATA CAACTACTTT TAAGTTTAAT 60

GATGAAGGTA CGCATTGTGT AATCACTTCA TCTAACTTTT TTAAATCAGG TGTCATAGTT 120

GAACCTTGGnG GT 132

## (2) INFORMATION FOR SEQ ID NO: 2233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233:

GATCTTGAAG CAGTTGAAAC ATATGTATCA GATGCATTAA GACAAGTACA CTTACAATCA 60

GACATTTTGT CTGTATCA 78

## (2) INFORMATION FOR SEQ ID NO: 2234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234:

TTTAGGCACA GACGGTAATA AGCTACAATT TTCATAAAAT CATCTCCTTn 50

## (2) INFORMATION FOR SEQ ID NO: 2235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235:

ATCCTGGA AAA ATCTGGTAAG ATATCTTGGA AATAACTAAT ACCAATTCCT AAAA

54

(2) INFORMATION FOR SEQ ID NO: 2236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236:

GGGTGATGGT CATTGACAAA GTCAACTTGT GATAAGCCAT GGATATTTT CGTT

54

(2) INFORMATION FOR SEQ ID NO: 2237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237:

TTATTTACTT TAAATTTCTC AATCTACAGT GTAATCTTAT TTCTTATTAT

50

(2) INFORMATION FOR SEQ ID NO: 2238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238:

CCTTAATGGG TTTTGGGGGG GGGCCCCCCC GGCCCAAAC CTTTGGCCCA ATTGGTTCCT

60

GGGTTAAGGA AAAA

74

(2) INFORMATION FOR SEQ ID NO: 2239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear



CCACCCATGG CGCTTGACAA AATATGGATG GAACATAACC ACACCGTCCA AGTTCACTGT 60  
TAGCACCGTG T 71

(2) INFORMATION FOR SEQ ID NO: 2240:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240:

CAGCTAGGTA GTTAGGGATT CGACTCGTAA AACGGATTAA TAGGTTTTAT AAGAAGGGGG 60  
TTTG 64

(2) INFORMATION FOR SEQ ID NO: 2241:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241:

CTTGACACGT ACATCTAATA CGACAGTCTG TGC GTTTAAA ACCTTTTGGG TCAAACCTG 58

(2) INFORMATION FOR SEQ ID NO: 2242:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242:

GACTCATCAC CGnTTGTAA GAnATACAAT TTATTACCCA GCAnTTAACA 50

(2) INFORMATION FOR SEQ ID NO: 2243:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

AAATTTGGAT TGGTTGAAA TTTACAGTTA AAATTTAAAG GGTGGATGGA AAAATTTTAG 60  
GAACTTCTAA G 71

(2) INFORMATION FOR SEQ ID NO: 2244:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244:

GGGGGCCCCCT TGGGGGTTTG GGTTTTGGGG GGCCCCCCTT TTAAAAAnTT 50

(2) INFORMATION FOR SEQ ID NO: 2245:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245:

TTATAATTTT TGAAAATAGA AGAGGGAAGC CTAAATTAC CAAATGGATT TA 52

(2) INFORMATION FOR SEQ ID NO: 2246:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246:

ATTAGTTGAA AAGTACAATA TTCCGCAAGT TACCAATCGA TACAGGTATT ACAAG 55

(2) INFORMATION FOR SEQ ID NO: 2247:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247:

## (2) INFORMATION FOR SEQ ID NO: 2248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248:

GGGAAGGTAA AACTTCCTGC TTTTTTTATA AGTATTCATA CTCTATTGCT ATATTAGTAG 60  
AAACCGTAAA ATCAGTCATT CACATACATT nTGAAACATC TAAATAG 107

## (2) INFORMATION FOR SEQ ID NO: 2249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249:

GTTGGATACC TGnAACTAAA TAACTATTCT TTAAAAGTTA AAAACCAACC ACTAGTGGCC 60  
ATTGGGGATT AAAATTCCAA CCTGGGCCCGG TCCATCCCCA TGGTGGGTAA AATGGGGGAG 120  
GGAAAATCCT TATTAGCCAA AGGATTCTT ACCTAATAAT AGGGGGAA 168

## (2) INFORMATION FOR SEQ ID NO: 2250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250:

TTTAGTTGTG ACATACTGAG AACTGTAGTA CTTAGTGCnA TACCAAAGGG 50

## (2) INFORMATION FOR SEQ ID NO: 2251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GCAGAACATA CCACGTGTCG CTGATTACCA ATACAGTAGA TCAAGATGGA CTCGATTGC 59

(2) INFORMATION FOR SEQ ID NO: 2252:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252:

5 GTTTGTGTTT TAATTTTAAG GGGAAGGGAT TTTTTCACCA AATGGGAATT TT 52

(2) INFORMATION FOR SEQ ID NO: 2253:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253:

25 AGTGTAATTA GAAAGGCAAG TACACCTGTT TAAAGTTTAT CTTCTAAGAT TTGTTTACTT 60

30 TAGAACTATA GCAGTTAATC 80

(2) INFORMATION FOR SEQ ID NO: 2254:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254:

40 GTAAATGACA GAGGAAATAT AACAAATGATT AATAATGTTA CAGCATTTAC TGCAAATATC 60

45 TACTAT 66

(2) INFORMATION FOR SEQ ID NO: 2255:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

ACATGTGTTA ACTCTTTGGC AATATATCCT GTTTCTTCTT CTAATTCACG

50

(2) INFORMATION FOR SEQ ID NO: 2256:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256:

AATCTTTTAT AGGAAAGAAA GAAGAAGATG TTATCAGTTG CGATTATCGG CCCAGGCGCT  
 GTCGGTACA

60

69

(2) INFORMATION FOR SEQ ID NO: 2257:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257:

TAGCGGGAGA TAGAAAAACC ATTCCGCATT AGCTTTGGTC AAGTTGGGAA TGGGTAAAAA  
 AATA

60

64

(2) INFORMATION FOR SEQ ID NO: 2258:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258:

GGTTAAGGTA TGGCGAAATA TCTCCAACAA CACTTCAAAA GGTTCAGAA AATAGAAGTC  
 GACTGAACAA TGTCATTAC ATGTGTGCGT CATGCACACC nTATGT

60

106

(2) INFORMATION FOR SEQ ID NO: 2259:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259:

CGGAATAACT GACTATGTAT CATTTGATGT TATTAACATC AATATTTTGT GTTAAATGAT 60  
 5 ATGCTAGAAA TAAAGCATA 79

(2) INFORMATION FOR SEQ ID NO: 2260:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260:

GCTGGnTGTT AnTGCCAGAG CATGTGAGCT GGATAATCAG TTGGAGAGGC 50

(2) INFORMATION FOR SEQ ID NO: 2261:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261:

nCCATTAATG ACCGAGATTA GTGAGCATGC ACAAATTGTT ATGGTAGGAT 50

(2) INFORMATION FOR SEQ ID NO: 2262:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262:

45 AATGAACCAC ATAATGACAA CTTGAATGAC AATATGAATA TGATGTCAAC A 51

(2) INFORMATION FOR SEQ ID NO: 2263:

(i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

CATTAGGTGC TTATATAAAT TACTTTGTGG TGGCTCCAAA ACTTCGGGTT AAAAC

55

(2) INFORMATION FOR SEQ ID NO: 2264:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264:

15

TTTCnTCCCC CCCCCGGGGT TTTTGGTCC CTTTTTTTTT TTAAATTTC

50

(2) INFORMATION FOR SEQ ID NO: 2265:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265:

TCATTCATAG AGGTGTAAAG ACATAAGGGG AGCTTAACTG CGAGGACCTA CA

52

30

(2) INFORMATION FOR SEQ ID NO: 2266:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266:

40

AGATGATGCA ATAATGGTGC AGTATAGAAG TACTGAGCAA TGCAAATTTT AGACG

55

(2) INFORMATION FOR SEQ ID NO: 2267:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267:

55

GTTTCATCACA TTTATTACAT TCAGCGTTGG AATCAGTACT GGGTTATCAT G

51

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268:

CTGTTGACAA CAAATTAAAA ATGACAACAT GTCGTAGTTA TAGTTAATTG ATTG 54

(2) INFORMATION FOR SEQ ID NO: 2269:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 312 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269:

AACCAAAAAG AAAGCAAGGT CAAGGAAATT TCAGCGnGAC GTATCTTTAG TTTTGAATAA 60  
 GCATATTAAT ATGGTGATAA TATGCAAGAn AACCTGTTTA TTCGATTCAA TGAAATTATA 120  
 TTATTAATAT ACTTAATCAG TATCATTTGC TATTTTTATG ATTTTGTACA AAAAAGTCAT 180  
 AAGATTAGAA GTTTAGGCAT ATATTTATTG GGGATTGTTT GGGTTTTACA AACAATCTCT 240  
 TTATCTATTT TTATTATACA AACTAGACAT ATTCCATTAG GgNCTATTC AGATGTATTC 300  
 TATACTTTAA GT 312

(2) INFORMATION FOR SEQ ID NO: 2270:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270:

GTTGATGGAT TCTCTTGGTT TGGTGTAGTC ACAATTTCTG AACTGGCCCT TGTTTACG 58

(2) INFORMATION FOR SEQ ID NO: 2271:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271:

CGTTCAGACG CTAAATCAGG CACCAGGTTG TACAATTGTC CTGGTTCTTC 50

(2) INFORMATION FOR SEQ ID NO: 2272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272:

CAGGTGTTGG TAAAACATTT GAGATGCTTT CAAATGCCAT TGAACATTT CAAAGTAA 58

(2) INFORMATION FOR SEQ ID NO: 2273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273:

TTATAAATTG GTGTAACAAT TTCATACACA TGATCATTCT TTGATTGAGG TAAAAATGAT 60  
TCTACTAAAC GTACACGTTT ATGCTTCTTA TATTCTTTCA TCAATAAATA TCTATGATTA 120  
GCTAATGATA AATTTAGTAG AAGCTTGTTA TCTCCATAAA CTAAATTCAC GATATTAGGT 180  
ATATTGAATT GTTCTTGATA TTTCAAAAAT TGTGATCCC ATTCTTCATT TTTAGGTAAA 240  
GGTAATACCA TCTCGTTAAT TTTCCAATAT GCTGGTTTAA GAATGACATT TTTATATCTG 300  
ATTCGTGGTG AATAACTAAA TGAATCAATA CTCACATCAT TCATAGGTTT AATGCATTTT 360  
ACAGATTCCA TTGAAATTTT TCGTAACAAT CGATATnAAT 400

(2) INFORMATION FOR SEQ ID NO: 2274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274:

GGGTACAAAT TTGTnGATGA TAGAAAAGTT CGTATCGCTA GAAAGTCTGG 50

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275:

TGATTTACCA GTTGATTACG ACAAAGAAGA ATTTTCAAGA ATTGTTGAAG CATCAAAACG 60  
CATT A 65

(2) INFORMATION FOR SEQ ID NO: 2276:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276:

ATGGCGTTCC ACCAGCAGTC AATAATCCTG TTGGGATAAA TGCCAATACT GTCGA 55

(2) INFORMATION FOR SEQ ID NO: 2277:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 76 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277:

TAATAAATCA CGTGCAATTA CGCTCACTAG CTTTCATCTC CTCATTTTGG CTTTCAAAT 60  
TTATTAAGTA TGAATA 76

(2) INFORMATION FOR SEQ ID NO: 2278:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278:

GTGGCTTTGT CTGTGTTATT GTAGTTTTGT TTCGCTGCGT CCAGCTTTGC TGCTTTTCCC 60

## (2) INFORMATION FOR SEQ ID NO: 2279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279:

TTAAGTGCCA AAGTCCTTGG TAGCCAGAAT GAACCACCAA CCTCCATTTT TCCAAAAATG 60  
 GTCTTACCT 69

## (2) INFORMATION FOR SEQ ID NO: 2280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280:

GGATGGAATT GGGTTAAGAA TAAAAAGGT AATAATTGAG TTTATGATAA TAATAATAAT 60  
 ATTGAGA 67

## (2) INFORMATION FOR SEQ ID NO: 2281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281:

TTGTTACTTC GGCACGGATA AATCCACGTT CAAAATCAGT ATGAATGATA CCAGCACATT 60  
 GAGGTGCAGT CATAAC 76

## (2) INFORMATION FOR SEQ ID NO: 2282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AACCCAGAAG ACTTATTATT AGAATCTTAA TCCACAACAC AAAATAGTTT ACTATTCCTA 60  
 AAAGCGGGAT TAAATCAATA ACAAACAGCA GTAAGATTAT TTCCTAGTCG AAATATCTTA 120  
 5 CTGCTGTACT TTATTn 137

(2) INFORMATION FOR SEQ ID NO: 2283:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283:

ACAAAGATTT ACTATTTAAC TAATTATAT GAAGAATAGC TTTCCCTAAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2284:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284:

ACTCCTGCAT ATCACAATA GATTAAATAT ACATCAAACA GATATAGTAA A 51

(2) INFORMATION FOR SEQ ID NO: 2285:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285:

CTAACATGTG TGAACGATAT GCAAATTCAA TATCTCATTC ACGCTTTGCA CTTTATTACT 60  
 ACAATCAACG TAACTAT 77

(2) INFORMATION FOR SEQ ID NO: 2286:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286:

AAACCTGTAT TTTTAATAAA CAATCGCTTG GACCTATTCA CTGCAGCTCT TCTGGGAC 58

(2) INFORMATION FOR SEQ ID NO: 2287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287:

AATTCATAAA ACCAATAAAT AAGAATTTTA TAGTAAAAGG AAATGGANTA GAGTTGGCAG 60

ACTTATACAA TATTAAAAAC AAAGAGCTTT TCACGATTAA AAGAGGAATT AATACATCTT 120

TATCTCTTTA TAGTCTAGAA CAGGAATATA ATAACAATTA ACGCCTTAAA ATATCCAGAA 180

TCATATAATT TTGAAGAATT AATA 204

(2) INFORMATION FOR SEQ ID NO: 2288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288:

GCTCGTAAGG CGTCAACTGT GGCCTTGGGT GCTACATGTA AAGGTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 2289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289:

TCGCTTCGGT GGTA AAAATG TCGTGGAGGT CCCGTTGCAG ATGGTTTTAA ACG 53

(2) INFORMATION FOR SEQ ID NO: 2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290:

TTGGAGGTCA ATGTTCCGGC TAATCTTCAA TGTTCCGTA CACAATTGCT GCGGTTGACA 60  
CACATACG 68

(2) INFORMATION FOR SEQ ID NO: 2291:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291:

TTCGACGAAT TAAACAAAT CCTTTTATAT GTTGAAGTGT ATTCGAGATT AAA 53

(2) INFORMATION FOR SEQ ID NO: 2292:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292:

ATCAATTGTC AACATCTAAT ATTCACTACC AATTATATCG CCACATGTTT TTTAGCAGTA 60  
ACA 63

(2) INFORMATION FOR SEQ ID NO: 2293:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293:

CGACTCAGGT CCATCAAGAG AGACACATTT CGACTACAGG TTATTACTTC TTTGA 55

(2) INFORMATION FOR SEQ ID NO: 2294:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294:

AAATTTTGGT TAATTTTAAA ACCAAAAAAC CTGGGAAGGA AATGGCCCTT TTCCCAATTT 60  
T 61

(2) INFORMATION FOR SEQ ID NO: 2295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295:

AATCTTAAAA CCTATGGCGT CTATTACATT CCCAAAACCT ATTTTCAGnA ATGTTACCAA 60  
TTAAACTTGC CGGGGTATGG ACCAGGGTAC CAGGCTAAAA ACTGGAAGAA AGGAAGGAAT 120  
TTTAGAAAAT AATTTATTAA CATGGACCAG GTAACATA 158

(2) INFORMATION FOR SEQ ID NO: 2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296:

TGTTCCAACG ATGAATGTTT GCATGCTTTG TTGCACTGAA ATTGATGAGT TGCTACTTGC 60  
AATCCTAG 68

(2) INFORMATION FOR SEQ ID NO: 2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297:

GTAGGGATTT TTTTAAACCG GGATAGCCCA ACCAAAATTT AATTAATTTT GGGTTTTTGG 60  
ATTGAAGGAA TT 72

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2298:

AAAAATTnTA CCAGGTGAAA AATTATTTTG GTAGGATTTA AATnTAATGG TTAAATGGT 60  
 GGTTTATTAC CTAATTTAAA AATGGTTAAA AGGGCCTTTA CCATTTTTAA AATTTAATCC 120  
 GCCTTTTGGG AGGGGGATTT TAGGGATGGT CCAGTTAGGA CCCCATTACC ACTGGAAACC 180  
 AACTTAAAAT TTGACCAAAT TTCCTGAAA AAA 213

## (2) INFORMATION FOR SEQ ID NO: 2299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2299:

TATTTTTAAA GGAGGGTAAT AATCTTAATT TAAGTTCATT ATTTTACTT TCATTATAAA 60  
 TATTTAATGT TACTTTCTTA TTTAGATAAC AATAAAAAAA TATAATCTCT nAAAACCCAA 120  
 TGAAACAGCT GCTCCAAACA ATTAGTTCCTT CTAATTGAA 159

## (2) INFORMATION FOR SEQ ID NO: 2300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2300:

ACAAGGTCAT TCGGATTTGA CTTTGTTTCA ATTGTAAAT TTTGCTCCAT CAATTGTCTA 60  
 ATTCT 65

## (2) INFORMATION FOR SEQ ID NO: 2301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2301:

TTTATTCTTA TTAAAAACC CAnTGAAAGT AnTCTTTnCA TTAnTAAAAA

50

(2) INFORMATION FOR SEQ ID NO: 2302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2302:

GAGATATATG CATGAGCTCT ACGACTTCTT TAGGTTTCAT GGCGACTATC CTGGCAGGGA

60

TG

62

(2) INFORMATION FOR SEQ ID NO: 2303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2303:

ACCAATCCCG TTGTTTTGGT TTTTAAAAA AAGGAAATTC CAAAAATCCC CCATTT

56

(2) INFORMATION FOR SEQ ID NO: 2304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2304:

TTTAAAACCC AACGGGTTTG GTTAAATGG CCTGGGCTTT TCCAAACTT GGC

53

(2) INFORMATION FOR SEQ ID NO: 2305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2305:

CGAACAGGTT GCCACTGTAA GATCTGGTGG CATTTAATGG CAATCGTATT TTATTTGGAG 60

(2) INFORMATION FOR SEQ ID NO: 2306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2306:

CTTTATAATG GCGGCGCACT TGGCATCTCT GCATTTCAGTT ACACGCGGTG GCAACACAAA 60

ATTTAGGGAA TTCT 74

(2) INFORMATION FOR SEQ ID NO: 2307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2307:

TGTCCATGCA CAGCTTTATT GGAATTTACC TTTTACAGG CAACCGCTAA AGA 53

(2) INFORMATION FOR SEQ ID NO: 2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2308:

TAAATGATTA TGGGAATATC CAAAATTATC GAGATCTAAT ATGAAGTGAC TGCACACATA 60

TCAGCTCTGA ATGAAT 76

(2) INFORMATION FOR SEQ ID NO: 2309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2309:

TCCTCAAAAT GTGAGTTAAT AGTCGAGTGG AAGCTGTGAC TTGAGCGACG ATACATCATC 60  
 5 AaACTATCAA TAATGTTTGC ACATCACTTT TACTACTATC ATTTGATGTA TAAATAC 117

(2) INFORMATION FOR SEQ ID NO: 2310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2310:

AAACTCATAT CGCTTCCGAT AACCAACCCT GCTGCTGTTG GTACAAATTG TC 52

(2) INFORMATION FOR SEQ ID NO: 2311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2311:

AACACTGGAG TCCTAATGTC ATCAAACATC TACCTATAAG ACCTTATATA ATCGTC 56

(2) INFORMATION FOR SEQ ID NO: 2312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2312:

GATAACATCA TAGGCCATAA CTTCCATTTA GGCCATCAGT TATAGCATGC GGACGACATA 60

CTGTGCCATA TG 72

(2) INFORMATION FOR SEQ ID NO: 2313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2313:

CATCTAATGG GAACGTGTCTG ATCCTAGTCA GTATAGTCAT CGGCAGGTAC GA

52

(2) INFORMATION FOR SEQ ID NO: 2314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2314:

TAAACTGAAA TTTAATTTTC GGATGGTATT GTTATTAAGA AATAGACATA ATTTGTGCTG

60

GATA

64

(2) INFORMATION FOR SEQ ID NO: 2315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2315:

CTAGTTTAAA TTTCTTAAAC TTCTACATCA GTAAAAGGCC GCTCTGGGAC CATACAATC

59

(2) INFORMATION FOR SEQ ID NO: 2316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2316:

GCATAGTAAC TTAATTGATA GGAGATGAAA ATCCGCAAAG TCATTGGAAG GATT

54

(2) INFORMATION FOR SEQ ID NO: 2317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

GSTATATGCTG GAAAGATAAA GTATGGAA~~AA~~ TGCATGGCGA ACATTTTGTA AGCAGAATGA 60  
 GCTATAAGCG TTGAATGGGT TTGAACGTAA ACAATCGAAC AATGATATGT CAGACATACT 120  
 5 TGCTTTAGAG CACATTTAGA GAGCGACATG 150

(2) INFORMATION FOR SEQ ID NO: 2318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2318:

AAATCATCGA TGTTAAATAA TTTAATGACA AGGATTAATG AAAGACGGAT TG 52

(2) INFORMATION FOR SEQ ID NO: 2319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2319:

TTAAGGAAAC CTTGGCCAAG GTTAAGGAAA ACCGGGGGTT CCAAGGTTTT TA 52

(2) INFORMATION FOR SEQ ID NO: 2320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2320:

ATGAAGTTGA TTTAGGATGA AAATTAATCT TGGGATATTT AATACTTTGT 50

(2) INFORMATION FOR SEQ ID NO: 2321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CTAACGCTAA GGGCGACGGA TGGTGGTnAT GTCAAAGAGA CAAATAGGAT

50

(2) INFORMATION FOR SEQ ID NO: 2322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2322:

CGTGGTGATT AATTTTTCGT CGCGTTTTGT TTCCTTTCCC CAGTCATGTT TTATCATTGT 60

GGGCATCATT GCACCTGGGT TCCATATTAT GACGTCATTT TTTAnAAT 108

(2) INFORMATION FOR SEQ ID NO: 2323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2323:

GTCACCGAAT TTCGATTTAT ATTATCACTC AATTATTAT CTTGAAGCAC GCGTTAAATC 60

GTCTTTTAAAT TGnAACAGTT GCTACTTTAT TGTCTTTACC ATTGATCTGA ATTTGATCCG 120

CTTTAAGTCC ACTATCTTTT ACAACTTGCh CTACCTTTTG TTGAGTAATT GCTTGTTTAG 180

ATTGGAAATC TACGCGTGTA CCACTTGAAA AA 212

(2) INFORMATION FOR SEQ ID NO: 2324:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2324:

TCATTTGTTT TTAATACGTT GTCAAAATTA CCAACAAATG ACAAATTAAA TTTTGCAATA 60

CATATCAAGG TGTTATTTTT TTCCTATTTT AATTATGTAT AACGCATTAA AAGTGACGTn 120

AATATTCAAA GGA 133

(2) INFORMATION FOR SEQ ID NO: 2325:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2325:

10 ATGAACGACC GTGGACAGAC AATATTTAAA GCATTTAAAA ACAGCGTTCC CAGAAAGACA 60  
 ATATATAACC AATATTAACA AAAGCAATGC ACATTACTTC ACAAATGAAA TCAAAGCAAC 120  
 ACACATATAC AATGCAATAA GCGGGCAACA ACAAACAGAT TTCAACACGC CTGTCATACA 180  
 15 GCAATATCGT TAACAAATGA CAnCCGCCnT TTAGGC 216

(2) INFORMATION FOR SEQ ID NO: 2326:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2326:

TGACCATATG ATTGAGGAAG GTTTTATTGA TCCTAAGTAT CGTGCTCTTG CACCGTTATG 60  
 CGACACTAAG GAATCATTA A TTGAATCAAT ATTAAATTTn AAACCTCTGG GTACTCGTTC 120  
 30 ATACGATTAA TCATTCTAAG G 141

(2) INFORMATION FOR SEQ ID NO: 2327:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2327:

TGAAACTGCA GCGTGCCGA GTGGGGGTTG TGCCAGGTGA CCCAGATGG GCGTG 55

45

(2) INFORMATION FOR SEQ ID NO: 2328:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

GAAGCCAGCC TAATTGGATA CCACCGGAAG TAACTTTTGA CCAGGGCCGT CGCA

54

(2) INFORMATION FOR SEQ ID NO: 2329:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2329:

GTTCCCGGGT CCAGGCCGTT GTCTTG TGCC GGGGTGTTG GTCCTTGGTT GTGT

54

(2) INFORMATION FOR SEQ ID NO: 2330:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 190 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2330:

TATATTATAT ATTAACTGC TGTGATGTAT TCTGAAAAA TAGTAGTATT GCCTATAATC

60

ATCTATGCCA TTGTGTTTGT AATAATTGGT ATCACTTATA TCTTTATAGG CGACAGCTAT

120

GATCAATTAA CAAATTTCAA TGTGATTTTG TATATGGGGA GTTTGTTTGA TGCATGGATG

180

GCTATTAGAA

190

(2) INFORMATION FOR SEQ ID NO: 2331:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2331:

TTTTCACCTC GTGTTTAAAA TTCAATTGAA TCTAACTAA AAGTACCTTT AAGT

54

(2) INFORMATION FOR SEQ ID NO: 2332:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2332:

5 TTCTAAAAAT ATTAACGAAT TATACAACTT TAAGAGTTTT TAGTATGTAA ATATTCTTTT 60  
 CATATTAATA CAATACACCC CTATATATGC TCACTTGTTT GAATTAATAA ACTTTAGCAT 120  
 TCTGCAAATA ATATTTTAAA AATAACTATA CTTTTTATTT ACCTATTGAA AAATAGTGTT 180  
 10 ATCATATTTA TTAAGAAGCT ATTTTATAC TAGTAGGTGT CAGTCATGAA TAACATTTTG 240  
 TTAAAT 246

(2) INFORMATION FOR SEQ ID NO: 2333:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2333:

25 CCTTCTAACA TCTTTTTACC ACTCATTGAA ACATGTGATC CTAATAACAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2334:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2334:

AGAAAAGAGA CTGAAACAAC AAATTCAGGC AACTTTTGAA CAACAGAGAC ATCGATTAAT 60

(2) INFORMATION FOR SEQ ID NO: 2335:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 193 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2335:

50 CCTCAATCAG CTCCTAAAGA ACAAATAGC GACTCGATTG ATGAGGAAAC AGTAACGAAA 60  
 AAAGAACGAA AAAGTAAAGT AACACAATTA AAGCCATTAA CACTTGAAGA AAAGCGGAAG 120  
 TTAAGACGTA AGCGACAAAA GCGAATCCAA TACAGTGTTA TTACAATnTT GGTATGTGTG 180

55

## (2) INFORMATION FOR SEQ ID NO: 2336:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2336:

CCTACAGTCC CAACACTGTC AGTACACTGC CGATACCCAA CCTCTGGCCG GTCCGGCA 58

## (2) INFORMATION FOR SEQ ID NO: 2337:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2337:

ATATTTTTThA TTTAATGGTT TTACTACTGC TACAACTATC ATAGGTGGCA 50

## (2) INFORMATION FOR SEQ ID NO: 2338:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2338:

CTCCTGTAGA TTAAAAATCT CCTAAATAAC AAACGAATAA TCGGCCATCT TTATGTATTT 60  
 TGATTGCTGC AGGATTCGCT TTGTGACTTA CAAAAGGTCG TTTGATTTCCT TTCGTTTCAG 120  
 GATTGATTTT GAAAATATTG CCTTCGAATA CATCCAATAA AAAGAGTTGT CCCTGCCGAT 180  
 CAAAGTTCAA TCCTTCTAGT TGCAATCCTT TTTTGGAAAT TTCAAGCCAT GGTTTCAGCTG 240  
 TAATTGTTTG TAATTCACCT TCAGATATAA TTGGAACAGC ACTATTGGAC TTCCCGChAT 300  
 AAAATAATGG AGGGnAAAnC TGGTGGGGAC ATCCATGAGC CATTCCTTTC CATTCCATTC 360  
 GGTTTTAACT AACCAATT 378

## (2) INFORMATION FOR SEQ ID NO: 2339:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2339:

ATGAAAATAA ACTGTGTCTC CnGATGTATA CGTCCCTTCA AGCAGACTTC 50

10

(2) INFORMATION FOR SEQ ID NO: 2340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2340:

20

TATCCATATG TGAAAAATGT CATATATGAG TCTAGTTTTG TATAAATGGA GACTCGAAC 59

(2) INFORMATION FOR SEQ ID NO: 2341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2341:

ATTGATAAAA TATGATTAAG CGTTGTTGCA AATGACATTT TCTCAAAAAG CGCTTCACTA 60

35

TCAATTGGTA CTTGTGTGTh AATTTCAGCC AGTCGCTTCG ATAAATATAG TTCATCTAA 120

TTGTCATTAA TCTTATTACG TTGCCAGCT GATAATGCAT CAATGTTTTTC AACCACATTT 180

TCAACGCTT 189

40

(2) INFORMATION FOR SEQ ID NO: 2342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2342:

ATCAATTAAA ACAAAGCATA CAACAATTTG TTGATGTTGA ATCTAAATCA ATTTTAGAAC 60

AACAAATGAT TCATCAGCTT CAACAAATGG ATCGTTCTTA TG TAGAGATG ATTACAGAAT 120

55

## (2) INFORMATION FOR SEQ ID NO: 2343:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2343:

CTTAACCCCC CTTTTTCCC AATTTTAATG GGGAAAATT GTAATTAACC TGGGC 55

## (2) INFORMATION FOR SEQ ID NO: 2344:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2344:

GACAAATAAA CATGACCTGG ACAAGAAGA ACAATAAACA AGCCTGGCAA 50

## (2) INFORMATION FOR SEQ ID NO: 2345:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2345:

GTATTGCGAT GATGCATACG GGTATTGTTT TGATTAAATA ATATTTTATA TTTAATGTTG 60

ATAAATGTTG AATAACAAT CCGCAAAGnG CACTTGATGA TAGTGCTAAG A 111

## (2) INFORMATION FOR SEQ ID NO: 2346:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2346:

GCAAACAGTT TCCGTGTCCG TTTTCCAATT AAGTTAAGGA ACCCAAAGAG A 51

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2347:

TCGTAGGTGC CATAACACAC GTTACCTGGG ACTCATATGA AGTATTATGT CGAGACGACC 60

(2) INFORMATION FOR SEQ ID NO: 2348:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2348:

GTTTTTAATA GGCTCTTTAC GTATCTAAAA ATAATTGCAT TATTGGTGTG CCTTGATGTA 60

ATTGAATTAA AGTACCGTTT GGTGTGAACG TTTCAGGTAT ATCATTTTCA AChATAAC 118

(2) INFORMATION FOR SEQ ID NO: 2349:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 176 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2349:

ATGACAGAAA GCAAAATCCC AATGTTGATA TACCGTTTTT GACACCACTT GATTATCATT 60

ATTTTTTCTT TAGCGATGGA TTTTATATTA CGATTTCAAT TCTTACTATC GTTGCAATTAT 120

TGTCATTCAA ACTGTATCGT TTTTACTTnTT ATAGACTTTT CGCAATAGTA ACATGG 176

(2) INFORMATION FOR SEQ ID NO: 2350:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2350:

CTACGACTGA CATTAACTGT GCAGATGTAC CTGGATTCTA TTTTTTCAAG AACAAATTGT 120  
 AATAATTGAT AGTTATATGG TGCAATGTCA CCTTCATCCA TTGAGCGCTC AATAATTTCA 180  
 5 GCTGChAGAG CGGCnTGA CT G 201

(2) INFORMATION FOR SEQ ID NO: 2351:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2351:

ATCGCTATAA CCTATCAGTG ATAATATTG ATTGCATGGT GCACCATTG AnATTTCAC 60  
 20 TAGAATGGTG GTACCTAATT GCTTATTTTT ATATGTCATT TGAAGATTTA AAAATTAAAA 120  
 ACTTTGATAC AGAGTGAAAC CATATTTCAA CAAATTAC 158

(2) INFORMATION FOR SEQ ID NO: 2352:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2352:

TCGTAATCAA AACATTTTGA ACAGGATTAT AGTAAGGGAA TTTTGGATT TTAAGTTGTG 60  
 TTTGTTTATT TTTTAATAAG AGTCGAGCTA AGTCTTGCAA CATCATTACT TGCTTGGCAT 120  
 40 CTAAGTGTTC GTCATTAAAT TTTATGAAAC GATCACTCAT GTTTTATCCC TCTTTAAAAG 180  
 TTTAGTTCTA CAGCATTATA TATTGCTTGT TGTTACGTT CATCTTCAA TTTATCAATA 240  
 ATTGTACGTT TAATTGCACG TTCAACTGGC ATTACAGTGA TTAAATCACA CAAGTCTAAT 300  
 45 AATGCACGGG ATACTAGCGG CTTCTTCAGA AATTTGTCCC TGCTTAGACA TAGTACGTAA 360  
 ATCTTCATTG AAACCTTAAAT AATTTGGTTC GATTTGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 2353:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2353:

ATTAAATGGGG TTAAATAACA TTTTGACTGC GAAAGATTTA TTCTTTTCAG GTAAATCATT 60  
 5 GATAGATGTA TATAGTCAAT TTGCTGGATT AGCTGAAATG ATAAATGTnT TTGCGAATGC 120  
 ACCATTT 127

(2) INFORMATION FOR SEQ ID NO: 2354:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2354:

ATCTCGCTGT TTTTATGAAA GAAAACTACA TTTTCGAGAG AATAAAAAGA TTTTCTGAA 60  
 ATTTAATCTA TCAATTACAT TGATTTACTA ATATAATTAG AAAGTAAATT TTATTTGATC 120  
 AAAGTAAATG GGGGAAGTAC TGTGATAGAA AATAAGAAAA CAGTTGAAGA TACATATTCA 180  
 25 ACAGGCGCAA TTGTTGATTC AATATCATCT TCAGTnCAAA TGn 223

(2) INFORMATION FOR SEQ ID NO: 2355:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2355:

ACACTTGTC AACACTCAC AATGATAAAG CATATTATCA GTATTGTAGT GTGTGGAAAA 60  
 40 TGACAGCCAT CTAAGGAGAA AAATGATGAA AAGAATATTG GTAGTATTTT TAATGTTAGC 120  
 AATTATATTG GCAGGTTGTT CTAATAAAGG TGAAAAGTAT CAAAAAGATA TTGATAAAGT 180  
 45 GTACAAAGAA CAGAATCAAA TGAATAAAAT TGCCTCGAAA GTACAAAACA CTATTAAAC 240  
 AGACATTAAA CAAGAAGACA GTAATACACA TGTTTATAAA GATGGTAAAG TCATTGTTAT 300  
 TGGTATTCAA TTATATAAAG nTCGTGAAAA AATGTATTTA TTTCGCATAT GAAntAAAAG 360  
 50 GTGGTTAAGG CCAGAGGATT TAATCAGnGG AAAnTAGACC 400

(2) INFORMATION FOR SEQ ID NO: 2356:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2356:

AATTTACTTT GTGCCACAAG GTTATCAATG TCTTTTGAAC CACCAAACAT TCTAGCGATT	60
10 AAGTGACCTC CATCATCGTC TGGTAATCTA TCCTCTCCCC CCACAGTTCT TTGTGCATGG	120
CTATTACGAT CCCCATCTTT TAGAGAGAGA TTGTCTACAT AAATTCTTT TATGCGACCT	180
TTATGATCGG TTCGATATAT GTGACCAGTA GGTGTTGTGT ATTCAATATT CGCCTTTAGT	240
15 TTCTTAGGTh CTAAGTCTTG GCATAGTGTT CTCCGAATTC nAACCTTGGT GTTAGTTTGG	300
TGATTCAACA TACTTTTGAT GGAATTCATT ThCATGGGCT ACTT	344

(2) INFORMATION FOR SEQ ID NO: 2357:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2357:

30 TATGCGCCCC TGCTTGATCT TTCATTTGCG TCCACTCAAT TAGTTGTTTG CGC	53
---	----

(2) INFORMATION FOR SEQ ID NO: 2358:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2358:

ATTTTTTCAC CTTCTGAAAT TGATAAATCT AGGTTATCGA ATATAGTCTT ATCGGCATAA	60
45 GATTTATTTA AATGTTCAAT TTTATATGCT TCCATACCCA TCTTCCTTCT TCTGTTGAAA	120
TCTCTACGTA CTTAAATCAG TTCTATACAT TATACACCTT TTTGAAATCA AAAGAAATCG	180
ATACCGTTAA GTGTCATAAT TTAATATATT GTTGCTTCAA CTATAAATAA AACTTGTTAA	240
50 GGCTTTGATG ACTATGCTAA TGATCTTTAT AATATACCTT TTTATCAACA CATATAATGT	300
AAACATAAT ATAnAAGAAC ATAATAAAAA CCCGATTGA TATTTTATCA ATCCGAGTTC	360
55 GTGTTTAGAT ATTATTTTTT AGAGTTTGCT TTAGGTCCTG	400



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2359:

TTAATGTCGC CATT TTTTGT TAGGTAGACG TATAAATCTG GACCTTTTGA TGATTGTAG 60  
 TTAGTAAGCA TTAATTTACC ATTTTAAATC TCAGCTTTAC CTTCAACAGT TTCACCGTTT 120  
 TTAGAACTGA nTG TACCTGT TAGGTGTTTT GTTT 154

## (2) INFORMATION FOR SEQ ID NO: 2360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2360:

ATATGTCTTG TGATTTTCA GGTGTAAGTT AGTATGCAAG TGATTATGAT TGATAGT 57

## (2) INFORMATION FOR SEQ ID NO: 2361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2361:

GGCATCAAAT TAGTAGCGAC TCACAGTGA TGCATCCTGT GTTTTGGATC TCATTTCT 58

## (2) INFORMATION FOR SEQ ID NO: 2362:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2362:

TGTTATTATC GnAGAGGCTT TTCGCTTTGG AATAAGGTAT TACGTGAATG 50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2363:

CTCTTCTGGT CCCTGACATA CATAGGAGAA ATAGCnCCAT GTACAACGTG

50

(2) INFORMATION FOR SEQ ID NO: 2364:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2364:

ATTGCCAATG TCGTTAGTTC GTGAGGCTGT TGGTGAAAGT TGTGTTTGAA

50

(2) INFORMATION FOR SEQ ID NO: 2365:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2365:

CCATGATTTA AATCATTGAT TAATGGTGCT TGTCTACAT CTGTGTAAAA TTCATACAAT

60

TCTTTAGCAT CGTCGAATAG TTCATCACGA CGTTGGnTAA ATTCTTCTTC T

111

(2) INFORMATION FOR SEQ ID NO: 2366:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2366:

TAATGCTGAG CGTGTTACTT TAGTTGGATC AACGATACCT TCTTCTAACA TATTAACCCA

60

CTCnTTTGTA GCAGCGTTAA AACCAACACC CGGCTCTGCG TTTTTCAAAC GTTCTACAAT

120

## (2) INFORMATION FOR SEQ ID NO: 2367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2367:

CCTGATTGCA AAGTACAGCA AGCACTACAG ACGCCTAA<sub>n</sub>C ACT<sub>n</sub>ACACTA

50

## (2) INFORMATION FOR SEQ ID NO: 2368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2368:

AAAATGGTAT TGCAATTAGT AATGTTACAA CAAGTGTGT AATAGCTGCA TAAAT

55

## (2) INFORMATION FOR SEQ ID NO: 2369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2369:

TATAGGATGA AAATCCTGCC AAAAGATTAA GGGGTGGCCT AATGAACCAT G

51

## (2) INFORMATION FOR SEQ ID NO: 2370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2370:

TTGCTCGAGG TGGTAAATAC GCAAAGTTTA TTTGGTTGTG CTAAGAGAGA AA

52

## (2) INFORMATION FOR SEQ ID NO: 2371:

- (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2371:

10 TAATTTGAAT AAGGTGGAAG TGATAAACAG TGCTTTGCGA ATCTAGAGTC ATTAATCAAA 60  
 ACCCTA 66

(2) INFORMATION FOR SEQ ID NO: 2372:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2372:

25 AGACAGGTAC TGTCTTACGG TATGGAGCAG AAGCGGGAAA GCTGCCCAGA GCCAACTGTA 60  
 GACAA 65

(2) INFORMATION FOR SEQ ID NO: 2373:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2373:

40 TTGCAGTGAC GGCTTATAAT CATTCCAAGC GAACAATTAG ACATTCCATA TAAAATATAC 60  
 AGATGGCTTT CAGTAGAGTA GTGGATTCCG ATTACGAAAC TATACTGGAA GCTTTTTTATT 120  
 ATAAATGAAG AGAAGTTATA TTTTTCAGCAT GTATAGTTGA ATACTGGGTT AAAATACCAT 180  
 45 ATTAATAATG AAGTAAAGGT ATGAGTGATT ATGAAAGTGT TTTGAATGAA ATATATTTAA 240  
 TTGGTGATGC TTTTAATTGA AAAGATTAAC AGGATTCAAC TTGGTAAATT GTATTAAATG 300  
 TGAGAAAATA AAAGTATATT CATTGAGAGA TATATGAGTC AATGATCGTT TTAAACAAGA 360  
 50 TAAGTGTATT TTAATATGTA AAAGTTATGT AATAAATATT 400

(2) INFORMATION FOR SEQ ID NO: 2374:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2374:

CCTATCATGC CTCTCTCTCA CTGAATCCTT TAGATCCCCT TCCCTCCCTC TCCCCCTCT 60

10

TTTCCCCTCC 70

(2) INFORMATION FOR SEQ ID NO: 2375:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2375:

CCAAGTCAGA GCAGCAGTTC AGTTCGTCAG CnGTTcAGTT CAGAGCnGTC 50

25

(2) INFORMATION FOR SEQ ID NO: 2376:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2376:

35

GTTGGTGAAG CTGTTGCCGA nGGAGAAGCG GGTATGGATC CTGACGGTGn 50

(2) INFORMATION FOR SEQ ID NO: 2377:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2377:

AATTGCAGGA CAGGTCAAAG GCAAATGCAC GTATTCAGGT CATGCTCATG TGCATGTTG 59

50

(2) INFORMATION FOR SEQ ID NO: 2378:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2378:

5 TTTATCATCG TATAAATCTA TATCTAATTG ATTAACTTC GGGTGCTTAA CTAACCTCTCT 60  
 CAATACACTT ACACCAGCAG TTCCCATGCC TATTATTGCT ACACGCATAT ATCATCCATC 120  
 CTTTTGTAAT TCAAAATATT ATATTTAAAC TATTACCTAT AATTATAGCA ATTTGGTATT 180  
 10 TCCAATAAAA TTTATnAAGG TAAGCnATTA TTTCACTTTC ACAACCATT 229

(2) INFORMATION FOR SEQ ID NO: 2379:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2379:

AGTTTTTTTGT TTGACGTATT TAATTTACTA TTTGCTTGAT TGATATTTTT AGACATTAAA 60  
 25 TAGTGTTCTC CTAATCAATT TATTCTTCTT TATnTCAGCA TTATTGCGAC TGACAT 116

(2) INFORMATION FOR SEQ ID NO: 2380:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2380:

CAAATCTTAG CGGATGATTG GCATGTATAT TCTGCTGGTA TCGAAnCACG CGGTGTTAAT 60  
 40 CCCAAAGCGA TAGAAGCTAT GAACAGAAGT CGGCGTTGAT ATGTCGAATC GTACGTCAGA 120  
 TTTAATCGAT AATAAT 136

(2) INFORMATION FOR SEQ ID NO: 2381:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2381:

55

TTAATTGATA GCTTTTATCT GTAGGAAAAG CTATTTTAAA GATTTCTAGT GTATCTATAA 120  
 CTTTTTTGGG ACGATATTGA ATATTACAAT CTTTAAATGC CTTTTTAATA AAATTCAAAT 180  
 5 CAAAATCTAC ATTATGAGCT ACAAAAATGC AATCTTTTAT CTTATCGTAG ATTTCTTGTG 240  
 CAACTTGATT AAAATATGGC GCTTGTGTGA GCATATTTTC TTCAATGGAT GTTAACGCTT 300  
 GAATGAACGG CGGAATCTCT AAATTTGTTC TAATCATAGA ATGATATGTA TCAATAATTT 360  
 10 GGTATTGCG CACAAACGTT ATACCAATTT GAATGATATC 400

(2) INFORMATION FOR SEQ ID NO: 2382:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2382:

TATTTTGTTA ATAAAGTTAA TATATGTTTG TTGTACAGAT AGTTCAGGAT ACA 53

(2) INFORMATION FOR SEQ ID NO: 2383:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2383:

CCCGAGCTTG CCCTCCTTCC CCCCTCTTCG CCTCCAGACG AAGTGCCCTT CTGTCCTTG 59

(2) INFORMATION FOR SEQ ID NO: 2384:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2384:

AGCCAACATC CCnGATGGTA CTTGCATTAA TGCATAACCT AGAGAGAAGA ATGATGCCAA 60

TAAACCAAAT TGTGGTTTTG TCATCCCTAA ATCATCCATC ATTTGCTTAG 110

(2) INFORMATION FOR SEQ ID NO: 2385:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2385:

10 TGAAAGTTCT TTTAnGCATC AATTTTAAnA CTACGAGCGG ACnCTAATAT 50

(2) INFORMATION FOR SEQ ID NO: 2386:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2386:

GGCAATTTAT TGACACAATG CTTGAGCnAT TGATAGCAGG ACAAGAAAGA ATACTTGATG 60

25 AGTTAATACC AAAAATGGAT GCGACTGAAA AATTAACGCT TTATTTAACT AGTCATTATA 120

AACAGATAGA TTATGAATTT TTGTATCTCC TTTCAATGGA TAAATTGTTT GGAAATAAAA 180

GAAATAGATT AACATTAATT GATTTAGAAA ACATATTGGG AGTAGGAAGA GTAAAAATTA 240

30 GTnGT 245

(2) INFORMATION FOR SEQ ID NO: 2387:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2387:

CACAAAATTC GAAATCGTCA TCGGTGATAT GTTTAATACT TGGGAAAATA TAAAACGCGC 60

45 CTTCAGGTTG AGCGGTAATC TCAAAACCTA ATTTAGTTAA TTCAGATACT AAATAATTC 120

TTCGTTChAC ATAAGCTTCG 140

(2) INFORMATION FOR SEQ ID NO: 2388:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2388:

ATATAACATT GTAGGGCCTA ATAATTTATT TTATGTCTCA GACTCATACA ATGGTTATTT 60  
 5 AACTTATTTA CCACAAATTG AGCACTAAGA CTCACTATTA TCGATTCTTC TATTGAACAn 120

(2) INFORMATION FOR SEQ ID NO: 2389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2389:

TCTAAATCCA GCATGATCTA CATCAAAGCT GAATTCACCT TTTTCATCGA CTTGCAAATC 60  
 20 AGGGAATTCT TGACCTTCAC CTAGT 85

(2) INFORMATION FOR SEQ ID NO: 2390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2390:

GGTGTTTATA AAGCAGGGGC TGAGCCTCGG TCAGGACTGG ATACACAGGC AGTACGGGTG 60  
 35 A 61

(2) INFORMATION FOR SEQ ID NO: 2391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2391:

TAAAGTAACC ACTTTAGATG ACATTTTAGA AGTTATGGGC CGAATGCAAA C 51

(2) INFORMATION FOR SEQ ID NO: 2392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2392:

GGTCGGAnTC CCGGGTCGAC CCACGCGTCC GCATCAACCT AGnAGAAGCn 50

(2) INFORMATION FOR SEQ ID NO: 2393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2393:

ATTTCCAAAC GAATTGAAAA ACGGACGTAA ATTCTTAACT AAAGGCGATA AATGT 55

(2) INFORMATION FOR SEQ ID NO: 2394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2394:

ATAGGTTGCT ACTATTTATA TCGACTCATT TTCACCTACA AATATGACAT TGTCTCTAGA 60

ACACnAAAAT TAATTTGCGT CATATCTGCT ACAGTTTTGA GTGTGTTATC AAGTGTATTT 120

(2) INFORMATION FOR SEQ ID NO: 2395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2395:

TGGACCATAG TAAAGCATT ACGTCGGTTT ATTATTTTCT AAGGAAGTAT GTTTATATAA 60

ATCTATGCTC ATTTGTTTTT TAGCGTCTGT TTGACCTATT ATTTAGAAC CAGCCATCTG 120

CTCTTTATAA AAATTTATTA CATCATCTTT TTTTAATGTT GTATATTCAT AGTTTATTTT 180

TATTATnTCA GAATCGTGAA AACTATTTAG TGATTGAnAT ACTCTTTTGT GAGGATTCTG 240

AATATAGATT TTCTTAATAT T 261

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2396:

GTTTTGAATA TAGGGGCTTT TATCACTCTC CGAAGTCTnT TCTAAGTTAG ATTTGGAAAA 60  
 TAACACTTTT TTAGTTTCAT TCAAGCGAGT CGAGTGACTC CAGA 104

(2) INFORMATION FOR SEQ ID NO: 2397:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2397:

GATTATCGAT CACAGTATGA TTTACGTAGC AATTTCTGGT ACATATACGC CTAT 54

(2) INFORMATION FOR SEQ ID NO: 2398:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2398:

GCTTCACCTT GAACTAGCAA ATAAGGATAA AACAAGCATT CTTTACATGT TTCTTTTAAA 60  
 TACGTTTGAT ATTTAATAA TACTTTTTTCG ATTTTACTCA TATAAGTTTG AAGTTCTAAT 120  
 TTTTCATTCT CACTTATTTT GTATATATTA CATTCAATTAT GTTCTGTCAG AAAAATATAA 180  
 GGGTCAATAT TAATTCGTC TATCAATTCA TAAATTCAC TTAAGTATTT nTnCT 235

(2) INFORMATION FOR SEQ ID NO: 2399:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTTGATGCAC TTATTTGTGT AATGACATCT TTACAGTCTT TTCCTTCCTC CATCATTTTA 60  
ATAATTCCAT TTAGTTGCCC TTGTATTCTA TTAATACGAT TAATCATTTT n 111

(2) INFORMATION FOR SEQ ID NO: 2400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2400:

AAATGCTGGC TGAGTTTGG GCCACCCGCA AAGGCACTGG ACCGGTGCGA AACC 54

(2) INFORMATION FOR SEQ ID NO: 2401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2401:

AACCACTCAT CACTACTAAA ATGATACTTA AAAACAAAGT CTTAATACAC TTTTTCATAA 60

TATCAACTTC TTTCTATATT TAATACATTA ATTATACATC TTTnTnAAAT AAAAATATGT 120

GTAAAATTTT AAAACTTATT TAATTGATGT TTTAATAATG TATTATAGAA ATTATTGACA 180

TATGATTAAA AACCCCTTAGG ATAGT 205

(2) INFORMATION FOR SEQ ID NO: 2402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2402:

AGATAATCAT AGAGAAAGTC CACAGTCGGT AGAGGTGGTA GCTGAAAACA ACATACTATT 60

AATTATGAAG TGCTTTGTAA CTTGTCGAGA CGTTTGCCGC GAATCTATCA TGATGGTGAT 120

CAACGTTTTG TnACAAATGA 140

(2) INFORMATION FOR SEQ ID NO: 2403:

- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2403:

10 ATTTAACCAC TCCTCCAATG ATAAGATTGA AAGGCAAGAT GACCTTCCAA TCTTATTT 58

(2) INFORMATION FOR SEQ ID NO: 2404:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2404:

CAGCTTCTAC AATACGGCGT GCTATAGCAA GCATTAAATGT AAATCCTAAT TCTGCAGTTG 60

25

T 61

(2) INFORMATION FOR SEQ ID NO: 2405:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 217 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2405:

AATAATCATT TTAATACGGT CTTCAAGGAAT TGAAGTGTCT ACAGGTACAT ATCCACATCC 60

40

TGCTTTAATG GGCACCAATC ATCCCAACAA TCATATATGG TGACATGTGA CCGAATAAAA 120

TCATCGGGTT TCTnACTACC TTGTAATCGA TGTGGCTAAT TTACTAGACT CATCCATTAA 180

CTGTTGATAA GTTAATTCCA TCAGTTGTGT GTCTAAC 217

45

(2) INFORMATION FOR SEQ ID NO: 2406:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2406:

GTAGTATCCA ACGTATTTTCG GATTGCATCG AGTTGATTTT TATTATTTTC TTCAATGCTA 120  
TCAAGCGCAn CTGTATTACG TCTTACTTTA GGTTTTATTT GCTCTATTGC CTTGATTGTT 180  
5 TGATnTCTAA CATCAGTAAC AGCAGCATCT TGATTGTAT TGTCTATT 228

(2) INFORMATION FOR SEQ ID NO: 2407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2407:

CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG CAGCTCCCGG 60  
20 AGACGGTCAC AGCTTGTCTG TAAAGCGGAT GCCGGGnAGC AGACAGCGAT 110

(2) INFORMATION FOR SEQ ID NO: 2408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2408:

GGAGACCCCA AAAATTTTGT CGTTGAAGAT GCCTTTTTTTT AAGCGTTATT TGGCTATATC 60  
35 AGTTTCTAAC TGT 73

(2) INFORMATION FOR SEQ ID NO: 2409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2409:

AAATCATTAG AGAGGAATAG TTCCCTTTGT TACGCCAAAG ATTCGATATT GAC 53

(2) INFORMATION FOR SEQ ID NO: 2410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2410:

CCATATGATT GTATAGGATC CATGACGTCT CCACTGACCC CTGACTCTAG TATC

54

(2) INFORMATION FOR SEQ ID NO: 2411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2411:

GTTCCTCTTC AATTGTTATA TGTATATCAC AAAAATTATT TCATTATTTT ACCATTATTA

60

TTTACAAAT ATTATCCCAA GAATACAATT CAAGAAATGA TTAACCTTAC TTTAGAATTG

120

TACCTTATTA CATTATTTAT GAAAGTACTC TCTCAATTAT AACnAAAAAG AAGGTGTTCA

180

ATACATnCAT ATTTAGTCTT ATAT

204

(2) INFORMATION FOR SEQ ID NO: 2412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2412:

CAGTGGCGCA GAAACATAAC GCTCAGGGAA GCACAGCACC TCATTATGCC AAAGCT

56

(2) INFORMATION FOR SEQ ID NO: 2413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2413:

TCGCTGGCGG GTCCCGCGG CCTAGCGTGC TCATGTGCGG TGTTCTAGGT GTTGGGGTTG

60

CAGTCA

66

(2) INFORMATION FOR SEQ ID NO: 2414:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2414:

10 GGATAGAAAT GGAATCCAC CCATCGGTGG GGGTACCAGG CTCTTCATAT GGCCTTGTGG 60  
 ACTTC 65

(2) INFORMATION FOR SEQ ID NO: 2415:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2415:

25 TTAAATAGAT AGAATAGAAT TAAAGAGACG ATGATAGGTG CTGCTATCGT CTTAAAAACG 60  
 ATGATAAAAG GATCAAAAAC ATATGATACT TTTTCGAAA TAAAAATAAC AATACCCAAC 120  
 AATACTAGCG CTATTAATGA GAAGACTAAA TCATTCCCAC CAACAACTT CATATACCGT 180  
 30 GATTCGGTAA ATTTTnnAAA ATTCTTTCTT ATATTCTTTT CATTTTCATT CAATTATAGA 240  
 TTCACCACCA CTTAAATAT TCATAAG 267

(2) INFORMATION FOR SEQ ID NO: 2416:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2416:

45 TTAAACAAAT GAATATAGTA GTTCCATTAT CCTCACTTTT AATCGTTTAT 50

(2) INFORMATION FOR SEQ ID NO: 2417:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55



TTTGCTGGGA GTTGCAATTA GAAAATATAC ACATTACTT GACATTCAAC TTGATAAAAA 60  
 ATTAGTTATT GCCATATGTT GCATCACATT TATAGGGATT TTAATATTTT ATGTACGCCT 120  
 5 AATTAAAAAA TCATCTTTAA ATATTTATAA TACTAAAAAT AAAAGGTCAA AAATnTT 177

(2) INFORMATION FOR SEQ ID NO: 2418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2418:

AAAATGAAGC GGTGCAAAA TATAATGACG TGAAAGCATT TTATACTCAT GGACATTTAT 60  
 20 ATCAAGTCAA TCGAACAAGA GATTTATTAG CTGAAAAAGG ACTTGAATTA GGTGTTTGT 120  
 TTGCATTTTA TGGACATACA CATGTGGCAA AATATGAGTA TATTAATGGT GTTCATGTTA 180  
 TTAATCCTGG AAGTATATCT CAATCTAGAA GTTCAATGGA AGAAACATAT GCTGAAGTTA 240  
 25 TTATTGATGA TCAAACTTTA CATGGCACCA TCAATTTCAA AAATCGACAT CACGAAACAA 300  
 TCAGTCATAC TACTTTTTAA ATAGAAATAG CTATGGCTTT TTTTAGTTTA TAGACTGATT 360  
 TAACTAGGAG GTCGTGTCAT CCAATGTTTG TTTAAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 2419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2419:

AGGGTGCCGA GTTAACCAAG AAAGGCCGTT GGTTGCCCGG GGTATTTTCC CCC 53

(2) INFORMATION FOR SEQ ID NO: 2420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2420:

## (2) INFORMATION FOR SEQ ID NO: 2421:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2421:

ACCAGAAGAC AATAAGTGTA ATGATGCCTG TTCTAATACA GAATCTTTAC TTTTATTGTC 60  
 CTTTCAAGT CGTTGTTCCA CTTTCTTAAT TTCATTGTTT ATGTTTAACT TTGCCAnGTT 120  
 AATCACCTTT GGTATTATCT TTTTCTTTAT AG 152

## (2) INFORMATION FOR SEQ ID NO: 2422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2422:

GTACGTTTTTC ATTAGTTGTT ATATTTCCAT CTGATAATT TTTTAAATCT TTAAATCAG 60  
 CATACTGACT AAAAAATTTA AAATTTTCAA TTTTGTGnT AAGTTTTTGT CTTCTACATT 120  
 ATCCAAAAGA ACAATCTnAT TATTTTTTAG TTCAACACGA TATTTTTTCT CATTATGATT 180  
 TTTGCTAATA TCATCATAAA CTTTATTTAC AAAATAATAA CCTGTTGCCT TTTTGGTATT 240  
 TCTATTAAGA TATAACACCA TGCCTTCATC ATCTAATACT CCTGGTTTGT TACTTTTTGA 300  
 AAAACCTn 307

## (2) INFORMATION FOR SEQ ID NO: 2423:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2423:

ATTGTGTTGT ATTTTAGACA AGACCTTCAA TTTTGGAGAT TTCACGATTT ACCACC 56

## (2) INFORMATION FOR SEQ ID NO: 2424:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2424:

AGTCCTTTGG ATCGTCAAGA TTTCACACAT TTACAnTTAT TAnCTCGTGA

(2) INFORMATION FOR SEQ ID NO: 2425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2425:

ATGTAATATT ACAATTCAAT TAGnAAAGAA CTTTATCTTT AATTGCTTTT CGATTTCATT 60  
 CATGTCATCT TCTGAAATTA TTATCGTTCC AGTAGGATCA GAATCATTTA TTTTGCTTAT 120  
 ACGTCTTTTG CTTATTGTTG TAATTGCTGA TATATTAACG TATGTATCTT TCCCTTTGTG 180  
 CTTGGAATAA ACACCTATCA CTCTATACAG TTCATTAGCT TTTTGAnTTA AGTTAGACAA 240  
 AAGCTTTT 248

(2) INFORMATION FOR SEQ ID NO: 2426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2426:

CCTTATTATA TGACAGGTTG CCTAAACAAG TGCCTAGAGA AAAAAGTAGC CCC 53

(2) INFORMATION FOR SEQ ID NO: 2427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2427:

TATCCACTAA AATGATTGTC GCGTATTGTA ATATTAATCG TTCTACTTTT TATGATTATT 120  
 ACAGGGAGCA ATTTGATTTA TTGGATACCA TCAACTCnAA GCATAGGTGG AGG 173

(2) INFORMATION FOR SEQ ID NO: 2428:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2428:

TACTTATGTT TATGTCGCAA TAATTAATGT TCGAnTTAGT GGAATTGAAC 50

(2) INFORMATION FOR SEQ ID NO: 2429:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2429:

AGTCATCATA TTATCAATAA TACGCCGCGT TAAATCTGAT AAATTCATAT AGTCTGTATC 60  
 TAACTCTG 68

(2) INFORMATION FOR SEQ ID NO: 2430:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2430:

TGAATTGAAA ACGGTCGGTG AAGCGCTAAA AGGTAGACGT GAAAGGTTAG GAATGACTTT 60  
 AACAGAATTA GAGCAACGTA CTGGAATTAA ACGTGAAATG CTAGTGCATA TTGAAAATAA 120  
 TGAATTCGAT CAACTACCGA ATAAAAATTA CAGCGAAGGA TTTATTAGAA AATATGCAAG 180  
 CGTAGTAAAT ATTGAACCTA ACCAATTAAT TCAAGCTCAT CAAGATGAAA TTCCATCGAA 240  
 CCAAGCCGAA TGGGACGAAG TAATTACAGT TTTChATAAT AATAAAGACT TAGATTATAA 300  
 GAGTAAATCC AAAGAGCCAA TACnATTATT AGTAATCATG GGnATTACAG TTTTAATAAC 360

## (2) INFORMATION FOR SEQ ID NO: 2431:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2431:

TGACTTCGTC CAAGTACAAC TGCAGTCAGT ACCTACGAAA TCAAGATCAG CATGGAT 57

## (2) INFORMATION FOR SEQ ID NO: 2432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2432:

ATTCTTAATC GCATCATAAT TAATTAACGG ACGCATAACA AATCCGATAA TACTATTATC 60  
 TTTCCAAGTC ACTGACACTC CAAATTGATT TGCTTCnTCT ATCCATATTT GCTCAATAGT 120  
 ACCATCATTT TGAGTACACA CTTTAAATTC ATGTACATCA GACTGCCTTG TATAAGATTT 180  
 GAAAAGTTTC CTAAACTGCC AATAACTGnA CTCTCGCTTC AAATT 225

## (2) INFORMATION FOR SEQ ID NO: 2433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2433:

CGGCCTGACG TIACATTTCT TCAACTTCAC GTCAAAATTG CTTGCAATA ACCAGGA 57

## (2) INFORMATION FOR SEQ ID NO: 2434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAACGTGT CTTTAATGTG GAAGTTGAAA TATTAGTCCG TAAAAAATG AAACCTAAAA 60  
 AAAAATAATA TTTATATTG TCGTACAAAG ATGAAAGCGA nAGA 104

(2) INFORMATION FOR SEQ ID NO: 2435:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2435:

TTTGCTAATC GTTTCACGGA TTGTGGGGAT GGGTAAAGAC TTTGCTAGTG G 51

(2) INFORMATION FOR SEQ ID NO: 2436:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2436:

AAAnTTAATT TTTGGGGGGC CCTTTTTTAA CCGGAAAATC CAATCGGGGC TTTTAAGGAA 60  
 TGGTTTTGGT TAACAGGCTT TGAATTTGG TTTGGCAAAA CAATCCTTGG TTTGGGGTTT 120  
 CGGTCCGGAG GGTCTAATT 140

(2) INFORMATION FOR SEQ ID NO: 2437:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2437:

GAAGCGGAAC CACCGTTGTT TTTCTTTTCA GGTCCAATTG AATAAATGTT ATGAATAGAA 60  
 TGGATAAAAA TATAATTATT TAAGTGTTAA AGTAAACCAA ATCATGATTT AAGATTATAA 120  
 GAAAGAAAAA TTGACTAATG TTAAAACCAA CAATCATATG GGTGTAAACG TTTATACAAT 180  
 CATCGTAAAA CTCAATATGC TTAATTTATT CAAAATGTTC GTCAATAAGT ACAATGAAAA 240  
 GGAGATTGAT TTTTGAATAA AAAATATCTT ATGATTGTAA TTATAATTTT AATATGATTC 300

AAGATACGAT TTTGAGACCA TGTGAAGGGA TTAAATATAG

400

(2) INFORMATION FOR SEQ ID NO: 2438:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2438:

TCTGTTTTGA AAGTTGCAGT TTGGACAGCA CCCGATGATT AGGTGAGTCT TTTGGTTTA

59

(2) INFORMATION FOR SEQ ID NO: 2439:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2439:

TTGGTnAAAC CGTTACAGTT GCAAGTTTTG AAGTGAGTTA TTTTTTGGTT

50

(2) INFORMATION FOR SEQ ID NO: 2440:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2440:

ATTAAAAATA AATTAAaGT TCCAGAACCA GTTAACCAGA ATATTTACGA

50

(2) INFORMATION FOR SEQ ID NO: 2441:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2441:

TGCTGTTTTG GCGGTTTTTC TCCGTTTGGT TGAGTATGTG GTGTACCTTT TGTC

54

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2442:

GTTGTTGGGT GTGTGGTTTT GGGTGTGTG GGTTCGGGT CTGGGTTTCGT TGGTGG 56

(2) INFORMATION FOR SEQ ID NO: 2443:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2443:

GAGACAACT AGTCGTCCAG AACGGAATTT AAGTAATCAT AATAATTACG GAAGTGCACT 60  
 TTTGTTTTTG ATTTATCATT GATGGAAATT AGAACAATTT ATCGAATGAT ATTAAAATTA 120  
 CATAACATCA TGTGAATGT GAAATTAGGA TTGAACATTA CCTGTnTATT TGAAAAACCT 180  
 TCAGTTTTTA AATCACTAGT ATCACAAATA AAGCGACTTA AATTCGATTC GTTAATAATA 240  
 GATAATGCAA ATTTAnGTAG CCCT 264

(2) INFORMATION FOR SEQ ID NO: 2444:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2444:

CCGTCTTTAG TACGTACGTT GTTTCGGGG CTTGGGGTGC TTTCTGGGTG TTGGTCATTG 60  
 TATTGGG 67

(2) INFORMATION FOR SEQ ID NO: 2445:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2445:

AGCTGCATTT CTCGTGCAGG CTATCAGCAT CGATATCTGT ACCATTTAGT GATCATGC

58

5 (2) INFORMATION FOR SEQ ID NO: 2446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2446:

15 AACCAAAACA AACATTTGTT CGTTAAAATA TTGACACAGA ACATAAGTTC TGA

53

(2) INFORMATION FOR SEQ ID NO: 2447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2447:

25 CACAAATTAC ACCCATTGTT AnTACTAATA CTThcCTnTT CATTGTGTTA

50

30 (2) INFORMATION FOR SEQ ID NO: 2448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2448:

40 GCACAAACCA AACGCACCTT AACTGCTTTA AATGGCTGGA CGGGGGGTCA ACTGGCCTTA

60

ATGACACTTG AATCG

75

45 (2) INFORMATION FOR SEQ ID NO: 2449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

GCAGCCTTCA AGTGTGTTGCT ATTTGCTTTG GTGTCACAAG CCATTATCTA CGGTCCCGCA 60  
 ATTTAGCCCCG C 71

(2) INFORMATION FOR SEQ ID NO: 2450:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2450:

TGGCGTGAGG AAAAATATCA TGTATTGTTA CACAGTCAAC AGTCTTACCA AATGATAAGG 60  
 AATGCTTTAA AAACGGATTT ATCACTTCAT CAAGTTCAAC AAATGATTGA TGTTGCTTTG 120  
 TTAATTGAAC CGGGTATAGG AAGTGTATGT AATGCTTTTG ATCATATGTG GGGATATTTA 180  
 AAAAAATGTG CGAATGAAGA AGGAAAGACA ACAATCAAAA CTACTTAAAA GCTGATTTTA 240  
 TTTAATGGnA AAAATCGACA CCCCAACTTT ATTAGATTTT TTAGCAGAAC TTGCCTAATA 300  
 AATATGGAnG TCAATATTTA CTACAAAGCC GnGTTTTTAA ACCCCAAAAA G 351

(2) INFORMATION FOR SEQ ID NO: 2451:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2451:

GTGTACCGCC TCGGCTGGCG TTCGCGGTGG GTGGTGC GGT CGGTGCGTGT CTGG 54

(2) INFORMATION FOR SEQ ID NO: 2452:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2452:

TGCCATTCCA ATGTTACCAT CGTCTTGGTA CTACTATATA CTGCGGCTAT 50 50

(2) INFORMATION FOR SEQ ID NO: 2453:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2453:

10 AGACGTGTTT CCACGGTATG GGATAAATGA AGCACCGACT GATAAATCAA TATAGCCTCG 60  
 TGTTTTTAGT TTACCCGAAC TATCCCTTGA TAATGATTGT GACATCTGCG GATAATATTT 120  
 CATTTTCTTA GATATCGTCG AAATATCACC GATTACTTGA AGTCCATCTG TCGTAAACAA 180  
 15 TTCAATTCTG CTTTGTTTGT TTTTACTTGG GCGGTATGTC ACTTCGGCAA TATATCGTCT 240  
 AACITCAGGT GTCATTTTCA ATAACGCCTT AATCATATCA TCTTCTTTTG TACCTTTGAA 300  
 ACCATCCATG ACAGGTGCAT CATTAAATTTT GACATCATTT GAACCTTTAA GCAATTTACC 360  
 20 ATTTTCTAAT AAAGGTAAAT ATTTACCTTT ATATTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 2454:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2454:

AGAAAGAAAT ACCATTTGGA GATAGAGACT CGTGTTATTT CTTAGCGATG GGAGATTTTT 60  
 35 ATAATAAAGA AGATAGnAAG AAAATTATCA AAGGTTATGA AAATAATTAT GGTAGAGGTA 120  
 TTAATATTCC TCGAGCACAT AGTATATATT TATATG 156

(2) INFORMATION FOR SEQ ID NO: 2455:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2455:

ACTTAGGTGA TATGAAATGT GGTCCGCGAC GATCGTCAGT AACAAAATAA CAGGCAGTCA 60  
 50 TTGGATTATG TTTAACG 77

(2) INFORMATION FOR SEQ ID NO: 2456:

55

- (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2456:

10 AGTGAAATCG CTAAAGAAAA AGATGGAACC TCGGTATCTA ATACACAACT TCTTGAACGT 60  
 TTTTA 65

(2) INFORMATION FOR SEQ ID NO: 2457:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2457:

25 TATCAATAAT TGCCACTTGC AATGACTGAT TAATTTGAGG TGCACATAAG CCAG 54

(2) INFORMATION FOR SEQ ID NO: 2458:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2458:

35 AATTTTATTT CGAGATTCTT CAATATAGAT GTTCTTCAT TAATTTGATT CTCTAACTCT 60  
 40 TGCTTACTAC CTAATAGTTT ATCTAATTCA GCTTTAGCTT TTTCATTTTC TTTAATTATA 120  
 TTAATTTTCAT TATTTATGTT CGTnATCGTA TTATTTAGTT CGATAA 166

(2) INFORMATION FOR SEQ ID NO: 2459:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2459:

55 CCAATGATTA AGCAATACAA TCGTCACTAA AATTACACCG ATAATCTGAA TCATCGTCAT 60

## (2) INFORMATION FOR SEQ ID NO: 2460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2460:

AAATCAAAAA AATGTATAAT GAAAAGAAAA AGAAATTTGG AAAAAATTGG GAAGACGCTC 60

AAAAAGCTGG AAAAGCTGTA GGTGAAGATT TGAGTGTA AA TGG 103

## (2) INFORMATION FOR SEQ ID NO: 2461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2461:

TTTATATCAG AATAGAATAG TAACTAAGG CATTTGGAGA ACTTATTCCA TG 52

## (2) INFORMATION FOR SEQ ID NO: 2462:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2462:

CAGCAGCGAA TTTTGTACGT CCAGTGTAGA ATGGATGTGA ATCAGATGAA ATATCTAAAC 60

GAATAACTGG GTATTCTTTT CCATCTTCCC ACTCCATCAT TTCTGAAGAA GTT 113

## (2) INFORMATION FOR SEQ ID NO: 2463:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2463:

CTAACATAAT TGTTAACT AAAATATTTA CTACTTTTAG AACTGTGCGA TTAAATACAA 120  
 TTGTCAGTAT TGTTATGACT AGGCTAACGA TACATAAAAT AAAGAAACCG TTAAAGACTA 180  
 5 AAATTAAGCG ATCGATTCCT TGTGTGTAAT CATTGATATT ACCCAAATTA ATAnTTAATT 240  
 GGATGCATTT nCCAA 255

## (2) INFORMATION FOR SEQ ID NO: 2464:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2464:

20 TATGCGACAA TTCGAAACAT TTTATATGCA AAAGGTTATA CAACAGAGAA TGTGATT 58

## (2) INFORMATION FOR SEQ ID NO: 2465:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2465:

30 TGAATTTTCAT TACCACATAT CGGACATTGA TCTCCAATAT TTACAGCAGA TTTAATTTCA 60  
 35 CTTAT 65

## (2) INFORMATION FOR SEQ ID NO: 2466:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2466:

45 CGTGACCTTC AAAGACCGAA CGAGAGAGTT GAAGAGCATT TGCGAAGGCC A 51

## (2) INFORMATION FOR SEQ ID NO: 2467:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2467:

AGTTTGTTAA GTTTGTAGTTT ACTAACTTTT CCATTAGATA TTATTAATGA AAAAC

55

(2) INFORMATION FOR SEQ ID NO: 2468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2468:

TTGTTGGTAA GGCACCTTCTT AAATATCAAC AACGCGATGA TATTTTCATT GGTACAAAAG

60

TAGGCAATCG TTAAAC

76

(2) INFORMATION FOR SEQ ID NO: 2469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2469:

CTTCTATAAT AAAACCATCT GCAATTAAGT CTTCAATAGA CGATGGATTT CTATTATGTA

60

TCAATGCATA C

71

(2) INFORMATION FOR SEQ ID NO: 2470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2470:

CTTCGTCATT GTATTCGAGC GCCTGTATAG CTTGCTCAAA TGATGCATAA AT

52

(2) INFORMATION FOR SEQ ID NO: 2471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2471:

5 AGAGGTTATG TTGATGTGCT TTATTTTCAT CAATGTCATT AACACAATCA TATTTCTTCT 60  
 GTTAATGCAC TGTATTATAT TCAAACGCGC TATCGACAAT TAATTTGn 108

## (2) INFORMATION FOR SEQ ID NO: 2472:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2472:

15 GTCCCCAGTT GATATAGGAT CACAGTTTAA TATACTTGGT GAGATAGTAA TACTATTATT 60  
 20 AATTCAAATA GGTGGTCTGG GTATCGTGAC CGTAACCCTA TTGACACTAG TATTTTAA 120  
 TAGAAAGATA TCAATGAAAA ATAGATTCTT GATTATGGTT ACATGGAATA TTGACGAACC 180  
 25 TGGTGGTGGT ATTAAGCTAA TTAAACACTT GGCTATTTAT AGTTTAGTCA CTGAATTAAT 240  
 TGGTATGATT TGTGTGTGTT TATCTTTTAT ACCAAAATTT GGTATAGGCA AAGGTTTATT 300  
 30 TTTAAGCTTA TTCACATCAG TATCAGCTTT TAATAATGCT GGGATTGCCC CTTTTTAAGA 360  
 ATAACCTTAAT AGATTATTCT AGTGATCCAA TTGTCATTAT 400

## (2) INFORMATION FOR SEQ ID NO: 2473:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 147 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2473:

40 CTTCAAATAC TAAATCAGCG TTGCTAAACA TACCGTATAC ATTTGATGGC GTTGATAACG 60  
 CGTCCTGCGC TTCTGTTAAT AACTTTTCAG TTTCAGCATC TAAATATGA GGACGTTTTT 120  
 45 CATTAATCAA CTTCAAATCA AATGCGA 147

## (2) INFORMATION FOR SEQ ID NO: 2474:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2474:

CTTTAGGTGC TTGTGGTAAT TCTAATTCAC AAGATCAAGG TAACAAAACCT GAACAAAAAA 60

CA 62

(2) INFORMATION FOR SEQ ID NO: 2475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2475:

CCTTTAAAT CATCTAGAAT ATCTCTTGAG AAAAATTCGA AATCTACAGT 50

(2) INFORMATION FOR SEQ ID NO: 2476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2476:

ATAGTGGTTA GTCAATGTAA TTAAATGAGA ATAGAATGGT GATTTTCATCT TAGCTTGATA 60

ATTAGCAGAA TCTTTAAAGA AAATTTTGTC TTnCAAGCCT AAGTTTACAA CGT 113

(2) INFORMATION FOR SEQ ID NO: 2477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2477:

CGTAACTAAC TCAATTTACT GAAAAAATCG CTTGCGATGC AATAGCATT T G 51

(2) INFORMATION FOR SEQ ID NO: 2478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2478:

TAGTTGCCGC TACGTTTATA CTCGTATTAA TGAACAAAAC TAGCAAAGAA TCTAAAAAAG 60

(2) INFORMATION FOR SEQ ID NO: 2479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2479:

TCGGACATGA TGGTAAAACC GTATTGGGTA TTCGCACTGA CACCTTAAGG GA 52

(2) INFORMATION FOR SEQ ID NO: 2480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2480:

TTCCTAATTA AGGATTAAAA AGGGTTTCCT AATTAGATTA nAATTCCGGG ACCTGGATGG 60

AAAAAAGTTT TTAACCTTTC CATCTGGTCC CGTTTTTTGA TTTTCGATAT AAAAAAAGCG 120

CAATTATCTC TAT 133

(2) INFORMATION FOR SEQ ID NO: 2481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2481:

AAATGTTTTG GAAGAACGTA AGAnAAATCA ATCTGAAACA AATGCACGAT ATGAAGAAGA 60

ACAAGAAAAT TTAATGGAGC TTTTAGAAAA TATATCAAAT GAGATTTCTG AAGCTCAAGA 120

TACTTATAAG TCTCTGAAAA GTAAACAAAA AGAACTCAAT GCTGTCATTC GTGAACTTGA 180

AGAACAACCTA TATGTTTCAG ACGAAGCACA TGATGAAAAA TTGGAAGAAA TTAAAAACGA 240

TACTATAGAA GAGAATGAGG CTAAAAAATC CAGACAGGTT CTCGTTAGTT GGAGTTTGA 360  
GCCATTGAAA GTATTGnGGG GGCCAATTAA AACCGCCAAA 400

(2) INFORMATION FOR SEQ ID NO: 2482:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2482:

AAGGTGCATA GTCAACAACA TTTACAGCAT CATTGATTC TGAAC TAACC GAAACATTAT 60  
ACTTACCG 68

(2) INFORMATION FOR SEQ ID NO: 2483:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2483:

ATGAGCCnAC ACAGTGGTGA GGTAATCAAC GGTACAGTGG TTAGTGTGAT 50

(2) INFORMATION FOR SEQ ID NO: 2484:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2484:

CGGAAC TCGT CGAATAACTT TTTAGATTCT TCGTTAGCTT TTACATTAGC GAATGCTTCT 60  
nTGATTGCTT TGTATTCTTC GCTTTCTCTT AAAGCTTGTT CTAATTGATT TGCATAATCA 120  
TATAAATTTA CTGCCATGGT TATAGCACTC CTTGGTnGTG ATGTTTATTA AAACGTT CGA 180  
TATTACTTTA CCACATCTCG CTTTTTTAGA CAA 213

(2) INFORMATION FOR SEQ ID NO: 2485:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 376 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2485:

	GACCAAAATT ATCTTTAGCA CTTATAGGTA TCTTTTAAAT ACTTTGTGAG TTTTCTATG	60
10	GCATTCCTTT TTTAGGTGCA ACGTTTATTT TAAGTTTGG ATGGCAGCCT TTA CTCTTTA	120
	ATGCATTACT TTATCTAATT CTTACTATTA TATTATTAGT GAATAGACAA AATGCGATTA	180
	GACCTATAGC GATTATTCCA ATATTGGTA TAGTAGGTAG TTTT TAGCT ATTATCCCCT	240
15	TCTTAGGAAT TTTGATTCAT TGGATTTTAT TTTTCCTAAT GATTCCAnTT GTCCTAGTTG	300
	GATTATCAGC GCCAACCTAT ATACCCAATA AAAATGCTCG TGnChTTTTA CACACAATAC	360
	AAAGATGGAC CTAGAG	376

20

(2) INFORMATION FOR SEQ ID NO: 2486:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2486:

30

	TTGACCTTGA CGGAAACTTT TTTCCAAGTT CTAAAAGTGG GCCAAAATCT T	51
--	--	----

(2) INFORMATION FOR SEQ ID NO: 2487:

35

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2487:

	GAATTTTGGC ATACACATAC ACTTTAAAAG ATATTATTGA AATTACAGGT GTA ACTAAAA	60
45	GAACTTTACA TTATTACGAT GAAATAGGAT TATTAGTTCC AGn	103

(2) INFORMATION FOR SEQ ID NO: 2488:

50

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2488:

AATTACATTA GCACCAATCC ACACATCATT TTTAATTGTT GTACGGCTAG GTTGGTCATT 60  
 5 AAAGTCTATA AACGTTTnCT TTAAGTTAAA TGGATTATTA TTTAGA 106

(2) INFORMATION FOR SEQ ID NO: 2489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2489:

TGAATTTGCT TGAGTCGTGC TGCTGATAAC AATAAAATTG CACATGGATA AAGAATGACG 60  
 20 C 61

(2) INFORMATION FOR SEQ ID NO: 2490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2490:

GCTCGTATGA TACAAATTCA TAATCTGAAA CTTCTGTCGT TTGTCGAACA TGTGGTAACC 60  
 35 AATTCTTCAA GATGCTGTAT ATTTCTGCGT AATTTTCGTC ATTCTGAAT AACCTCAACT 120  
 TTAAATGTC ACCTTGTTTG ATATAACGCA TTAATAAATA TTGATCTATA TCTCCCTTAT 180  
 CTTTAAGATG TTTTACAAAT GGATACAAAT TGTCGATGAT AAATGTATCT TCGATGGCT 240  
 40 TATCGATATG AATATGTAAT GCAAACCACT CTTTGTGATA TTCAATATCT GTATTTTTAT 300  
 ATTTTGGAAT TTCGATTTTCG GGTCTCGAT AAGATGATTT TTTATAAATT GGTGTAACAA 360  
 TTTCATACAC ATGATCATT CTTGATTGAG GGAAAAATGA 400

(2) INFORMATION FOR SEQ ID NO: 2491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GACTGTTTTA TCGCAACTAT TTACACCTAT ATTATCGTTA GTAGGACATC TCGTCGG

57

(2) INFORMATION FOR SEQ ID NO: 2492:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2492:

CATTGAACTT GCTTTTGACG TACACCAGTA ATCAATGCCA TAATACGATC CGG

53

(2) INFORMATION FOR SEQ ID NO: 2493:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2493:

AATACAACATA ACATACACTT ACCCATGTCC GAAGTCCnTG TTGAGGAATG

50

(2) INFORMATION FOR SEQ ID NO: 2494:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2494:

GCTGTTTAGC TTGCTCAAAT GATGCATAAA TATCTGATGC AACTATCATA TCAGCTAGTT

60

CATCA

65

(2) INFORMATION FOR SEQ ID NO: 2495:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 322 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2495:

ATTAAGCTTT CTAAATCATT GATGTTAGGA GCTAATGTGC TCGATAAGCA GAGTAAAGAA 120  
 GAATTGCTTA AACAAAGCTAA ACATATAACA GGTTTAGAAA ATCCTAATAG TCCTACACAG 180  
 5 TTATnGGCTT GGTAAAGGA TGAACAAGGA TTAGATATAC CTAATTTACA AAAGAAAACG 240  
 GTTCAGGAGT ACTTAAAAGA AGCAACAGGA AAAGCTAnAA AAATGCTAGA AATTAGATnG 300  
 10 CAAATGTCTA AAACCAAGTGT GA 322

## (2) INFORMATION FOR SEQ ID NO: 2496:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2496:

ATCAGTGTTA ATTCGCACGG AATTTCTTC CATTAACTA ATCCGATCAT ATAATGGAT 59

## (2) INFORMATION FOR SEQ ID NO: 2497:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2497:

CTAATTAAGC CAAAAGGGGA AGGGTCCACC AACCTTGGT TTCCCCCAT TGCCCGGAAA 60  
 35 CCACCAGnAA GTTTAAAGCT TCCCTTTAAG CCGTCCGATG GGTAGTCCGA ACTTTACCGT 120  
 TCCCCG 126

## (2) INFORMATION FOR SEQ ID NO: 2498:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2498:

CACTTTGCGC CAGTTTTCAG TTGAGTGGCA TAGAGTCTGC TCATCAGTTC CTTGCTCC 58

## (2) INFORMATION FOR SEQ ID NO: 2499:

- (A) LENGTH: 90 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2499:

10 TCATGATGCA GACGCAACAG CATTGTTA TGAATATGGA CAAATACCAC AGATGCCGGT 60  
 AGCATTTCAA TCAAGTAAAC CTTTAATAGA 90

(2) INFORMATION FOR SEQ ID NO: 2500:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2500:

25 TGCTCAAAGT CGTGTAGACA GCCAACTAAT GCATTTTCAA GATCAGTGAC ATCTCCGACA 60  
 CCAAAGAAAT CACCGAATAT TTTTGCATGT TCGATTTTAC CTCGTTTAAAC ATCAAACCTTA 120  
 ATTTGTACAA ATCCTTTTTC AAATTTTTC TCGCGTTCAA AGTTATATTT AGGGTTTCTA 180  
 30 CCATAATTCC ATTCCTCAAGT TCTATATTTG TCGTTACTTA ACTTTTCAAT ATTTCCCAA 240  
 TCTTCATCCG TTAATTGATA TTCTTCnACT TCAGTTTCGC CAAAGATAGT TT 292

(2) INFORMATION FOR SEQ ID NO: 2501:

35

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2501:

45 GGTGTGTGTA GAGGTCGAGA GTTGGGGGGG GAGTAACGTG GAAGTTGCCC GGACAGCA 58

(2) INFORMATION FOR SEQ ID NO: 2502:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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ATACGGGAGG TATCAGCACG TACGTGCAGT CGGTAATGGA TCnAAATACG

50

## (2) INFORMATION FOR SEQ ID NO: 2503:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2503:

15	ATCCCCACTC TTTTAAAT GATTAAACCA TATTTATTT TAAAATAAA TATCCATCAA	60
	AGTGTATCAA TAAATTTATC ACATGTCAGA AAGTATGCTT CATCTGAATA CACCAATACT	120
	CTCATGAAAC TTATTAAAAA TACTCTCTC AACGTAAAA ACCATTCAA TTCATGAATG	180
20	GTTTGGAAGA ATGATTCATT GTTACGCTAT TTAATCACTA CATCTTAATT ATTGTTGCTC	240
	TAAACGATTA CGCTTACCAT TTAAGAAAGC ATAAACGAGA CCTACAAAA TACCGCCACC	300
	GACAAAGTTA CTAAGAAAG CAAAACGAT ATTTTAAAC ACGTGTAACT ATGAAACTGC	360
25	ATCAAGGGTA AAGAATACCA TACCTGCATA TAGACCTGCA	400

## (2) INFORMATION FOR SEQ ID NO: 2504:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2504:

	ATTATCTATG AATAAAATTT ATAATAACA TATATTGAGA AATTCTCTAA TACCTATTAT	60
40	TACATTTTTA GGTGCTGATA TTGTAAGTAT TTAGGTGGA GCCGTGATTA CGGAGACTAT	120
	CTTTTCATAT AACGGTATCG GTAAATTATT TTAGAATCG GTAATAGGCC AAGACTATCC	180
	ATTAATGATG GCATTAACGT TATTTTCTC ATTTTAGGT TACTGGGTA ATTTGATTTT	240
45	TGATATTACT TATGGATTTA TAGATCCAAG AATTAGAAGT AACTAGGGG GATTAGAATG	300
	CAAAATAAGT CAAAATCGCC TTTnAAAATT GCATTTTCTA AATTnATTCA TAnTA	355

## (2) INFORMATION FOR SEQ ID NO: 2505:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2505:

5 CCGTTAGTTC CATACCATAT TTTTCTCTAT AAAATAATTT AACATCTAAT TGCCTTTCTA 60  
 ATTTTCAAT AGGGGTAGAT ACAGTTGACT GTGAATAGTT AAGTAACTCT GATGCTTTAG 120  
 TAAGGTTCTT TGTTCACTA GTTACTAAAA ATGATTTTAA AATGTTTAAG TTCAAAGTAG 180  
 10 TACCTCCTTT AGGGTTCCTT TTTATCGAAT CCTGAATTCT AAGAATTCTG ATTTAATAAT 240  
 AATATATnAn ATAT 254

## (2) INFORMATION FOR SEQ ID NO: 2506:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 268 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2506:

25 AACTCCACCG TGTAGTTGCG CTTTCATCGCC TTGAGGATGC GATTGGCGCC GTGCTGCGCG 60  
 GCACGTGCAG ATAGTGCGAG CACTTGGGCA GATCGCGCAC CGCCTCCAGC AGGTCGTCGG 120  
 TCATATCCTT GGGATAGTTC GTTACGAnTT GGATCCGGTC GATGCCGTCG ACATCCGAGA 180  
 30 TGCGGCACAG CAGGTCGGAC AGTCGCGTTG nCCGCTGGCA GTGTCGTAGT GGTAATGTTT 240  
 CACGGTTTTG ACCTAGCAGC GTTCACCT 268

## (2) INFORMATION FOR SEQ ID NO: 2507:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2507:

45 AAAAGTGGCT AATATCATCA GCAGAAATGTA TAACATAATC GAATTGCAAC CAGCGATTAT 60  
 ACCTTT 66

## (2) INFORMATION FOR SEQ ID NO: 2508:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2508:

ACCTCCGCTT CAAATGTCAT TGATAGACAT TTAAAGCGGA GGCATGTACA TGT

53

(2) INFORMATION FOR SEQ ID NO: 2509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2509:

ACCCTATGAn AGATGAAGTh ATTAACCAAA AACCACGTGT TGTAATATTA

50

(2) INFORMATION FOR SEQ ID NO: 2510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2510:

TTAACCTATT ATATTAAATTT TAGTATCAAT TCTTCTCCA GTTCCTGCGT CATTTTT

57

(2) INFORMATION FOR SEQ ID NO: 2511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2511:

ACGTGTTTCAT AACCCATAAA GGCGAATATG GTAACACCGA ACATCATGAC A

51

(2) INFORMATION FOR SEQ ID NO: 2512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

GTAnAGCGGT CCGCGCTTAA AGCGCTTGCT AACTTCGAAC AATGAATCTG CGGAACATCT 60  
 TGCGAATCCA CGAGATGATC TCATATGACG GGCAGCGAGG T 101

(2) INFORMATION FOR SEQ ID NO: 2513:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2513:

GGGTAATGTA ATAGTATTCA TCTACATCAT CTTGATCATC GTAATGCTGA TTGTACCCTT 60  
 CTAAATC 67

(2) INFORMATION FOR SEQ ID NO: 2514:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2514:

CCCGTCGTTT TCGTGnTTTT CGCGGCGTGT CTCCTGTTTCG CGCCTCTACT 50

(2) INFORMATION FOR SEQ ID NO: 2515:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2515:

AAGAAAATAT CTCTTGAATA CTGATCGATT GCCATCGAAA AACACTGTTA AATCAAGTTG 60  
 CCCAGTCCAT TGTGTTCAT CCATTATGAT AATCCTTTGA GTAAAGTGTC GCGTTCAATC 120  
 CAATCGATAA CTTTCATCAA ACCTTCGTCG GTTTTTAAGT TAGTAAAAGT AAATGGACGT 180  
 TTACCACGAA ATACTTTAGT ATCTTCAGCC ATTTGTTCTA ATGATGCACC TACATAnGGA 240  
 GCTAAATCAG TnTTGTAAAT TACAAAGACA ATCTG 275

(2) INFORMATION FOR SEQ ID NO: 2516:

(A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2516:

10 CTGCACCACC AATAACGTAA ATACTGTATA TACTAGTAAT CGCTAATACA CCGATATTA 59

(2) INFORMATION FOR SEQ ID NO: 2517:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2517:

TCTGCTACTA CGTATACGAT AGAATGGATT TCTTTTGTAA CCTAAACGTG TTAAACGAAT 60

TTTAACTGCC ATTTATAAAA TCTCCTTTAA GTCATGTTTT AATTTTTTATT TTCTACAnG 119

25

(2) INFORMATION FOR SEQ ID NO: 2518:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2518:

ATTTCCTTTT AAGTTTTTAA AAATCCAAAA TCCTGTGGT AGGGCCATGA AAGGGTTGGG 60

(2) INFORMATION FOR SEQ ID NO: 2519:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2519:

ATAGAAGTGA AGCACGTAGA TTGAAACGAT GGTAAATAA CGAGAGACAT TTAGAAAACA 60

50

ATAAAAATGA GGAATAATCA ATGATACATG GAATTGGTGT AGATTTAATC GAAATCGATC 120

GAATACAAGC GTTATATAGT AAGCAACCAA AATTGGTTGA GCGGATTTTA ACTAAAAATG 180

55

GGTTTGCTAC AAAAGAAGCG TCAGTAAAGC ATTAGGCCCC GGCCTnnGGA AACA

294

(2) INFORMATION FOR SEQ ID NO: 2520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2520:

TTTTAGGCCG AAGAnGTAGT AATTTCCGGT CCTTTAAGGG GCGGGTGGTT AACCATGGCA

60

ATTAATCCCA GGGATGACCT TACCTAATAA CCACCTAATA ATTACCCGGA CCAAAGGTGG

120

AAATAATCCC TCCGGTCCTT CCCGG

145

(2) INFORMATION FOR SEQ ID NO: 2521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2521:

TTTTAGTCAC CAAAATTCTC GCATTTAACT GATACGAATG TGCAATAACT AAAAATCGAT

60

CTAATAATTG CGTTGAAAAA TTTGGCTCGA CAGCACTCAT TACAATTACn AGTGTATCTA

120

TATTACTTAC AGGTGGTCTT TTCAACTCAT TTTCCCGCTC AAACACTTG

169

(2) INFORMATION FOR SEQ ID NO: 2522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2522:

ATCCAGCCTT TCAACAAATA AATCTGAAAT TCGATGTTCT AAAATTTCTG CTTCTTGATG

60

TACTTCTTCC CAATTATATT TCAATATT

88

(2) INFORMATION FOR SEQ ID NO: 2523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2523:

CAGTAACATC AATCTGTCCT GTAAGCTTGT GGTACTCCGA TACAACCATA AGTCAACGCA	60
CCACCAAAAA CGCCTTGGAG CCGTTCTACT TATTAGTCCA AGTTTAGACA TTGAAATACC	120
AACAACCTTG CAnTCCATAG TATCTGAAAA TGTAGACATT GCCTGCAATA AATTTAACnC	180
ATCATTTTTA TTATGTGGCA TTACTGCTAA TTTAACGTAT TCTGGGTT	228

15

(2) INFORMATION FOR SEQ ID NO: 2524:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2524:

CTCATCCATA GCGCTGGTAT TAGTATAGGT GTCAAACCAT TAGCGTATAT CATATCTTCT	60
GGATGTnCTC ACATATTCAT AGATGCACAT TTTACTTCTC TCGTACCTTA GTACTGGGA	119

25

(2) INFORMATION FOR SEQ ID NO: 2525:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 357 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2525:

TACCAATATT AAATTTGAAC ATTATAGTTT GACCATCATA ATCTATCTTC TCTATTTTCAT	60
TATAACTAAT ACTTCTATAA TAAAATTGGC CATTTCATATC TACATTCATA ATTAATCTTT	120
CATTTGTTGC TATAAATGCC CCTTCAAATT CATTCTCACC TTGAACTTGA TACTCAATTA	180
TTCCTAGCAC TGACGGACCC TTTTTTTCAG TTGGAAATAA ATCATTTGGA TTCACATTAT	240
CTAAAATCAT AATATCCCTC CCACTTAAAA CTATAAACTA TTCTTCATAG GTATATGAAA	300
TACAAGTGAT TAACTATTnA TnATnAAGCT TAACTTGTAT TCCCTTTTCA AGATAAT	357

50

(2) INFORMATION FOR SEQ ID NO: 2526:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2526:

	CACGCGTCCG GCCACCTGGA CATGGCCGAC CTAGAAGCCA AGCTGCAnGA GGCCCAGAAG	60
10	CATCGGCTGC GCCTGGGTGG CCACTGATGG GGCCTTTTCC ATGGATGGCG ACATCGCACC	120
	CCTGCAGGAG ATCTGCTGCC TGCCTCTAG ATATGGTGCC CTGGTCTTCA TGGATGAATG	180
	CCATGCCACT GGCTTCCTGG GGCCCACAGn ACGGGGCACA GATGAGCTGC TGGGTGTGAT	240
15	GGACCAGGTC ACCATCATCA A	261

(2) INFORMATION FOR SEQ ID NO: 2527:

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2527:

	CTnTAGAGGA TATGAGTTCC TCATCATAAG AATTTCTGGA TCCTTAATAG ATCTCTTGCT	60
30	ATATATAATG TAATAGAAAC ATCTTTTAAG GATCCAGAAA TTCTTAGA	108

(2) INFORMATION FOR SEQ ID NO: 2528:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2528:

	TTTTAAAATA CTTGGTAGAA GTTGAATGG ATTAATCATT AATTATCTCT CAAGATGTAA	60
45	TGACTGTTCA GCACACTTTT CCGATATGAA AAGAGATTTG AAnACAATA	109

(2) INFORMATION FOR SEQ ID NO: 2529:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55



GATTAAATTT GTTATACCTG GCTTGTTGTC ACGATCAAAT TTAATAATAC CATCTGAATC 60  
 AGTTACTGCG CTTTAAATTT TTTTAGCTGC AACATTCGGC TCGTCTAATA ATGAAATnGA 120  
 5 GTTTTTAGCA TTATCATCAC TCTTACTCAT 150

## (2) INFORMATION FOR SEQ ID NO: 2530:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2530:

TTCTTTTGG CCAGTGGCAG GAAGTACGGT CTTATTTGGT GTTATGTTAA GAAGGTATTC 60  
 20 CCATTATTT ATCGTTAAAT ATGnATATAG TATAGTAATT TTAATTTGTT GCATCATAAT 120  
 ACTAGGT 127

## (2) INFORMATION FOR SEQ ID NO: 2531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2531:

CACATAATGA TTCGAATTAT TGTTTAAATT AAACCTTTTT CACATATGTA TAAATTTTAn 60  
 35 AGAGCGCATG CGTGAATATT TTCATTTGAT TCAAAGGCAA AAGATAGCCT TATACTCTTT 120  
 TC 122

## (2) INFORMATION FOR SEQ ID NO: 2532:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2532:

AAATAATAGA GCAATTGGCA CATGTAAGAA TGCAAATTGA CTATGGCATC CAGTATTTTG 60  
 50 GTCACAAATG GGTGTATAT GAGCATGTTG AAAAATAAGT CTTATGnTAA AACTTAGTA 120

## (2) INFORMATION FOR SEQ ID NO: 2533:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2533:

GAGAGCGGCC GCGTGTAAGG AGAGCGGCGT TCGTTCGCGT GACGCGAGTG TGGTTCGCGA 60  
GAAGnGGACC AGAGTTCCCC ATCGAGGCTG TTCGGGTAAA T 101

## (2) INFORMATION FOR SEQ ID NO: 2534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2534:

TTGCTCATTA AAGATTATCC CAATCAATAT CATCTATATT TGTGTACCA CTATTATCTT 60  
TTTCTCTTTC TCTTACTTTG TnCATTTGTAC CAGTAGATTC AAGATATATT GT 112

## (2) INFORMATION FOR SEQ ID NO: 2535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2535:

ATAACGAATC CAAAAATATA GAGAATGACA GTGAAACTTA AATAGGACTC T 51

## (2) INFORMATION FOR SEQ ID NO: 2536:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2536:

## (2) INFORMATION FOR SEQ ID NO: 2537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2537:

GGATGTACCA CCAGCATAAT AAACAAC TTC AAATGGATTG ATAAAGAAGA nACCAGCAGA 60  
 GATAGGTAAT TCATTACCAT GTTCTTCTTG TAGACGTTTA CCTTCTTCAA TCTTTTGCTC 120  
 ATTTGCATCA AGTTGTTGTT GTAAGTTATC TCGCTTGT 158

## (2) INFORMATION FOR SEQ ID NO: 2538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2538:

TATATTCATT AAATCCACAA AGCGGTCCCG TATAACATG GGTTTCCATT 50

## (2) INFORMATION FOR SEQ ID NO: 2539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2539:

AAAGTATACA TATCACTCAA CTAATCAATA ATCATACTTA CCTTCAACAA ATTCTTTAAC 60  
 ATGCAGTGTT ATCCCTTGAT AATATGGATA TTTnGTTAAT CTA 103

## (2) INFORMATION FOR SEQ ID NO: 2540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAATCAATTT GTCTATCTGT TGAGTGGCAA CCTCTAATAA GCCTTTTATA TTGTCA

56

(2) INFORMATION FOR SEQ ID NO: 2541:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2541:

TGGAATAAC GAAAGTATTA TTAATTTAAA GCATCTTTCT CCCAATACTT TAATGAGTGA 60  
 TATTGTTTAT ATACCGTATA AAACACCTAT TTTnGAGGAA GCAGAGCGCA AGGGAAACCA 120  
 TATTTA 126

(2) INFORMATION FOR SEQ ID NO: 2542:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2542:

ATCAGTTTCT TCAAAAATAA CTGAAGTATC TGATGCTGAA AATTGGAATA GTTGATGGGT 60  
 CGGGnTATTG ATTTTATCT GATGTAAAAA TCCATAAGTG CCATAAGATG TATATAGTTT 120  
 CTTCATATGA AAGGTCCCCC TTATGTnTTT ATTTATTATA CGATGATAAA CTAGTCATTA 180  
 CCACTATTAA TAATTGATTA A 201

(2) INFORMATION FOR SEQ ID NO: 2543:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2543:

GAACTTTATT ACAGGAATAG ATAAGCACAG TCGTGTTACA CAGACGCTAA ATGCGCGTTC 60  
 GTATG 65

(2) INFORMATION FOR SEQ ID NO: 2544:

(A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2544:

10 AGCTATTAAT GGCGCTATAA TTGATACAAT AGTTATGATT AATAAAAAAA TAACCGATAA 60  
 CATTGCAATT TTATnATGAA TAAATTTAGG AAATGCAATT TT 102

(2) INFORMATION FOR SEQ ID NO: 2545:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2545:

25 AATCTACATC CAGCATGATC nACATCAnAG CnGGATTCACT CCTTACTTCA 50

(2) INFORMATION FOR SEQ ID NO: 2546:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2546:

AACCATTCAA CACACGACAC TAAAGTGCAG TACAATCCTA CAAAACGATT GTTTTTATCG 60  
 GGTGGTCTAA CCATTGAATA AATAATGAAT AATGGTAAnA 100

40

(2) INFORMATION FOR SEQ ID NO: 2547:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2547:

ATTGAAAATC TTTTATCATT TCATACGTGT GCATAATTAA AAAGGTGAAA CCTCTTATTT 60  
 TGAGATTTCA CCTTTTTTAT TGTTAATTAA AATTTAATTT TAATGATTAT TTTGTTTCAC 120

55

## (2) INFORMATION FOR SEQ ID NO: 2548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2548:

AAAGTGAAAA TTGGAGGTGT AATTTTGACT AGAACTTATA ATATTATTGG TATCCTTTCT 60  
TGTCTTATAT CTTTATTAT TATGGCGTTA CCAATHATTT GGTACACAGC TTCAGCATT A 120  
TGGTTCTTCC CAGGTGCAAT CA 142

## (2) INFORMATION FOR SEQ ID NO: 2549:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2549:

CCCAACCCTA CnAACGACAT TACACAATCA GTAACAGATC GGTATTAAGA CTGGATATCG 60  
TGGCATCTGT TGAGTTAATA TCAACAGTCG TCCAGAACTC G 101

## (2) INFORMATION FOR SEQ ID NO: 2550:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2550:

TGTAACCATG ATTTAGATGA CTAAACGTGC TTGCCAACAT GCTTCATCCA ATGCCGAATC 60  
CTTTAGCTAC AT 72

## (2) INFORMATION FOR SEQ ID NO: 2551:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2551:

CAGTAAGAGG ACAAGGCTAT AAGGTGGAGA ATCATGTTTA AAACACTCTA TGCTAGAATT 60  
 5 GCGATTTATT CCATTACGGT TATTTTATTT AGTGCATTAA TAAGTTTGT ATTAACAAAT 120  
 GTTACTATC ATTATAATTT AAAAGCATCT AATGACGCGA AAATCATGAA GACGCTTAAA 180  
 GAAGCAAGAC AATATGAACA ATCAGCTAAA CCAACGCACA TTCAACAATA TTTCCAnACA 240  
 10 TTTAGGGTCA AATGGAATTA CCAAATAATG ACCATGGATC CATAAAGGTC nTnAGACCTT 300  
 TTT 303

## (2) INFORMATION FOR SEQ ID NO: 2552:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2552:

25 TTTACTTTAG CCTTTATTGC ATTTGTAATT TATAGAACTG CGAACAGGTG ACTACTGTnA 60  
 ATTTATGTGA TTAAAGTTTC AATGATATTT GATTTATTAG ACCATTGCAA AAGCGCAAGG 120  
 TTCTCATGTG CTGCTACAGT TTGCGGTCTT 150

## (2) INFORMATION FOR SEQ ID NO: 2553:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2553:

40 GCACTCGTCA ATAAAGATGA AGCAGCATTT AATCAATATA CGGCAGAATA CAAAAATT 58

## (2) INFORMATION FOR SEQ ID NO: 2554:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2554:

AAAATCGTTG AATAATCAAT CATAGCAGTA AGCTATGTnA TATATTTTnA AAAATTGA 118

(2) INFORMATION FOR SEQ ID NO: 2555:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2555:

15 ACAACTTCAA AGAAATCATG TCACAAAAAA AGTATTTGAT TTTAATCATA nGTGGCGACA 60  
 ATCCGCATAC CAAAGCACAA CCTTTAGTCA ACCAATTCAG AT 102

(2) INFORMATION FOR SEQ ID NO: 2556:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2556:

AGATGCATTA GCAGCATTAG ACGTTAAACC AGTTGGTATT GCTGATGATG GTAAGAAAAA 60  
 30 ACGTATCATT AAACCAGTTA GAGAAAAAAT TGGGGATTAT ACTTCTGTAG GTACACGTAA 120  
 ACAGCCAAAC TTAGAAGAAA TTAGTAAATT AAAACCGGAT TTAATTATCG CTGATAGCAG 180  
 TAGACATAnA GGTATTAATA AAGAATTAAAn CAAAATTGCA CCAACATTAT CATTAAAGAG 240  
 35 TT 242

(2) INFORMATION FOR SEQ ID NO: 2557:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2557:

TGCACTCATA ATCATCGGAA TATGTATAGA ATCAACTATC ACTTTGCCGT GTTTATCTGT 60  
 50 GTTAAATGTG TAACCATAAC AGTGTGTCCC ATTTGGATTA TGAATCTCAG AATAATCATC 120  
 AAAAATATCC TGAATTTnCA AATTAATTTT ATTATAGCGG nAGCAATGTC TATAAAATTT 180

55



TATTTCAA

248

## (2) INFORMATION FOR SEQ ID NO: 2558:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2558:

TTTGGGTCGT GATTGAAAAA ATCTAAGGCT AATAAACCAT GTTGTTCTGC GCTTAATAAT	60
TGTTTGAGTA TACGGTTAAT AATTA ACTCT GTATCATGAG GGTTGACGCG AAAGTCAGAG	120
CGCATATAAG TCATATAATT CTCGAAGATT TCTCTATCAG TATTGCTTAA TCTTAATGAT	180
TTAACATTAT TTTCTTTTGT TAATTGCGCA GTACTTTTCA TTGTTACTTA AGCGCTCCTT	240
TAAAAATGTT TAATTCCTAAA TTAAAATGGA AATGATTTTA TAGTATTAAT AAGGTCAATC	300
ATATCATATT AAACGCATAA ATATAACGAT TAATATTGGA GAGGAAAATG AGGACACTTA	360
ATAAAGATGA ACATAATTAT ATCAAGCAAA TAGCTAATAT	400

## (2) INFORMATION FOR SEQ ID NO: 2559:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2559:

AAGGGAAATT TAAAAGTATC ATTTGATTAT ATAGATTGGA TTAAATTAGG TTTTGGCCCA	60
TCAGGAAAGG AAAACTACTA TATGTACAAA AAATTTGGTA TTTTACCAGA TATGGAATAT	120
GAAATGGAAG AAATTCGAGC AGTAGAGAAG TATGTTAAAG AGCAAGAGTA GCAGACATGT	180
TATAAAAGAC TGTGCAAAAT CACCCTCGTT TTACATTTGA TTCAAAGAAG AAGGTAAAAG	240
ATAAGATAT TTGCAACTTA AAAAGTCAAT TAGCTTATCG GTATCCATAC ATCATGGATA	300
AATGAGTACA ACTAATTAAC AAATCACGAT ATA	333

## (2) INFORMATION FOR SEQ ID NO: 2560:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2560:

GTAAGACATT CACATTTATC ATTTACCAC AATGGGTTTA CCAACCATGG TTAAACGAAT 60  
 CCAAAACTTT GATGCTCGTA TGTCTCA 87

(2) INFORMATION FOR SEQ ID NO: 2561:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2561:

TTGCATTTTG ACGTAAATGA TTAAACAAAT CGTGATTATC TCTTAATTTT CTAACCGCCT 60  
 TTTCAATTTT TAACGGCGTA ACTTCCTTTA GAACAATGCC AAATTTATAT TTnTCAT 117

(2) INFORMATION FOR SEQ ID NO: 2562:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2562:

AAGTCAAACA AAATAAGCAA ACAGACTGGT CAGAAGATAA GTTGAATAAT ATAGCTTTGA 60

(2) INFORMATION FOR SEQ ID NO: 2563:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2563:

AAGTGTATT ATTGTGATCA TAAAGTGAAG TATTACCTTT TTTATTCGTA ACCCGATTCC 60  
 ATGCGCCTTC AACATAAACT 80

(2) INFORMATION FOR SEQ ID NO: 2564:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2564:

AGACATGGGC TTATCAGATA AAGTAAAAGC ATTACCTAAA GGGGGAGGCG GTAAGTCATT 60

10

ACCG 64

(2) INFORMATION FOR SEQ ID NO: 2565:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2565:

GTTTGTTTAT AGTACCCTGG ATTTTCITTA TTTCATCAT GTGAAACTGT GTCAGTGAAC 60

GCTGAT 66

25

(2) INFORMATION FOR SEQ ID NO: 2566:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2566:

TTAATTATTT GTGACGTATT ACACGCATTA CTTTAGAAAG TGATTCCCAA AGCGAATTAT 60

CTTTACGATA AACTA 75

40

(2) INFORMATION FOR SEQ ID NO: 2567:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2567:

ATATTATTAT ATTGCTTTTT TTCAGTTTGC CGTTGTTACT TTCATAACTT 50

(2) INFORMATION FOR SEQ ID NO: 2568:

55

(A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2568:

10 TTTTAGGATT TGTAGTAGGT GAGCGACGTA TTnnGGATGC AATCCAGAGA ACAATAAATA 60  
 TTGAGAGAGA GCAATTCATA ACGCAGTTGA AATACATGTG TTACGAATTG CTTTTATGTT 120  
 AGTTTTTATC ACACAAGTTT TTTGATGCAA CCCC GTGATA GCGAAACTCA TATGTAGATA 180  
 15 ATACAGCTTT TTCAGCATCA TCTACATGAA TTCCAAAACA TCA 223

(2) INFORMATION FOR SEQ ID NO: 2569:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2569:

AATAATGCCA TACAGTGAAG ACCATGCGCA TCAATCGATG TCTAGTGTGT ACTACGTC 58

(2) INFORMATION FOR SEQ ID NO: 2570:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2570:

40 CGTTTCATTA GTTTTAAATG ATCCCCAATA CTTTTTGTAC CTTACCAAC TATCGTTCCA 60  
 AACTATCTA CAGCTTTTTC TGTGGTATTT TTAAACAGCG TCTATTTAAT GTCTTATCCA 120  
 ATTAGTTTTA TCTCTTAATC CAAATTTATT AGTATGAAAA GTCCAATTTT TAAGAATTGT 180  
 45 CTAAACAGAT TCCGCAACAA AACCAGCTAn AAACCGTCCA TACTATTGGA ATnAAAACGC 240  
 CAATGTTATA 250

(2) INFORMATION FOR SEQ ID NO: 2571:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2571:

AGCTCCTTTC TTTCTAGTTA ATATCATThA ATCTTGTTTT TCAGTGTCAA AATTACCTGT 60  
 5 AAAACAACA TTTTATCTT TTAATAGG GATTACACTT TCCACTTCTA TTTTATTAAT 120  
 CTCAGATATT TTCATATGAA TTTTTTGAAA TCCTGAATCG AAAAGTTTAG TTGG 174

(2) INFORMATION FOR SEQ ID NO: 2572:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2572:

CATGCGGTAG GTATTCTAA TCTATGGACA AATGGCGGAT TTATGCCAAA TGGTATTGTT 60  
 20 GGTTCCTTCT TTGCATTATC AATTGTAATT GGTTCATACC AAGGTGTGGA ACTGATAGGT 120  
 ATTACGGCAG GTGAACTAA AGATCCTCAG AAAAATATCG TTAAAGCAGT GAATGGTGTT 180  
 25 ATCTGGAGAA TTTTAATTTT CTATTTAGGC GCTATTTTTG TTATTGTTTC AGTGATCCT 240  
 TGGAATCAAT TAGGAGACAT TGGAAGTCCG TTTGTTGCAA CATTTGCTAA AATCGGTATT 300  
 ACATTTGCAG CTGGATTAAT TAACTTTGTT GTAnTAACTG CAGCAATGTC AGGATGnAAC 360  
 30 TCAGGGnATT TGCAATGCGA GTCGTAATGA 390

(2) INFORMATION FOR SEQ ID NO: 2573:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2573:

TAGAGTACAG AACATACGCA AGGAACTCGG AGTTTACTCA CGGGACTThT 50

(2) INFORMATION FOR SEQ ID NO: 2574:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2574:

TACAATTACA AACGCATCGT GAGATGTTTT AAGCATCAAT GAGAATCTAA CTCTCCAAG 59

(2) INFORMATION FOR SEQ ID NO: 2575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2575:

GACACAACGT ATGACGCATG AAGAGTTGCG TGTTGACAAT CAAGATGATC ATAGCCAAGT 60

TAGTCTAAAT GGTTACACAA AGGGGTCTGA GAAAGATCAA GAAGCATTCA CTAATAATAA 120

GGATGAGGAA GCAGTTGCTG CTAAAAATCC TGAATCAGAA GAATATAAAG TGAATGAAAA 180

AATAAAAAAA GAACATAAAA ACTTTATTTT TGGTGAAGGT GTTTCAnGCG GTAAAATATT 240

AGCGGCATTA TTATTCGGTA TGTTTATTGC GATTTTAAAC CAAACATTAT TAAATGTTGn 300

TTTACCAAAA ATTAATACGG AATTTAATAT TTCTGCGTCA AnAGGGCAAG GTTGATGACG 360

GGATTCATGT TAGTAAACGG TATTTTAATA CCAATTACGG 400

(2) INFORMATION FOR SEQ ID NO: 2576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2576:

TTTAAATCGT ACCTTAAATT TGAAAGTAAT AAGACACACC AATTACCTTC TAACTCTATC 60

GATAGTTTCA AACAAGAAAT CGnTAGTACA TTCAGTTATT TAGAACGCGT TGATTACCAG 120

CT 122

(2) INFORMATION FOR SEQ ID NO: 2577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

CACATTGAGG TGCAGTCATA CCTTGTTTAA ATGTCCAAGC ACGTACTTCT T

51

## (2) INFORMATION FOR SEQ ID NO: 2578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2578:

AATTATGACT ACAGGTCTGA CTCCCCCTTG TTCAGATCCC TGTACTGGTG ATAAATCTGC 60  
 TAAATAAACA TCTCCTCGTC TAATCATTCA TTCGTTGAAT TAGAAGATAA ATATGTTTCG 120  
 TTGCAATCGC ATGCTTCACA CTCTATCGGA AAAGCTTCGT TCGCTAGGGA GAGATTTAAA 180  
 TCAGCCATTT GTGAATATCC TTCTTTTAAA GATTGTTCTA AGCTATGACT TCTATTTTGA 240  
 CTAAAAGATA ACATATGAGA ACCTCCAATT GATTCCAAAA GTTATTAAAT GACCTTTAAT 300  
 TACTCTAATG ATAACAAATT TTATATGCAC TGACCATATT ATTTTAACAA TTCATTTGTT 360  
 ACAAACGGT GGATCACCCA TCATGGATAG AGTCGCGGGn 400

## (2) INFORMATION FOR SEQ ID NO: 2579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2579:

ATAAAAACCT AATTGACTCA TAATCTTCTA ACGGTATATC ATCCACAATC ACAGTATGAT 60  
 TAGGATTATC GTTAGATACA TCTnTCACTG CCTTATCTAA CCCCTCATCA CC 112

## (2) INFORMATION FOR SEQ ID NO: 2580:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2580:

CATGAnTnTA ACGGATTCAT TCCATATATC AATTGCGTTT GTTATTTTAA TAATGCTATT 60

ACTACAAC TT CGATTTAAGC TATATTTATA AAAAAATGCG CCTACTCATA ACATTCTTTG 180  
 GCTATTTAAC TT TAATAAGC TAGGGCCAAG TTTGTCATAA GATAAGCGCA C 231

(2) INFORMATION FOR SEQ ID NO: 2581:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2581:

ACTTCGTAAA ATTTATCTTG AGTGGTTGTT TCTATATTAA GATTCATTTT ATTACACTCC 60

(2) INFORMATION FOR SEQ ID NO: 2582:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2582:

GTCAAATGCT GAGTTCTAAT AATGATGTTG GCCACCATGC ATACAAAAAT GCTAAAAGAG 60  
 AATTACGCAA GATTTTAGAT AGCTATCTCG AAAATGGTAA ATTAAAATAT TACGATATTA 120  
 TCGTTACAAG CAATTTAGCT ACTAAACATC CGTTTTTCGA GTATGCACGT TCATTTGATT 180  
 TTATCATTGT TTCAGATATC GGTTTAATAA ACGTTGATGT AAAAAGCTGG GGTGAAAAAA 240  
 CATTTTATCA CTTTGATGTA CCTGATGAGC ATGATACAGA nAnA 284

(2) INFORMATION FOR SEQ ID NO: 2583:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2583:

GAGTCAGTCG AAGTTTGTCTG TTCGACCCGT AGAAGTGTA AACGGCATTG TGAATG 56

(2) INFORMATION FOR SEQ ID NO: 2584:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2584:

TCGACTAATG TAATGTAGGC ATTGGACGTC AAATGTAATG TGGGGCAATC CGACGAGATG 60

10

ATGGTGTC 67

(2) INFORMATION FOR SEQ ID NO: 2585:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2585:

CGTAACCGCC CCTTGTCGG GCCCTCCAAG CCTTTTAAGG GGACCCCCCG GA 52

25

(2) INFORMATION FOR SEQ ID NO: 2586:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 238 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2586:

35

ATTAGCAACA ATGTCAGATA ATCGATACCA ACTAATTAGG CGAGAAGCGG TTTCTCATGG 60

TCTTAGTGGC CTAGAAATTG ATGTATTTGA TTTGCATTCA AATAAGTCTA GACATATTAG 120

CTCGTTATCA GGTGGAGAAA CTTTCCAATC GTCGCTTGCA nTAGCTTTAG GGTAAAGCGA 180

40

AATTGTACAG CAGCAATCAG GAGGTATTTT ACTAnAATCA ATATTTATTG ATGAAGGA 238

(2) INFORMATION FOR SEQ ID NO: 2587:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2587:

ACTGGAAAAA ACCGcNAACA CGACATTGTC AAAACGACGG CCAGTGCCAA 50

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2588:

GnGCAATTAT ACCACTATAT TTATTTCTTA TACTCCATTT GATTTATAGT TGTATTAATA 60  
 CATTGACTCA AAAACTAATT AATCAAATAT GTTTTTTAGA TT 102

(2) INFORMATION FOR SEQ ID NO: 2589:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2589:

GCATAATATC GGATATGCGn GTGTGTCAGT CnCATAGTCG nTGGATTGCG 50

(2) INFORMATION FOR SEQ ID NO: 2590:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2590:

TTAnAAATTG CcTnTCCAAT TnTAAGAATC CTTTTTCCAA GGTAACAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2591:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2591:

CTTCATCCCT TACTTTTAAT TGTCACGTCA AATAATATTT GTCTTTAACT AGTAATAACT 60  
 CCAAATATAT TTAGTTTGTG GTGCTAGCTA TAAACACAAA TGAnTCATAA CACTATATTT 120

TGATTTTnAA TTATTTATAT

200

(2) INFORMATION FOR SEQ ID NO: 2592:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2592:

TGCATTAATC ATCTTGGATA CTCTTTCTAC CAAAGTAATG ATTGCACTAC CATGACGACG 60

ACCAGCAATA GTAT 74

(2) INFORMATION FOR SEQ ID NO: 2593:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2593:

CACCTGCTCA CCTCTATTTT CAAACAATTA TGATTGAATT GAATCATTCT AATTTTTGTA 60

AAGTTACTTG TTTAATTTAT TATATTTATT AACTCTATGA TAACAAAAAT ACTGTTTGTG 120

TATAACAATA AATTGAGATA CTCAATAATT TGATAATGTG AAATTGATAC TTTTCAAAAT 180

AGTTGAATAT GACAATTAAT GATTAGTTTT GCAATGGTGC TATAAACAAT ATTTAGCAGT 240

TATC 244

(2) INFORMATION FOR SEQ ID NO: 2594:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2594:

ATATGGTATG GAACTAACGG AAGAAGGCTT AGCATACGTT AAATATGCTA AAGTGATTTT 60

AGATAGTAAT AGCGAATACG AGAGAGAnAT AAAAGGACTT TACAATAAGA AGGTAAATAT 120

AAGTATTAAC ATGCAAGAnA GTCAGTATTT GTATCGCTAC TATAATAAGA TTAGTGAATG 180

## (2) INFORMATION FOR SEQ ID NO: 2595:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2595:

AAAAAGTATT AAAAATTGCA ATTCTTAAAC TGTTATTCAT ATTAATATTT CTAGCAAATA 60  
 ACATTGTAAA ATAAAGAAAA ATAATTAAAG TATTGCACTT TATTGAAATT TATATTACGA 120  
 TAGTAATGCA GAAATTTATA TATGCAAAT ATTATA 156

## (2) INFORMATION FOR SEQ ID NO: 2596:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2596:

TGATCCGCAA ATCGCTGAAC ACGTCTTCT ATTGGAATCC CTCCATTCAC TTTTAGCTAG 60  
 AC 62

## (2) INFORMATION FOR SEQ ID NO: 2597:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2597:

TTACCTTTAG nTTTTAAAAC CTGACCCTCC AACCAGCCTA ATTGGTTAAA TGGGGATCCA 60  
 TTTATATAAT CCCAGGCCTA ACCTTCCAAG GACCAACCTA AGGGATTAAT CCCCCCAATG 120  
 GCCAAAGTGG GATGGGTAAT 140

## (2) INFORMATION FOR SEQ ID NO: 2598:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2598:

5 ATTAATTGGG GAGTTAAATT AAAAAAAGG GGTCCTTCC AACCGGAnCC ATTCCCATT 60  
TGGATTAAAA ATTCCCGCCT TTGAAAAAAT TGTTTGCCGA ACCGCCCTTA AG 112

(2) INFORMATION FOR SEQ ID NO: 2599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2599:

20 ATACCGCCCC CAGTTCAATA AGAAGCCCTG GATCAGACCT GACCCTGGTA TGGGGGGAAT 60  
CCC 63

(2) INFORMATION FOR SEQ ID NO: 2600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2600:

30 ATACTATGGA ATGCCTTAAT GGTGGATAAT TTCACCAAT TAATTTTAA AAC 53

(2) INFORMATION FOR SEQ ID NO: 2601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2601:

45 AACTAAAGGT TCTAAAGATA CAGTAAAAAT TGAAAATAAC TATAAAATGC GTGGCGAGAA 60  
AAAAGATGGT AGT 73

(2) INFORMATION FOR SEQ ID NO: 2602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2602:

CGGTTGCCAG CCAAACTTG GCA<sub>n</sub>CCAAGG CAATTATAGC AAGGCACCCA CCTAAATTG 60

10 CGGACCACCC GGAATGCGGC CACCAAAGTT GGTGGGAGGC CATTTTAA 108

(2) INFORMATION FOR SEQ ID NO: 2603:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2603:

AAGCTTATAA CTATTTGTGT TTGTGATCGA GATAGGTTTG CCTGTAAAAA TGGCCATCA 59

25 (2) INFORMATION FOR SEQ ID NO: 2604:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2604:

35

ACGTCCAAAG GGCCGTTTCG CCCAG<sub>n</sub>GTG CTGGCAAGGT TCCACAACG<sub>n</sub> 50

(2) INFORMATION FOR SEQ ID NO: 2605:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2605:

GTCCAATGTC ACATTAAATTG ATTGGTATAA GCGATCACAA GG<sub>n</sub>CATAGTG AATATTTTGC 60

50 ACCAGACGGT GTACATTTAG AGTACAAAGG AGTCCTAGCT TTAAAG 107

(2) INFORMATION FOR SEQ ID NO: 2606:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2606:

GTTTAAAGCA ATTTGGAAGG ACATTGGTTA AAGGATGGGA GTGGCAAAAT CTGG 54

10 (2) INFORMATION FOR SEQ ID NO: 2607:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2607:

20 GTTTTAGCTG AAGTTAATGA TGAAGATATC GGAGCTATGG TAATTAAACT AGTTAAACTT 60  
ATTTTCATGC TTGATTATGT TTTATTTTCAT TCAATTCAAA AAAGCTATAC AACACATATG 120  
25 AATGAGCTTA AAAATTGTTT CGATTACATA GCTGAATTAG ATAATCATTA TGCATTAGCA 180  
ATGTATCGTA GAACGCTAGA ATGTTATACT GAACCACAAA TTGATGATTC AAATGATGGC 240  
ATAGTATTCT CTGAGTTAAC ACATCCACTC ATAGCAGATG GCAGTAGCCA ATGATTTnC 300  
30 ACTATCACAn AATATACTGT TAACTGGGGT CGAATGCTTC GGGnTAAATC AACATTTTAT 360  
GGAAAT 366

(2) INFORMATION FOR SEQ ID NO: 2608:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2608:

45 TTCTTAGACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 60  
TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGTA TAAATGCTTC 120  
AATAATATTn GAAAAAGGAA GA 142

50 (2) INFORMATION FOR SEQ ID NO: 2609:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2609:

GGGTCGTCAA TTGA<sup>n</sup>GGCAG GTAGAGCATT AAGTCAGAAT TG<sup>n</sup>AGTAAAT

50

(2) INFORMATION FOR SEQ ID NO: 2610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2610:

ATTGGGTGAT GAATTTTGAC GGTATTGTCA AGTCCAGTGG CTA<sup>n</sup>ACTTCCG G

51

(2) INFORMATION FOR SEQ ID NO: 2611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2611:

ACAAACTTCG GACTGCCAAT TACATTTACC TTGGGGGGTC AGAAACAATG GGTGCATAAA

60

GGCCCGTGTT TCGAAACGGG AAAAAGCCCA GCA

93

(2) INFORMATION FOR SEQ ID NO: 2612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2612:

ATGATGTTTT TCGGCTAATT TTTATACTGA ATTTAGTTTA ATTA<sup>n</sup>ACTTAT GATATTTT

58

(2) INFORMATION FOR SEQ ID NO: 2613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2613:

TTCTCACCAT TAACTATGCA TACTCACTTT ACACATAAAT TTGCTTAACA TGCAGAACGG 60  
 5 AAATAAATCA TTACCACATA TAGATCCCAT CATATATTTA nA 102

(2) INFORMATION FOR SEQ ID NO: 2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2614:

TGAACTACAA GACGCTTATA TCATTGACGC ACATTTCTCG CAGTGAAAGA AACACTTGCG 60  
 20 TA 62

(2) INFORMATION FOR SEQ ID NO: 2615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2615:

TGGAGCATTT CACATACATT GGCAACCTCA TGGAGCTTAT CATTCTACCT TGGGGnACAG 60  
 35 ATATAACAAC ACTAACGCAA CATGGATGGT GTCGTTGATA ACTTTCAATC TATAGAATTA 120

(2) INFORMATION FOR SEQ ID NO: 2616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2616:

CTGTAGTAAA TTGCCAGAAT CCGTATCAAT ACCAGTCTGT GACTGCGTTG GCC 53

(2) INFORMATION FOR SEQ ID NO: 2617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2617:

ACATATGATA TGAGTATATT AACGTTTAAA TTATGGATAC TCTAAAGACA GGCGATTTTG 60  
 5 AAAAAATCAGC AAAAAGTTAT ATGATGTAAG TGGGACAGAC ATACTAGATG TAACACATTA 120  
 ACCAAGTG 128

(2) INFORMATION FOR SEQ ID NO: 2618:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2618:

CCTAACCGTG TGTGTATGTA TACCTACAAA AAAATTTACA TTGTGACACT GCGTACGTG 59

(2) INFORMATION FOR SEQ ID NO: 2619:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2619:

GCCCATGGTC AATCAGACAC ACGGATTGAA CGTTAACAAT TTATGACTTT AACA 54

(2) INFORMATION FOR SEQ ID NO: 2620:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2620:

ATCATTGTCA CATTGAGTAG CCGTAAAATG GTCAGACGAT CAATGCGAAC TGA 53

(2) INFORMATION FOR SEQ ID NO: 2621:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2621:

CTAAGTGTCG CCCGAATAAC CGTCAATCCA CGGAGCACAT AGGATCTCCC ATG

53

5 (2) INFORMATION FOR SEQ ID NO: 2622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2622:

TGGGACCGAT AATCATTCGC ATGAACACCT TCCACCGTCT CTTACTCACT ACCTACGGC

59

(2) INFORMATION FOR SEQ ID NO: 2623:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2623:

ATTA AATTGT TATTTCGTCA TTAGGTGACA ACTTGTATGT AGATATTTTA ACATATTTTA

60

30 TGCT

64

(2) INFORMATION FOR SEQ ID NO: 2624:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2624:

CCGTCCCAGA ATATCATATG ACAAATGTTA AGAGACTTGA ATGATCATAC ACGTG

55

45 (2) INFORMATION FOR SEQ ID NO: 2625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2625:

GTGGTCACCA GGTACGGGGG ATACAGGGGG TTAATCCCAC CTTGGATAAG TGGAAAACGG 60  
 5 ATTTCC 66

(2) INFORMATION FOR SEQ ID NO: 2626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2626:

CCACCAATGG GTGGGGGATG GAATAACCCT TAATGCGGTG GTACCCGGGT AATGGTAGCC 60  
 20 CC 62

(2) INFORMATION FOR SEQ ID NO: 2627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2627:

CATGTTTTTT CATTCTTGA TGACGACACT AGAGGTTCCC GTGTTTATTA TTAA 54

(2) INFORMATION FOR SEQ ID NO: 2628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2628:

TTGGCCAATG GCGGATACAC CCTCTCAATT CGATACATAA CTCAAGGCTC AGTCAT 56

(2) INFORMATION FOR SEQ ID NO: 2629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2629:

TGTCGCTAGG TAACCGTGCA TCGTTCACAG GTACnTATGA TTTCACcGA

50

(2) INFORMATION FOR SEQ ID NO: 2630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2630:

GAAGGnCCCA AACCAGGCGT TAAAGGCCGA TTGGGTTTAA ACCAAAGGTT

50

(2) INFORMATION FOR SEQ ID NO: 2631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2631:

CGCGAGTGTA TCCGTCGATA TGTCGAGAGG AAAGATTGAA GTGTGGAAGA GTGTTGAGTA

60

ACCCT

65

(2) INFORMATION FOR SEQ ID NO: 2632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2632:

TGAAAGAACT TTAGCTAGAC GTTCGTAAAG GTCTTTTGAC ATAAAGCTAG AGA

53

(2) INFORMATION FOR SEQ ID NO: 2633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

AAAAGCCAAA AGGAATTAAT TAACCCCGGG GTTTAATTTC TAATGGGAAT TTG

53

(2) INFORMATION FOR SEQ ID NO: 2634:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2634:

GGTGTTCACA TTCTGAAGGT TTAGAGAGTT AAGATTATAT ATATATAAGT TTTGGGGTGA

60

TAGATATG

68

(2) INFORMATION FOR SEQ ID NO: 2635:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2635:

CCAATTTTAC TTGGTGCTGC CATTTCCGTC TCTCGTGAC TTGTGATTGA GGTGCCATTG

60

TTCCCGTAGA TGGTTCACAT

80

(2) INFORMATION FOR SEQ ID NO: 2636:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2636:

CTTACACCCA ACTTATTGAC TTATAATCTA TTAAAGTGCC ATTTTACAAT CTGAATCCCT

60

TAATATAGCA ATAATTACAA CTTCCGACAA ATGACTTGTT TTATGTGCGT GATTCATCAA

120

TGAACATCGT AATGCGACnT AATA

144

(2) INFORMATION FOR SEQ ID NO: 2637:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2637:

5 TAATTCGGCA ACTAATATCA AGATCATGAT CAAATACTAC TGCCATTTTC TTATACCTCT 60  
TAATGTGAAA TCACTGnCAA CACATAACAT CTTAAACTT TGAC 104

(2) INFORMATION FOR SEQ ID NO: 2638:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2638:

20 CATTTCATCCG TTTTTTTGGT TCATGTACAT ACCATTGTTT TGTACACAGC GAAGTCAGTT 60  
AACCTTATAT CCTTGTATAA CAGTTGAAAT CGGCAATATT AAACAGTACT TTCCCAATTG 120  
CTTTCCTCCT CAATTGTGCG ACGGACTGTA n 151

25 (2) INFORMATION FOR SEQ ID NO: 2639:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2639:

35 AAGATCAACT GAAATTCATG TGTTGCCCTT TATTAAGATC ACATGGAAAT A 51

(2) INFORMATION FOR SEQ ID NO: 2640:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2640:

TTAGCTAGTT GGTAGGACGG CTACCAGGCA CGTCATAGCG CCTGGAGGGG TC 52

50 (2) INFORMATION FOR SEQ ID NO: 2641:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2641:

CAGGCTTAAA CCTGAGTTAG TGCCATTCAT AATTGCAATC CCAAGCGACG GAA 53

10

(2) INFORMATION FOR SEQ ID NO: 2642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2642:

20

ATGTTTGTCA TCTGGAGCnA TAGAACAGGG TTCATCATGA GTCATCAACT TACCTTCGCC 60

GACAGTGAAT TCAGCAGTAA GCGCCGTCAG ACCAGAAAAG AGATTTTCTT GTCCCGCATG 120

GAGCAGATTC TGCCATGGCA AAACATGGTG GAAGTCATCG AGCCGTTTTA CCCCAGGCT 180

25

GGTAATGGCC GGCGACCTTA TCCGCTGGAA ACCATGnCTA CGCATTCACT GCATGCAGCA 240

TTGGTACAAC CTGAGCGATG GCGCGATGGA AGATGCTCTG TACGAAATCG CCTCCATGCG 300

30

TCTGTTTGCC CGGTTATCCC TGGATAAGCG CCTTGCCGn CCGCA 345

(2) INFORMATION FOR SEQ ID NO: 2643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2643:

40

CTTATACGGA TGTATAGGTC GGTCCAAACA TTTGATTTTA GTGGAGAGCA GCCTTTCACA 60

AATTATGTTC AATGT 75

45

(2) INFORMATION FOR SEQ ID NO: 2644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

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TACCGGTAA TTAACCAGGG CCCCGGTAAA AAAATCCCCG GTATTCCCCA TTCCAAC 57

(2) INFORMATION FOR SEQ ID NO: 2645:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2645:

AAAGCAATTC GCCCGATAAG AGTAGAGACG AATTGCTTTT AAGGTTAAAA CAAAGTGAGT 60

TCAATT 66

(2) INFORMATION FOR SEQ ID NO: 2646:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2646:

CAGTATAACT TGTGACCTAT TTAGAGGGGC ACGGTTGGTA CAATGAGTCT GAAACCGTAT 60

CAA 63

(2) INFORMATION FOR SEQ ID NO: 2647:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2647:

TAGAACATGG ACCGGTATTT TACATCCTGT ACGCCTAATC TGTGTAAAGT ATCTTTAGTG 60

AACCGTTGCT CTGGAATAAC CGCGATTCTG GGCAAACAGT GTGTAAACCG ACTnTATGGG 120

GATGTGTGAG TAATCATTGT GnACTGTTGA TTCTGTTCTG GAATCCCATT TCACAACACG 180

ATCTTGAAG TGCTGTCATT TTAGATGC 208

(2) INFORMATION FOR SEQ ID NO: 2648:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2648:

TTTTAACCTA AAGAATACTA AACTAAAAAG AGAATGATTC TGTACCGCTT TCCTTTTTCA 60  
CTCAATAACT TTATATTTAG TTATCCTTAT AATTGTAATT TATGTTAGTT GGTAAATnTT 120  
TACATATATG TATTGATAT GCTTGTAAT 150

(2) INFORMATION FOR SEQ ID NO: 2649:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2649:

AGTTTAACTG ACATCGAGTG GTACACAATA GCAATGGTTG TGTGTAAAGT CCTGGTGACA 60  
ACATATGAGA GTAACATTTG TAGTGATTAT CTTGTACTGA GAGAATTGAC ATCTATGnAG 120  
TTTATCACGT GCAAATAT 138

(2) INFORMATION FOR SEQ ID NO: 2650:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2650:

TCACAATTGC AAACCTTCTGG CACGCACTCA TCTGCGATTT CACAAGCTAC AT 52

(2) INFORMATION FOR SEQ ID NO: 2651:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2651:

GAGTCAAATT AAAATGCCTA TTGGCCATTG TGATGTATAA TCACTTAGTT CACATATACT 60

55

## (2) INFORMATION FOR SEQ ID NO: 2652:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2652:

GGGCGGTAAT TGTCAACATC ACAAATTGCT ACGTTGAAAC ATCGAGGATT CAAGCTGGAC 60  
 AGCAGAG 67

## (2) INFORMATION FOR SEQ ID NO: 2653:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2653:

ACACATCTTA TATGTCTTAC TGATTTAAGG AAAGAATCAG TGGATCAAAC TG 52

## (2) INFORMATION FOR SEQ ID NO: 2654:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2654:

CAAGCTGTAA ACCAAGAATT CCAGCATTAA ATATCTCTCh TGGTATCGGT TGAGATAAAT 60  
 ATTCCGTGTG CTCATTAAAT GTAGTAATCT TTATTGTAGT TCCTCAACCT ATGACACGAA 120  
 TATTGCACAA TATTAGTATA GACAAATATT TCCTTTATAA TCTCATTCAA TTTTCTCCTT 180  
 TAATTATGTA TCATACATTG TATATTCTCA TATAGACGTT TTGnCATATT CATAGCTTCA 240  
 ATATTAGTGC ATTTATGTAT T 261

## (2) INFORMATION FOR SEQ ID NO: 2655:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2655:

AATCCTATTA GCACCTATAA TGATCATGAA AAGATGTCAT CGAGAATCAC CTAGTACACG 60

(2) INFORMATION FOR SEQ ID NO: 2656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2656:

CGCCGAAAAC AATAAATTCT CGGAACATAG AATTTATCAC ATACCACGCT TGGATTATCA 60

CAATGGACTG AGTCG 75

(2) INFORMATION FOR SEQ ID NO: 2657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2657:

TATTAAATAT GCGGTTGCAT ATATCTACGG CATGATTTAA CCGTGAACCA TGAATCATT 60

TAATCGGGCA CGCGTAAAT GCTCATTGAT CCGCAnATAC CACTATATAT CTAATAGCAA 120

GCGTCCAGGA TTCTGTGTTT TATAAATTTA AACTAACTGA AACGTGTGTA TCAGTTCAC 180

CCGnTCGATT ACCACACTTC AA 202

(2) INFORMATION FOR SEQ ID NO: 2658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2658:

CGTACATGTG CATCATGTAT CTACGTCAAT AAGATGATGG GGTCACATGA TTGGACCATT 60

(2) INFORMATION FOR SEQ ID NO: 2659:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2659:

10 CTAATCATGT CATGTCTACA ATTATTTGGA GTATTGCTGA CGAAATGCGT TGTACAACTT 60  
 TTTCATTCTA GCACCTTGCG GGGGCCCCACA AAnGAATTGG TCCATTCTCA nCATCAGTGG 120  
 GGGGCGCGAA TAATTTTCGAA ATTATTCTGC CACTCCCACT TCATCGATTA AGTTGTAACT 180  
 15 CTACATTACA TTTGTCTTAA ACCATTG 207

(2) INFORMATION FOR SEQ ID NO: 2660:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2660:

TTAATTATGT ATAATACTTA ACAAGATCAC CTGATAGATG TCTAAATATT ATCT 54

30

(2) INFORMATION FOR SEQ ID NO: 2661:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2661:

40

ATTAAAAAAA AATGGGGTAA TTTCCGCCAA ATCCCGTTTC CCCCTTGCCA AGGCCAAATT 60  
 TAACCACCCT TGCCAAATnA TTAAGCCAAA TTTTCCGATA TTTGTTTCCG TAATGTTTCT 120  
 45 TTAATTAATA 130

(2) INFORMATION FOR SEQ ID NO: 2662:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

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AAAGTAAAC CAGTCTATTC AAAAAGGTGA AAAATGGTGA CGCAGCGTAA ATAAnTGGTC 60  
 TCTGGTAGGG TAAATCGCGT TGTGGGTTTG TCACATCAGG AACT 104

(2) INFORMATION FOR SEQ ID NO: 2663:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2663:

AAAAAGAATA AAAGGACTCG AAAAActCAA AACTTATTnT AGATAGTCAT CGTGACAAGA 60  
 AACAAACATT TAACTAGACT AAGAAAAATG CTTCCATTAA AAGGCAGACT CATCA 115

(2) INFORMATION FOR SEQ ID NO: 2664:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 164 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2664:

GCATGCGCCA CGGTGTCTCA GCAGAGTGAC TGCCACCTTG TGTGCGCAGA GTCTGCGCCT 60  
 AGTACAGTCA GGGTGAAACA CnCTATACGC ATTAGGTACA GTACTTCCTG TCTCCGACTT 120  
 GAGTAGAACG TGACATATCT ATCAGCATTC ACTCGAAAAA GGGA 164

(2) INFORMATION FOR SEQ ID NO: 2665:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2665:

AATTACGCAA TnTCCCTGTC TTAnTGAAAG GAATTGACCT GTTAATTCGT 50

(2) INFORMATION FOR SEQ ID NO: 2666:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2666:

5 ACAATTCAAT AGAATTTACC CGTAACAGCG TTGCACTGCA CTCAAGACGG CTGACGTATA 60  
GCAC 64

(2) INFORMATION FOR SEQ ID NO: 2667:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2667:

20 GTAGAACCAG CGACGGCGCG GCGGCTGAGC AACATCTGAC TACCTATCGG CCGCGC 56

(2) INFORMATION FOR SEQ ID NO: 2668:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2668:

GGATCGATTG ACTACATGAC GTGGnGACGC AATTATACGG ATAGTCCACT 50

(2) INFORMATION FOR SEQ ID NO: 2669:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2669:

45 GCAAGATCGA ATTACAATCA CGACGATCAA CGCACGTAAT CATCTCTGAT CACAGTAA 58

(2) INFORMATION FOR SEQ ID NO: 2670:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2670:

5 ATACCAGCCA GACTTCGATC AACAGTGTTC AACTGCATTG CCCAGTAAGT TGGATAGCTC 60  
 GCACATAGTG CTACAAGTTA ACATATACAn CGAGTTTGTA TCTCAAGCTT GAAGCTTGAC 120  
 TACC 124

10 (2) INFORMATION FOR SEQ ID NO: 2671:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2671:

20 CGCTTACTGC ATAAAAGCCC CTAACACCGG GGCCTACGC TCGTTCGCCG GCTT 54

(2) INFORMATION FOR SEQ ID NO: 2672:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2672:

TCAGCGATTT AACACTAATT CTTCTAGCTA TTCTCTGTAT TTGGACGACG A 51

35 (2) INFORMATION FOR SEQ ID NO: 2673:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2673:

GATAAGTTGT ACCATATTTTC GATGCAATTC AATGGACAAT GAGGTCACCT GGCTTGT 57

(2) INFORMATION FOR SEQ ID NO: 2674:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2674:

5 TCCTTTGGCC AATTTTCCA AGTTTAAACC CAAACGGCCC GGGTTGGGTC CCCAATTCCA 60  
ATCCAAAATA ATTTTA 76

(2) INFORMATION FOR SEQ ID NO: 2675:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2675:

20 TCCGGGAACC TTACCCAGTG GCCCTACCCT ATGGGTAAAC CCAACCAGTG GGGCCA 56

(2) INFORMATION FOR SEQ ID NO: 2676:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2676:

TGCGGGGTCT CGTGCCGCCG TCTGCGGTGG TTGTTTGTC GGTGGTGTGT CGGAGTCTTT 60  
GCCAGCT 67

35 (2) INFORMATION FOR SEQ ID NO: 2677:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2677:

GGACAGAGGC CTTGACCCCC CCACAATCCT GATTACCGT AAGTTGCTCT CCCCC 55

(2) INFORMATION FOR SEQ ID NO: 2678:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2678:

AAATTGGGGC TTCCATCCCC ATTCCAAATT ATTAAAACCG TTTAGGGGCC TTATTGGCAC 60  
CATGG 65

(2) INFORMATION FOR SEQ ID NO: 2679:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 176 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2679:

ATTTTGGGAT TAAACCCTTA ATTAAAATTG GCCGGGAAAA GGAAAAGGCC GGTGGGAAA 60  
AGGCCAAGGA AAAGACCTTG GGAACATTA AAAACCTTGG GCCAAGGCCT TCCAAAACC 120  
GGTTGGTTTT TATTTTGGGA ACCAAATTGG GGGGCCGGA TTGGGCCAAA ACCTTG 176

(2) INFORMATION FOR SEQ ID NO: 2680:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2680:

GCCCCAAGA ATTCAAATAA CCnTTCGGAC CCGTAATGG CCACnTAATT 50

(2) INFORMATION FOR SEQ ID NO: 2681:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2681:

TGTGCATTTA TTGCATAACC TATATATGTG TGACCGATAT TTAGTGCGCA CTTCAATGGT 60  
GCG 63

(2) INFORMATION FOR SEQ ID NO: 2682:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2682:

TTATCCAAGC TTCCGGATAG TTTCAAGAGA AACCAATGAA ATCCGTTATG GGACCAATGG 60

10

GT 62

(2) INFORMATION FOR SEQ ID NO: 2683:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2683:

AACAGCATTG AAGTGAGTTA CTGGGGTTTA TGCACCATCA TTGGATATCT GCACAAGGAA 60

25

TTTCAACGTG 70

(2) INFORMATION FOR SEQ ID NO: 2684:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2684:

CTTAAAATTC CCCAGTTTCC TTCCTTTTAA ACCCCATGGA ATTATCCCGG CCAAAAATGG 60

40

ACCATTAT 68

(2) INFORMATION FOR SEQ ID NO: 2685:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2685:

TTTTAACAAA ACACCTAGAT ATGTTGCTG ATCAGAGATG CCTGGTGACC GGTGATCC 58

(2) INFORMATION FOR SEQ ID NO: 2686:

55

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2686:

10 ATCCATCCTT ATAGGCATTC ATCCTTTAAC ACCAACGATT TACATTATGG ATATAACGAC 60  
 TTGAGGGGGA ACGTGGGGTC CATCCTA 87

(2) INFORMATION FOR SEQ ID NO: 2687:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2687:

25 ATGGCTGGGC GCTTTACGTG GCCACATTAG GATTATGGCA CTGAAGCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2688:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2688:

AACGGTCGTA GGCAAGGGAC TCCCCCnGG nGCTAnATGA ACTGGTCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2689:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2689:

50 GCTAGCATCC ATGGCTCCTA TGCCGAAGCT GAGTAGACTT AGGTGACGGG TCGGTGACAA 60

(2) INFORMATION FOR SEQ ID NO: 2690:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 146 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2690:

ACTTAAAAAA GGAAGATTAG AAAATTCATA AAAAAATTTT GCTGGGGATT CTTGATCCCA 60  
TGGGCCCATT TCTGGATTTA GGTATTGGG TTGGCCAGCC AGGTTAGCGG GGCCCCCATT 120  
CTTCCAGGCT CGGTTTCTCC CAGGAC 146

(2) INFORMATION FOR SEQ ID NO: 2691:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2691:

ATTGGTGTCT AGATCATTTA ATACTAAACA TACAACACGA CTAATTCCAT TCA 53

25

(2) INFORMATION FOR SEQ ID NO: 2692:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2692:

TATTGAATTC AAACATGTA CTATTCCTA AATAATACAA TAAAAACGAC TACCATACTG 60  
GCCAGAAATA TATTTTATTT GTTACACATT AATTTCAATC CTCCATAATT TGC 113

40

(2) INFORMATION FOR SEQ ID NO: 2693:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2693:

GACTTATGTC CGTGTTCCGC TGAAGGCACG TCACGTAAAC TACCCGGTAC AGCT 54

(2) INFORMATION FOR SEQ ID NO: 2694:

55

(A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2694:

10 CTTCAGCATG AAGAAGTCGC GTGATATACA TCATATCGAT ATATACCGAT TATATCATCA 60  
 GAACATTCTC CTGGTATCAT TAGATAGATG ATAATTTGAC ACAGTCCACA ATTTGTnACA 120  
 ACGCCGAGAC TCAATGGCAT CCTGTACHTG ATCTATGCCG GAAAACACTA GTCTATATGC 180  
 15 CCGCAGACGT CCACTATATG CATC 204

(2) INFORMATION FOR SEQ ID NO: 2695:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2695:

ATAACTCTAA TTTGAATTAT CTCTCACTAT TAAAACGCGA GCTGTGTAAT AACGAACGCT 60  
 30 GACATAATCT TGTATTGTCG CATCATTCGC TGGTATTATC ATAnTGCGGT TA 112

(2) INFORMATION FOR SEQ ID NO: 2696:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2696:

TGGCAAAATT AGATGTCTGA ATAGTTTTAT TTACAAGTAC AAACCTTGTA CCATTTTAAC 60  
 GTAAACACAA TTTACTTATT GAAAAGAAAA TAAATGTATT CATGAAnACA CACTTTCCAT 120  
 45 AGCACTCATC TATAGTACTC AAATTCAG 148

(2) INFORMATION FOR SEQ ID NO: 2697:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2697:

CCTATAATGC TAAACTTCAT ATATCTCTTT GGCAACTATC TCCCTTCTAT TACCAAAGTT 60  
 5 ACGATAGCAA nACAATAAAG CAAGCATGTC ATGCTTACTT C 101

(2) INFORMATION FOR SEQ ID NO: 2698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2698:

TTGATAACAT TTGAAAAGCT GCTCCGATAT CAGCAACCAT TTCATCGACC ACAATATACG 60  
 20 ACATAGTCAC AAAACTGATT AGAAGACACC AATTGCTGAT TATCAAATCA CAAATTTAAG 120  
 nTGAGATTCA A 131

(2) INFORMATION FOR SEQ ID NO: 2699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2699:

GATAGCGGTT GTTAATCAAA CGATGGTACA TGCTTACATG ATGCGCCATG TTTGATAACA 60  
 35 GCTCTCTATG ATTACGATGG AAGAATGGTT TATTTTCATCT CAATTATTCC TATTAAATGn 120  
 AACATGCCCT AGCAAACGGA TACAACACAA TCACAACATC ACTTTGAAAT TGTAAACCT 180  
 40 GAGAACCACA TACGCGnAAC AC 202

(2) INFORMATION FOR SEQ ID NO: 2700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2700:

TTCGAATTTA ACAAACGTAT CACGCCATAA AGGTTGTATA TGTTGTTTGT AAATTC 56

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2701:

TATTGCGGGC TTATTAGTAC ACGATCTATA TGATGGTCAA ACTTATGTCT TTCATATTCA 60  
 AGTGTGACAT TGTGCGGTGA TTATATTTAC GCGTCGTTAT CTACGAACGC CACATTAAGA 120  
 TTCGAAACTG ACAATCAACT CATAACGCCA TGGTCCTAGA AAn 163

(2) INFORMATION FOR SEQ ID NO: 2702:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2702:

TAnACAATCG TAATCGAGTC AATGATGTGA ATTGCCCACG TGAGCGCTAA GAATGCGACA 60  
 TTCCACACGA TAAGGCAGTG CGCATGCGCA CTGACCTAAT AACACTGAGG ATGAGTACTA 120

(2) INFORMATION FOR SEQ ID NO: 2703:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2703:

CTGCTTGATT AGGATCGTAT TTATATGAAG ACTGTGTTCC ATAATGATGT GCGTTTTGGC 60  
 TGAAGTCCCT TAAATGTACn TGTGTATAAA TGCTATAATT TAG 103

(2) INFORMATION FOR SEQ ID NO: 2704:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



TCTATAACGC CTCTCATCGT TTGGTCACAT ATTACCATTA TTCATTTTAT GTTCTCGATA 60  
 ATTGTATGCG nTGTTTCTCA CTGTCATCAC ATTGATACAA CTCATTGTCA CTTTATACGA 120  
 5 TTCACACACC TCGATACGAG TGATGATATA TGACAAAGCT 160

## (2) INFORMATION FOR SEQ ID NO: 2705:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2705:

TTATTGTTTA AGATGGTTAA ATGTCATCAT ATAACanTTA ATTTTtagCA ATTcGATATG 60  
 20 CCTATAACCT ATAAATTTCA CGTCAACAGA AAGTGACAGG CATACGGATG TGTGAA 116

## (2) INFORMATION FOR SEQ ID NO: 2706:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2706:

TTACACCTGC AGTGATGGA CTATGGCTAG ATACAATAAT TTTAGTCATC AAnCTACATC 60  
 ATACAAACTT ACGACTTACA CATATCTGCT TCTAnATCTT CTAActGATT AAAGCTCGAC 120  
 35 ATCGGAAGCT ATTCTAAATT ATTATCATAT ATCTAACTAA CTGACCTAAT ATATACTACC 180  
 ATAAATAACC CGCCTCAAGG TTCGCATCCG CATATAATGC TTAGAAGTC 229

## (2) INFORMATION FOR SEQ ID NO: 2707:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2707:

50 TCCATATCAA TCCTGAAAGT ACACATATAT CGTACACCAT ATGGTACAAT TTCCTATAnT 60  
 ACACATCACG CATCTTTCAA GACACATGTT AGGCGCTGGT CGGTGTATCT CAGAAATGCA 120

## (2) INFORMATION FOR SEQ ID NO: 2708:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2708:

GGAAC TTTTC TGATTAAGTG TTCACACGCC AACCATAACA TGTATTCATG CACACAATTG 60  
 TTGCTAA nCT CACTAACAAC ATACGACCAT TTTACTTTCA ATACATATGA TCCGTATAAC 120  
 TCGAATT CnC TGCTTATAAA TGACCATTTT GACGTTTACA ATGTTAAACG ATTGGAAATT 180  
 TTAAAGTTAG CATGTCCACA TCCGAGCACT AACTATGCCG TACCATTGTG ATA 233

## (2) INFORMATION FOR SEQ ID NO: 2709:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2709:

TTGTACCTAC CAACGAGGAT ACAATGGATG TCACACGAAA ATTGGGATAT AGATGTCCCA 60  
 GT 62

## (2) INFORMATION FOR SEQ ID NO: 2710:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2710:

CTTTAAAAAG GATAAATGAT TGAGAnAAAA ACCCATTCGA AAATCATGCT GTCATGCTG 60  
 TAGACTTATC GTTTGGACAC TCGCGTAAGA GCGAGCAGTG AAAT 104

## (2) INFORMATION FOR SEQ ID NO: 2711:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2711:

GTCCAGAATA TTAATCTGAC ACAACCATTT TAGCnGGTGG ATTAAATATA TACGACCTCA 60  
 5 CCGCAAGAAT CTCTATTTAA CTTAACCTAT CATGAATAAA CTGGCGCTTG TGATATCATA 120  
 TGAAGATTAG CGAAAGATAG C 141

(2) INFORMATION FOR SEQ ID NO: 2712:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2712:

20 TGGTATTGAA TAGCAAAATT TTGACACTAT TTGCATACTC AATGATACAT CATATCGTTA 60  
 TATGGATTTT TATGGTCATT AATGGTAAGA ATTTGATACG GAATATTGGC AGGTTTGGAA 120  
 ATCAAATAAT ATGAGAAATT GTATTAAcna TTAGTCAAGT TAACGCTCAT AAATAGACTC 180  
 25 ATCnCGCGCT ATAACGCTTA CC 202

(2) INFORMATION FOR SEQ ID NO: 2713:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2713:

TTGAACTGTC TAAGACTTGG ACGCTAAATG AATGCGTTGA TACAAACGGT GAATCC 56

40 (2) INFORMATION FOR SEQ ID NO: 2714:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2714:

50 CATGACCGAC ATCAGGTGCA AACTCCCTCA TTAATCTGGG AAAACTGTAT CCCGGTAGCT 60

## (2) INFORMATION FOR SEQ ID NO: 2715:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2715:

CCTATAACTA CTCAATATTG CAATTACACA TCCTCACTTT TGTCAATTGT TTGACAATCn 60  
 AATACACGTT ATGCACAACCT CCATTTTAAC GGAATGGAGA GCACATATGG ACAGTAAATT 120  
 AAAT 124

## (2) INFORMATION FOR SEQ ID NO: 2716:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2716:

GGAATATGTA CTATTATCAT TTGATGTTAT TACTCATATT TTTTGTAATG AATGCTATCA 60  
 CCTACAAAAA ATTTACTTGA AACAGTAATA ATAATTAATT ACCACAAACC ATGATAAATT 120  
 TAATAnCTAA TCTAAATAT CGCATGTTCA nAGCCACAAG ATATAACGCG TTCCGTAGAT 180  
 GGAAGTAGAT AGTATAAGGC GCCGTGGAGC CTGGCCT 217

## (2) INFORMATION FOR SEQ ID NO: 2717:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2717:

ATGACATACG CGCATATACA TGCTATCCCG AACTAATATT GATGCGTATT ATGTAATTGG 60  
 AGCGAACACT CA 72

## (2) INFORMATION FOR SEQ ID NO: 2718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2718:

CATATCATCA CTATATCCAT TGC	CGTAATAG TGATGATATT GATTGGCATA ATGGTATATG	60
GCAGATACGA TAACATAACn AACACCTCGG	ATAATTGCTA TTAGCTGCGA AGTTATCGTG	120
CCTGATTTAA CGATGTAGA		139

(2) INFORMATION FOR SEQ ID NO: 2719:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2719:

CTCTATCATA TCTAGCCATA TGCATGAGAT	TATCGTTTAT CTCGACACGC TCTTAAAGG	60
CGACACCGGC ATATGATGT		79

(2) INFORMATION FOR SEQ ID NO: 2720:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2720:

CAATCACAAT TGAAATTACA CAAATACAGC	CCATTGCATG ACACAGACCA ATC	53
----------------------------------	---------------------------	----

40

(2) INFORMATION FOR SEQ ID NO: 2721:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2721:

CGCCCGAGGC TACCATTTTA CCATAAAGAC	CGGTCTAAAT CCTTCCGGTT TCCATGGGCC	60
ATTG		66

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2722:

TnCTCGCCG AAAATGACCC AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA 60  
 GAAGACAGTC ATAAGTGCGG CGACGATATC ATGCCCCGCG CCCACCGGAA GGAGCTGACT 120  
 GGGTTGAAGG CTCTCAAGGG CATCGGTCGA CGCTCTCCCT TATGCGACT 169

## (2) INFORMATION FOR SEQ ID NO: 2723:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2723:

CCGGGCCAAG CTGGTGATCA CCGATGTGGA GCGCCAACAT CGCATCGAGG AAAT 54

## (2) INFORMATION FOR SEQ ID NO: 2724:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2724:

ATCGGTGATC ACCAGCTTGG CCCGGGACAA CTGCAGAGCG TGCAGCAGGA ATTG 54

## (2) INFORMATION FOR SEQ ID NO: 2725:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2725:

AAAACCATTTG TCCACCTTTA GAAAGCTTTT GTTTTGGGAA TACCTAAACC GTGGTTAATG 60

## (2) INFORMATION FOR SEQ ID NO: 2726:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2726:

TTTAGGCCCT GTAACnGnTT GCCGnTTGGn CCGTGTGTAT ATCGGGGGAA 50

## (2) INFORMATION FOR SEQ ID NO: 2727:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2727:

GGATCATTAACGTTGTATCA CCATCCAGTT TGCAAGACGG ATAAACTGCT GCAACG 56

## (2) INFORMATION FOR SEQ ID NO: 2728:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2728:

ACCCATGGAG AATTAAATTT AAAAACCGTA TTCCGGGTGG ATGCTGGGTG GGTAAGTTGG 60

CCATACTGGG 70

## (2) INFORMATION FOR SEQ ID NO: 2729:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2729:

ACCACCTTCC CCAATAAGCT GGCCTAAAGC CCCATAATGG GCCATGGTGC GGCC 54

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 74 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2730:

TGTTTGGGGA CCTTAAATGG TTCCAAATTC CAACCACCCA CCAAAAGAAT TCCAGTTTCC 60  
AATTAAGCCA GCCA 74

(2) INFORMATION FOR SEQ ID NO: 2731:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 66 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2731:

AAGTTGGGGA TTAAGGCCAG TTATGGAAAG GATGGATGGT CCATTGGGC TTATTAGAAG 60  
AGCATT 66

(2) INFORMATION FOR SEQ ID NO: 2732:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2732:

TTTGnAAAAG CCnGTAAGAG TATTTGATTT TGTGGAGGC CAAACCAGAA 50

(2) INFORMATION FOR SEQ ID NO: 2733:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 102 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2733:

AGTACCAGCG GACAATTCGG ACCCAACTTG GCAATTTGnG GTTTTGGACC AGGAAATAAA 60



## (2) INFORMATION FOR SEQ ID NO: 2734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2734:

CCAGGCTGGC AGTTTTTCTA AAATGGTGGT AGGAAAATTA nCCAAACCAT TTAGGATGGC 60  
ATGGTCTTCC ACGGATGGCG GCCGTTAACC CCAAAAAAGG CCATTCCATT T 111

## (2) INFORMATION FOR SEQ ID NO: 2735:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2735:

CGTATGGGAT GGCCATTCTG ATGACACACA ACGGTTAGGT TAGCAACGTT GTCAAA 56

## (2) INFORMATION FOR SEQ ID NO: 2736:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2736:

CAATCCGGGT GTGCGGGCGT GTGTACAAGA CCCGGGACGA TTACCGACAT 50

## (2) INFORMATION FOR SEQ ID NO: 2737:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2737:

TAACATTTAT TGTGGAGAAA GTnAGGTATC GTGGTAGTGA GGATTGTGTT 50

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2738:

TAAATTTAAA CCCGTCCCGG TTTCCCAAAT TTGGAATTTT TTGGAACCCC TGT

53

(2) INFORMATION FOR SEQ ID NO: 2739:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 85 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2739:

ATACCCACCT TGGATTCTTA ATACCCCAA AAGGCCGGGG CAACTTGGCT TAAAAAACTG

60

GCTTGTTTAA ATTGGATTTC CGGCT

85

(2) INFORMATION FOR SEQ ID NO: 2740:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 70 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2740:

GGAAAGTTTA GTAGTTTAGA GTCGAAAAT TAGTTTTCTA GTGTAACGAA TCCGGACCCA

60

AATTTTTTTC

70

(2) INFORMATION FOR SEQ ID NO: 2741:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2741:

CGCGCCAATT TACCTGGCGC AGCAGACGCT CAACGAGGAG CACGGCAGCT GCG

53

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2742:

TGAAGAAATC GCACACACTA TCGAACGCAG ATCGCACATC GAATGCATCA GAATCAGCTC 60

(2) INFORMATION FOR SEQ ID NO: 2743:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2743:

TATCACCTCT TTTGCATATT ATTAGAATAT ATAATGATCT TTATAGAAAG GAAAGAAGAA 60

GAGTTATCAT nGCGATATCG CCCAGCGCGT CGTACACTAT GCCATGAATT ACACAATCAT 120

GCCTC 125

(2) INFORMATION FOR SEQ ID NO: 2744:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2744:

GAATTTCCCC CGAAACCGGG AAAAATTTTT CCCAACCGGT GGCCTTCCCC CGTTCCCGT 59

(2) INFORMATION FOR SEQ ID NO: 2745:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2745:

TTTTCCTTAA GTTAGTTTTT TTATTGGGCC AAAACCGGCC CCAGGAATTG A 51

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2746:

TAATTTGGTC ATAATGTTGT TTCAGATGAA ATGCTAACAA TACACTGATT ACAGT 55

(2) INFORMATION FOR SEQ ID NO: 2747:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2747:

ATGGTGGAAT GGGATTTAGG TGGATGGCCC CCCCAACCAG CCGGTCCTTT TTAAGGAACT 60

TTGT. 64

(2) INFORMATION FOR SEQ ID NO: 2748:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2748:

AACAAGAGTT ACATTGGTTG TGGAAATCAT CGGTTTTAAT TAGTCCAAAA GGATGGATTC 60

AATCGGTAGG GGGGTAAG 78

(2) INFORMATION FOR SEQ ID NO: 2749:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2749:

GCAAGTGGCG GAGTCACACT TATAGACAAG AAGTACGACA TCTTGTATGT GGTG 54

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2750:

TATTTAGATT CAAAGCATCA AATTGGTTTC GTACCCTTTT GCACATCGGT TGGGATAA 58

(2) INFORMATION FOR SEQ ID NO: 2751:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2751:

GGAAAACCCC CCAAATTTTC CCCCCCGTT GGGAAAAGAG TTCCCAAAGT TGGAATTAGT 60

TCCCAAACCC GGGAGTTCC 79

(2) INFORMATION FOR SEQ ID NO: 2752:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2752:

AGAACCGAGA GATAGTGCCG AGAGAGCGAG AGGTTTTAAT AGAGATGTTT GGCCGTACTA 60

GTTAGCCG 68

(2) INFORMATION FOR SEQ ID NO: 2753:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2753:

ATAATCTATG GGGGGACCGT CTGGTAAGGA ACCTGGTTGC CCTGCCAATG AAGCCACCCT 60

## (2) INFORMATION FOR SEQ ID NO: 2754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2754:

ACAAAGGTTT TACGCCCAA TTGTTCACTG GCTAACTGGG CGATGGTTAG TATTGGCAGC 60  
 GCAAAAGTGG CAGGGG 76

## (2) INFORMATION FOR SEQ ID NO: 2755:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2755:

ACCTCAGGGA CAATTAAAAG TTTTCTTCG GAATGAATGA CAACAACAAA T 51

## (2) INFORMATION FOR SEQ ID NO: 2756:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2756:

ACGTATTCCC TCGTTCTTAG GTCTTCTAAA CATAGGTGAC TTTTGGTCG 50

## (2) INFORMATION FOR SEQ ID NO: 2757:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2757:

AAATGCTTCG TATTAACGCC TATTTTAGCT CCGTTATAGA CACAACTTAC ACA 53

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2758:

ACACGGCAGC GAATACTCGT TTGGTGAGCC TGTACACATC TAACACGAGA A

51

## (2) INFORMATION FOR SEQ ID NO: 2759:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2759:

GGGAAAACCA ATTAAGGATT TAAAGGTTnA TTTAAAGGGG CCGCCACCGG GTTGGGGATG

60

CCCTTTGGGC ACCTTAAGAA AGCCCCGATG GAAAGGGACC GGTACCTTA ACCGG

115

## (2) INFORMATION FOR SEQ ID NO: 2760:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2760:

TTTGGCCAGG CCAATTAATT CTGGTGCGC AATTAAATTT AAGGGGACCT TTGGGGGAAT

60

AAGGTTTAAA ATTGGAAAAT GTTCCAATTT GGACCTTTTG GCCAATTGGA TTCCCGGCTT

120

AAAAAGATTT GGACCGGTAA ATCCCTTTTT AAATTACCTC GGGCCAnGGC CCAACCAAGC

180

CAAACCAATT TAAATCCGCC TGGAAACCAA CCCATAnTTC CTTTACC

227

## (2) INFORMATION FOR SEQ ID NO: 2761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ACACTATTGT GCCAGCGCAC CTTGAGGTA TCTTGCATCA CTCAGCTGTT TTTTACTGT

59

(2) INFORMATION FOR SEQ ID NO: 2762:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2762:

TTATCCTGTT CCTAAGCCCG ACGGCTCGGC CACACGATTA ACCTTTAACG CCATCTTGTC  
 CAACCTGT

60

68

(2) INFORMATION FOR SEQ ID NO: 2763:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2763:

TGGAAAGTAC CATATAAGTA ATGGTAGTCG TTTCAGAAAG ATATAAATCG TTGGGAAAAG  
 AAGAAATGAC AATTAAATGT AAATATTGT TCATGTACAA ATAAATATAA TTTATA

60

116

(2) INFORMATION FOR SEQ ID NO: 2764:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2764:

TTGTTACAGT GGTGTAGCGG ATCGCACGGC CTTCAACTAA GTGGTTCAAT GCTTGATACC  
 AGTTATGAGT GTTGGTGC

60

78

(2) INFORMATION FOR SEQ ID NO: 2765:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2765:

ATATATTCGT ATGCACCTTT TGTAAGGCTT TGTAATACGA AAATTATCAC TACAATGATT 60  
 5 GCTGTAACGA GTAACGACAT ATATGGCACA CCGTTTTTAT TnGTTTTACC AA 112

(2) INFORMATION FOR SEQ ID NO: 2766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2766:

TATTGAAGAT TTTTTCGAAG ATAAAGGTGA CACATATTCA TGTCATGTTT AATATCGTTA 60  
 20 CCTTACGTAA CCATATAAGA CTGTAACTTG TGTCATATCA TTCGTAGAAC nTTTGGAAAT 120  
 GAT 123

(2) INFORMATION FOR SEQ ID NO: 2767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2767:

GTCCGCGCCA CGGAATGGCC CACGGGACGA TAAGTGAGGG CACCGACGGC CGAACCCAAG 60

(2) INFORMATION FOR SEQ ID NO: 2768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2768:

GTACGCGGAG CACGAATTCC GCGGATCTGG GAGCATCTCT AGGTAAnTTT 50

(2) INFORMATION FOR SEQ ID NO: 2769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2769:

CTTAGGTAGC TCAGTGTGTT ATTGAGAGGC CTGTTGGCAG GCCCCGGACG ATC

53

(2) INFORMATION FOR SEQ ID NO: 2770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2770:

AAATTGATAG CGTGCACAAA CCAGGTCCAT CCACGAACAT GCCAATCCAG CCCAGGAAGT

60

AATTGCCCCG

69

(2) INFORMATION FOR SEQ ID NO: 2771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2771:

ACGATCATCT GGATGGATAT ACAGAACAGT GTGATTGTAC GTGGTGGGGA AA

52

(2) INFORMATION FOR SEQ ID NO: 2772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2772:

TTAACAGTAT GATATTATCA CACGTGAATA GGATATGCCA ACACTGGCAT CGTTGGGGAT

60

AGCGTAATAC

70

(2) INFORMATION FOR SEQ ID NO: 2773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2773:

AACATTGTAT TCGTGATTAA GACTTCGATC GGTTTCAGTAT TCGGCAGATC CACATGTGAC 60  
 CATGCTT 67

(2) INFORMATION FOR SEQ ID NO: 2774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2774:

CACCCCTGTG ATATCACATT TGTATGTGTT AAGAGGGAGC CCCTTTCCCG ATCAACTGGC 60  
 GATAAAAACA GTTGAAAGT GGGCGGGGGT TATTATTTCT GATGACGGCG GGGTTTTTTC 120

(2) INFORMATION FOR SEQ ID NO: 2775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2775:

AACCGTTGCA GGTAAAGCTG GGCnCACCAT TCTTCTCTAT TAATGGTTCA 50

(2) INFORMATION FOR SEQ ID NO: 2776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2776:

CATGTACGGT GTCCACACAA GAAGTATTTA GGTGGTTGTT CCCGGATTTA ACCTGGC 57

(2) INFORMATION FOR SEQ ID NO: 2777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2777:

AACGACCCCG GGTTCACCG GGGTCCATTA AGCCAAGGGC CAGGGGACCC C 51

(2) INFORMATION FOR SEQ ID NO: 2778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2778:

TTGTTCCGGC CTAAAAAATT TAAATTGAAC CCAAGGGTTG CCTTGGGTTG GGTAATCCAT 60

TTTTTGAATA AACCTTTGnC CCTAATGAAT TTTTCCGCCA TTAAAGGGT GTCCGCCAAT 120

CCGG 124

(2) INFORMATION FOR SEQ ID NO: 2779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2779:

GTAAATTTGG GAATTACCGG AAAATTAAGG AAAGGCCAGT AAGGGGTTTC CAGGCCAA 58

(2) INFORMATION FOR SEQ ID NO: 2780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2780:

GCACTCCAGC CTGAGCACCA GGGTGAGACC CTGTCTCAAG AACAAAAACA nCAACanCAA 60

AAAATTGTT CAAAACTCAC TTCCTGCAGT AATCTTTCCT TGAACAACT CACCCTCTAA 120

TTCCACCTG CAATTGTGTG TAGAAATCCA TTCTCGTGTG TAATTTTGGG CTTATATGCA 180

CACATTGAAA ATCCAAGAGC CAGAAAGAGC TCTAAGGAAT TATCCAGTCC AGCTCTGTGC 240

AGCCTGGGCT AGGACCCAGA TCTTTCCCAT TTCCCTGTTC CAAAAATTTT nGGCACAGGG 360  
TGGCCACCCT G 371

(2) INFORMATION FOR SEQ ID NO: 2781:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2781:

GGGGTTGCCA AAGGGTGTT AAATTTAAGT CCGATGAAAA TTAAGnAAAA AAATCCCATT 60  
TTCCCTTCCG GGTCCGTGT TGGGGCCTTA ATTTCCCGCC AATCCAAGTT TGGTGAATGA 120  
AATTAATTAC CGT 133

(2) INFORMATION FOR SEQ ID NO: 2782:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2782:

GTTCAAGTTG ACGCTGGATC ATCTGGTACA CACGTATCCT GCATACTATA GATGTCAT 58

(2) INFORMATION FOR SEQ ID NO: 2783:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2783:

GCTAATTATA GGCCGTCAGG CATTACGnGA TCGAATCTGG CAACTCACAA 50

(2) INFORMATION FOR SEQ ID NO: 2784:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2784:

GCCnCTCT GTGACTGT GTATATACAC CCGCGGAAT ATCTCCAACG

50

(2) INFORMATION FOR SEQ ID NO: 2785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2785:

CTTTGTCTGA CATATTGGGG CAGTGATTTT TGGGACGGTT CTACATGTCG AGTACTTTAG

60

TCAGAGTTGT GAGTAGCGGA CGGGTnTACT TGATATACCC TTAATGTGTA T

111

(2) INFORMATION FOR SEQ ID NO: 2786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2786:

CATGATGATA CTTGCATGTA CGTTGTACGT GAACGTACAG TTACGTTGTC

50

(2) INFORMATION FOR SEQ ID NO: 2787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2787:

TCAGCAAGTA GTAAGGATAT CAACTATGA TCTATTTGAT GTTATGCCAT AA

52

(2) INFORMATION FOR SEQ ID NO: 2788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

GCATCATGGA ATATTAAAC AGCTGATATG TTTGAGTAAT GATTGATTGA CGAGATATGC 60  
GGCA 64

(2) INFORMATION FOR SEQ ID NO: 2789:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2789:

TGAGAGAAGT CACAGTCGCC AGCGGCAAAG AACCCGnnAA GATGTGnGCA 50

(2) INFORMATION FOR SEQ ID NO: 2790:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2790:

CAGTGTATGG AATCTTGTTT GAGTGTGAGA GTCAAAGACT TGGTGATTGA ATGGAAAAAT 60

TGAA 64

(2) INFORMATION FOR SEQ ID NO: 2791:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2791:

ACAAAnGGGTG AAGTTCTCCC ACATGCTGTA TACCGTGGA TTATTTTAA 50

(2) INFORMATION FOR SEQ ID NO: 2792:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ATTCTATTTC AACACGGAT ACATAATCTT TTATATCTTC CTTCTAGTCA TATGATACTG 60  
GAATAAGTGA TATTTCTTAT AAT 83

5 (2) INFORMATION FOR SEQ ID NO: 2793:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2793:

CATATGTCAT CGTACGTAAT CATCGATGAA ATATCAACAT CTCGACTTAA TAGGTCAACA 60  
AGAT 64

20 (2) INFORMATION FOR SEQ ID NO: 2794:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2794:

30 CCCTACTCCG CGCAATAACC GCATTACCAG ATGCGCTTCC ACTGAGGAAC GACGGAT 57

(2) INFORMATION FOR SEQ ID NO: 2795:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2795:

AGATAAAGTG TCATCTATAT CCATCTATCA ATATAGATAT GTTTACGGCC GATTTCAATC 60  
45 CGCAA 65

(2) INFORMATION FOR SEQ ID NO: 2796:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
50 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2796:

TATACGCCTC ATTACACCCA ATTGGACCCT TTACGTATGG AGTACATTAT AGAATCGA

58

(2) INFORMATION FOR SEQ ID NO: 2797:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2797:

ngCTAAGAAT TTATAAGAGG TTTCGGCAGA TATATATACG CAAGTATCTG

50

(2) INFORMATION FOR SEQ ID NO: 2798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2798:

AAGCAGTCTT TCACAAAAAG TGAATAATCA CTAGTTCATT AATTTGCATT TGAACCTTCA

60

TATAATGCAT ATTACTTAAT GTACAAGCAA AGATGTATTT ACCTATCAAA GAATTTnC

118

(2) INFORMATION FOR SEQ ID NO: 2799:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2799:

CCATAGAACC TGTGAATACC TATACATATC ATACTGTGGA ATTCGTTACG AGG

53

(2) INFORMATION FOR SEQ ID NO: 2800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

CCAATTCAGA CTGTTATTCT CTCTTCGTGA TAACCCGTGA TGTTTGTCTG C

51

(2) INFORMATION FOR SEQ ID NO: 2801:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2801:

GGGGGnGCAT ACCGCACCGA AGCATCAGAC GATGTGAGCG ACCTACCTCC

50

(2) INFORMATION FOR SEQ ID NO: 2802:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2802:

CCGTAGCGCA CATATGACGA GACCAAGGAT AACGTGCAAn GnCATATTGT

50

(2) INFORMATION FOR SEQ ID NO: 2803:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2803:

CACGTCATGA ACGTGCATTC AACACAATCA TTTACGAGAT GGACCAAGAC

50

(2) INFORMATION FOR SEQ ID NO: 2804:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2804:

TATGGTGT TT ATTTAGCGC TnGTTGTGCT TTGTCTTCAG CATCTATAAC CTAGTGCGAT

60

CTATTG

126

## (2) INFORMATION FOR SEQ ID NO: 2805:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 88 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2805:

AAAAGCGCAT ATGGTGT TTT TCTCATATCA CTCCAGGACT CAGCAGCTGG AAGGAGTTAA 60  
 GAAGTAATAA GGTGCCACCC TAAATCCA 88

## (2) INFORMATION FOR SEQ ID NO: 2806:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2806:

TGGATCCGGT ACCAAATAGG GACTACCGGG AATGTCCCGG GGGGCCTAAT GCCGAATGGG 60  
 GCAACG 66

## (2) INFORMATION FOR SEQ ID NO: 2807:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2807:

CCCGCTAACG TGGGGAAAGT TTTGAAGTTA AGAAGGAATG GATTCCTAAC GGGGCGGGGT 60  
 CCAAAC 66

## (2) INFORMATION FOR SEQ ID NO: 2808:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2808:

ACAAAGCAGT ACTGAACTGG TTTCGTTGGA GCCCGTGTG CTGTTTATTC ACGGCA 56

(2) INFORMATION FOR SEQ ID NO: 2809:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2809:

AGGGGGCGTA CAACATAGAT TTGCGAGATA CTCAGCATTA CACTTCCATT TAACTTATTA 60

TCC 63

(2) INFORMATION FOR SEQ ID NO: 2810:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2810:

TTAGGCGCCT GTTCCAACCG CACCCATATA AGGCGGTCGG CTGCACGCAC GACGTATG 58

(2) INFORMATION FOR SEQ ID NO: 2811:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2811:

AAACCCCAAA GGAATTAATT TTCCGGTTTT CCAACCCCTT AAAAAGGGAA AGGCCAAT 58

(2) INFORMATION FOR SEQ ID NO: 2812:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

CATCATTAAG GCAAAAACTT TCACAAAGTC ATGAGGCGCA AAAGGTATTA TTATAACACA 60  
TCCCGCGTTG GG 72

5 (2) INFORMATION FOR SEQ ID NO: 2813:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
10     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2813:

CCATTTAAG CGGTACGGGG CTTGGTTCAG GAACGTCGTT AGACAAATTC GTT 53

(2) INFORMATION FOR SEQ ID NO: 2814:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2814:

TAGTACCCAA TTTCCAGTCG AACCAGGATG GGACCAGAAG CCAAACCAAC GTT 53

30 (2) INFORMATION FOR SEQ ID NO: 2815:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 62 base pairs  
    (B) TYPE: nucleic acid  
35     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2815:

GAAAAAAGG CCTTGTTTAC CAAAGGGGCC AATTTTTTCG GTTCAAGGTC CAAACCTACC 60  
TT 62

45 (2) INFORMATION FOR SEQ ID NO: 2816:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
50     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

TCTGAATGAC GCCGAAATCC CATCTGAATT CATGGGATTT TCCACTTTCA

50

(2) INFORMATION FOR SEQ ID NO: 2817:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2817:

CGTTACTAAA GCTACATAGT GCGTCATTTA AGATTATAGC AAGTAGCATA T

51

(2) INFORMATION FOR SEQ ID NO: 2818:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2818:

CATTCACCAT AATATTCATT GTTCCATTAG CATATCAGGC ATGTCACGTG CACA

54

(2) INFORMATION FOR SEQ ID NO: 2819:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2819:

GTGTATCAAA TGAGCATGTT nCAATGGTTC AncATGGCGT TTATGGCACT

50

(2) INFORMATION FOR SEQ ID NO: 2820:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2820:

ACAATTGCGG CTGCTCATTG TGAGCACGAC TTTATCATGG TTGGGTTTCAG

50

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 102 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2821:

CAGTAGTACG TAAAAATGAA TCACTTGAAG ATGCGTACGT AGATTTTAAA CGTCAGTTCT 60  
AAAAAGTGGG CAATCCAAGA GACGTAACGG AATTTCGAA AA 102

(2) INFORMATION FOR SEQ ID NO: 2822:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2822:

GAGTACTTAA TCCGGCACCG TTTACTTCTG GGGGCATCGA CTAAGTGGGG CGGCC 55

(2) INFORMATION FOR SEQ ID NO: 2823:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 71 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2823:

ATTGGTTTCT CATAAACACT TTTCTATGAA TTTGTATGTA TTTGTTTATT AAAATCTCTA 60  
ATTCTTATGG A 71

(2) INFORMATION FOR SEQ ID NO: 2824:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 134 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2824:

CCATTGAGTG TGAGTATATC ATCGATCAAT ATGCAACATT TATCAGGTGC ATGTTGCTTA 60

TGGATAATTG AACA

134

## (2) INFORMATION FOR SEQ ID NO: 2825:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2825:

CCAGAATGAT GAGCTACAGG ATCAGCCCAG ATATGCAGGT AAACGGGCCA ACCATTG

## (2) INFORMATION FOR SEQ ID NO: 2826:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2826:

CAATAATGCT GAACAGCAAC GCATCTCATT CTAAAATCGC TCAGAATCAC ATCCCATGCA

CACATAATAA GTGGCACTTA GCTTAAAT

## (2) INFORMATION FOR SEQ ID NO: 2827:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2827:

CGGATTAGTG GTGTAAACTG GGTGACCCAT ACCACACCTC GCGTGTGTG AAAAAAGGAC

TTAA

## (2) INFORMATION FOR SEQ ID NO: 2828:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



TATACAGAAA ACAGCGTGCC GTTATCCATT ATCACATGAC ATATGTAGTC C

51

(2) INFORMATION FOR SEQ ID NO: 2829:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2829:

GAGATACGGT CTTCGTATAT GATATGTGCA TATTTAGATA GTCATTTATG AGAGAACGTG

60

GACGTGAG

68

(2) INFORMATION FOR SEQ ID NO: 2830:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2830:

TGATGATTGT TTATGATACG ATATGTAAAT GATAATCATC CAGGAGGTCT AGCATGGT

58

(2) INFORMATION FOR SEQ ID NO: 2831:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2831:

CCTAACAAAC ATAATTAAAC CCATAAATGC ATCCAATGCG GTTAAACCAT GAAA

54

(2) INFORMATION FOR SEQ ID NO: 2832:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2832:

## (2) INFORMATION FOR SEQ ID NO: 2833:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2833:

GTCTGCTACC CTTTCAGAGC AACATGCTGA GTGTATAATG CCGTGTATAG GGGACAATGC 60  
 CATTCACTA 69

## (2) INFORMATION FOR SEQ ID NO: 2834:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2834:

AACACCAGCT GGTAAGTATC ACGTTACATT TTGTGTCTTC ATGATTATA AAAAC 55

## (2) INFORMATION FOR SEQ ID NO: 2835:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2835:

AGAGCTTGGA TGTCGTTTCGT AATTGATGCT CTAGCTCCAT GGGGCCCATG 50

## (2) INFORMATION FOR SEQ ID NO: 2836:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2836:

TTTCGTCCT ATTGCTCATG CATAGACATT TGCAATACCG GCAAATGACG ATGGnATATG 60

TTAATGGTCA ATACAGGG

138

## (2) INFORMATION FOR SEQ ID NO: 2837:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2837:

GTTGGCAACT TCAGTCGCTA CTTTAACGCA TCTCACAGTC CTCCTCCCAA AGAGAACGTA 60  
T 61

## (2) INFORMATION FOR SEQ ID NO: 2838:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2838:

ACGTGAATCC CGTGAGGCCA ACAGTGATTT GGATAATTAC ATGGATGTTT GACTAATGGT 60  
CATTACACACC CAGATCAG 78

## (2) INFORMATION FOR SEQ ID NO: 2839:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2839:

ACTTAAAATC TCCTCTTGCC TAACTTCCAC ATTCTTATCG ATATGAATAC ACCATACGTT 60  
TTATAGATAA GTTGATGTTG ATGCATATGT 90

## (2) INFORMATION FOR SEQ ID NO: 2840:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2840:

TATATTTAGT CTGTTATACA AGGTGTATCA CAGCGGTAAT ATGCCTCTAC ATGGCCATAT 60

G 61

(2) INFORMATION FOR SEQ ID NO: 2841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2841:

GGGCCCCGGC GGCAGGGAGG AAGGGGGCAA GGGCGGCGCC AAGACCACGA CCGGCACC 58

(2) INFORMATION FOR SEQ ID NO: 2842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2842:

TGTACAGGTG CAGTTAGACC GCCTGACGGA ACGAGACGTG CAATTGCCAG CAACGCACAA 60

(2) INFORMATION FOR SEQ ID NO: 2843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2843:

AAACATGTGA AGTGATCGAG GTATGGACGG AGTAATGATC GCACAAGACA TAGCATCCCC 60

GT 62

(2) INFORMATION FOR SEQ ID NO: 2844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2844:

ACGATTTAGT TTGAATTTCT ATTAGGGTTT GGTGATTCTA CTACTTCTGA TA 52

(2) INFORMATION FOR SEQ ID NO: 2845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2845:

GATTATCACA ATTATGCAAA GTTGTCTAAT CGTTAGACCA ATTTCTGTTC AAACACCACA 60

ATC 63

(2) INFORMATION FOR SEQ ID NO: 2846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2846:

CGTTATATAA GAnCGACATG GAAGCATGAT GAAATATTGA ATACATCATA 50

(2) INFORMATION FOR SEQ ID NO: 2847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2847:

CCACAGGTGC ATCCGCCTGG TATGGAGCCG GCCAGTCTTC ACTGCTTTCA C 51

(2) INFORMATION FOR SEQ ID NO: 2848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AAAACTGTCC CAAGCTGTTT TTATTTAGAG CAACCAATCC AATTTAAACC CCCCACCATT 60  
 ATTTTAAATA ATACCATTCC AGCGAAAGCC CTTTCCAnGG TTTTGGAATA TAA 113

(2) INFORMATION FOR SEQ ID NO: 2849:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2849:

CATCTGGAAC TTTTAAATTC CAGAAGGGTT CCAGAAGGTT TCGAAATCCC TCCTAATGGG 60  
 CTCCATTAAC GGATTTTAAA TTTTAAATA ATTTAGGCC AAAAAATTAA TTTCCAGGAA 120  
 AAGTAAGTTT CCAACCCGGG TAAGAAATTA CnAA 155

(2) INFORMATION FOR SEQ ID NO: 2850:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2850:

CACAACTAA CATAGAAGGG CCATCATCAG GTGCTATTAA ATATCTACGC TAGATTGTAA 60  
 ATCA 64

(2) INFORMATION FOR SEQ ID NO: 2851:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2851:

AATTATTCAT CAATAGCTCT TTACGATTCA CAAATCTAGG TACTTTTCAG ATCT 54

(2) INFORMATION FOR SEQ ID NO: 2852:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2852:

AAGCCCCCTTT AAAGTGGGCC TTAAAGGAAC GGTGGCGAAA ATCCCCAAAT TCCGGGCA 58

(2) INFORMATION FOR SEQ ID NO: 2853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2853:

AAAGGTTTCC ATTCGGTCCC ATTAAGATTT TTTTGGAAAT TCCATGGAAG GATGGTTGGT 60

CCTTTAGGCC TGGTAGGTTA TCCTTTTTGn AGGTGGTATC CAG 103

(2) INFORMATION FOR SEQ ID NO: 2854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2854:

GGCCACGGTC ATTCCTCCAA GCCAACCAGT GGACAAGATG GGTGGAAGGC GCAGG 55

(2) INFORMATION FOR SEQ ID NO: 2855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2855:

TATTTGGCAT TCAAATAACG TAAACGGATT TTGAAGTAAT TTACATAAAG AGG 53

(2) INFORMATION FOR SEQ ID NO: 2856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2856:

ACAATTGAC AATGACTGGG ATGCTGACAC TTGATATGAA GACAATTGAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 2857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2857:

AACTGCGTTA CATGCTTTGC TTTTAACTGA ACCCAGAACA ACGGTTTCGG

50

(2) INFORMATION FOR SEQ ID NO: 2858:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2858:

CTTTnnTAnC TTCATCTCTA TTATTATTGT CCGAATTACT ACGTGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 2859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2859:

TCCAGGTCGA ATTTATTGCC AATTAGCCTC CCGGGTTAAA AGGGTGGGTG TCGGGTAAAA

60

TCGTAC

66

(2) INFORMATION FOR SEQ ID NO: 2860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear



GGTATCCAGT CCCCCGGAGG GGTGACAAAC TTCCACGCCC AGTGGGGGGA CTACCGTTTT 60  
 GGACCAAAGC CC 72

(2) INFORMATION FOR SEQ ID NO: 2861:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2861:

AGTGTCGAAC AATTAAAGAT ATTGAGTGAC AGGATTGCTT AAGGGCCGGT CGGAACAG 58

(2) INFORMATION FOR SEQ ID NO: 2862:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2862:

TTAGCGGTAA ATCCGAAGAA CTAAGAAGAC GTCAAGAAGG GGATATACGC 50

(2) INFORMATION FOR SEQ ID NO: 2863:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2863:

GCAAAAnTGA GAGCTCAAnC TGCAnNAAGC AAATCAACGA AAGATTAGGT 50

(2) INFORMATION FOR SEQ ID NO: 2864:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2864:

AACTATTCTG GATTTGTGCA GTGGCTATGG GGATGAGTGC GTTCCCCTCT TTCATGACGC 120  
 AGGCGAACGC CAGCAACGCA ACCACTGATC AATGCTGAGC CAGCTGTAGC CGCCCAGACG 180  
 5 GAACAAAATC CGCAGTGGGG GCAAGTGATG CCGGGCGTGC AnGGCGCTGA TGnCAGTTTCG 240  
 TGGCAG 246

10 (2) INFORMATION FOR SEQ ID NO: 2865:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2865:

20 ACAGATGATA CCTCTTGATC ACTTGCCAGA GATCGTCTAA GTCGTCCTTG 50

(2) INFORMATION FOR SEQ ID NO: 2866:

- (i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2866:

AATACCACGC TGACCTTAAT AAGCCATCAT GGGGGAAATC ATGACCGCAA T 51

35 (2) INFORMATION FOR SEQ ID NO: 2867:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2867:

45 CAACTTGGTA AGTGGTCGTT TTGGGCCCCA CCCTACCCGT TTGGACCTGG 50

(2) INFORMATION FOR SEQ ID NO: 2868:

- (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2868:

5      CCCAACCCGG TTCCGGGCTT TAATTTTTTn CTTTTTAAAG GAAAAAAGG AAAAACCGGT      60  
       TAATTCGGGC CCAAAAAaCC CGGAAGTTGG AAACCTTTTT TTAATAAAAA TAATGGACCG      120  
       TCCCAACCTT TGTGCCCCAA AGGTGGCCTA AAGGTTTAAA AAAAACCGTT AAAATCCATG      180  
 10      GCCAGGATCC AGCCTAAAAT TGAAACCATT ATAATTGATA AAC      223

(2) INFORMATION FOR SEQ ID NO: 2869:

(i) SEQUENCE CHARACTERISTICS:

- 15      (A) LENGTH: 66 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

20      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2869:

      TGGACCTTTG GTAATATGAA TTGAATGGTG CTTTGTGGAA ATCGGGAATT CGCCTCGTGC      60  
       CTTGTA      66

25      (2) INFORMATION FOR SEQ ID NO: 2870:

(i) SEQUENCE CHARACTERISTICS:

- 30      (A) LENGTH: 50 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

35      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2870:

      AAnAGCCaNG ATCATGGTAT ATCCATTAAG AGACGAGAAG ATCGATGCCC      50

(2) INFORMATION FOR SEQ ID NO: 2871:

40      (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

45      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2871:

50      TTATTTGGAC TTACAAGGAG AATAGTCaNT TCTAGGAAAG TGGTGCGAAA GTCACCTTACC      60  
       AATATACGGG GATTATTCAT CCATCGTCGG TCGGTCATAT GATACGGAAT TAACACGCCA      120  
       CTCCG      125

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2872:

CAACACCTGA CGTGTATAGA ACTCATCTCT TCAATAACGT CGCTGTCAGG TTACGAAGTC 60  
 GA 62

(2) INFORMATION FOR SEQ ID NO: 2873:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2873:

TATACATTCC ATTTAACACC TTAACACATG CAAGTTACTT CCTCCTCAAG CATC 54

(2) INFORMATION FOR SEQ ID NO: 2874:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2874:

GCTGAAAGGA GACTTCTGCA GGTGTGATCA CAACTGCAC ATCTACACAA GCCATT 56

(2) INFORMATION FOR SEQ ID NO: 2875:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2875:

AGCGCGACCG CGAGAAGGGA GGGGGAGCCA GAGCAGCAGC AGGCCCCAGG GCGAAACCCC 60  
 CAAGAGGAGC GAGnAAGAAG GAGGGAAAGC CCAGCAGGGG CGCCCAGGCC AG 112

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2876:

GnGCGTtnnA nCGGTCGCGT AGAGATGTCG GGTCTGTAGT AGATCTGGGG

50

(2) INFORMATION FOR SEQ ID NO: 2877:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2877:

ACCTTGACTT TGCAGACGAT GATGCTTTTG GCTGGGATCT TCACCATCTG GCAACTGAAT

60

ATGGTTGG

68

(2) INFORMATION FOR SEQ ID NO: 2878:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2878:

CTCCACCTGA TGCATGCCCC CATATCAGGA AAATGATAAC CTCGGACACC TTC

53

(2) INFORMATION FOR SEQ ID NO: 2879:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 75 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2879:

GGGAACTTTG ATCTGCCCTT GAAATCCTGA AAAATGTTTG CAAACGGGAA TGATCTTGTG

60

CCTTGCTTTG AATGA

75

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2880:

AGAGAGGCCG AGATGGCAGA TGAGATTGCC AAGGCTCAGG TCGCTCGGCC TGGTGGCGAC 60  
 ACGATCTTCG GGAAGATCAT CCGCAAGAAA TACCAGCCAA AATCATTTTT GAGGATGACC 120  
 GGTGCCTTGC TTTCCATGAC ATTTCCCCTC AAGCACCAAC ACATTTTCTG GTGATACCCA 180  
 AGAAACATAT ATCCCAGATT TCTGTGGCAG AAGATGATGA TGAAAGTCTT CTTGGACACT 240  
 TAATGATTGT TGGCAAGAAA TGTGCTGCGG ATCTGGGCCT GAATAAGGTT ATCGAnGGTG 300  
 GTGAnTGAAG TTCAGnGGTG GACATCCGTC TATCACGTTT A 341

(2) INFORMATION FOR SEQ ID NO: 2881:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2881:

GCGGTTACTG TGTAATGGCA TTAAATATGA AACGAGCCGA TGGAGCGTTG 50

(2) INFORMATION FOR SEQ ID NO: 2882:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 81 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2882:

CTCATCATTT GTAGTTGGAA AGGTTTATGT ACATTTGGAA AACACCGACA CATGACGTAT 60  
 CTCCATTGCA ATTTACACAA G 81

(2) INFORMATION FOR SEQ ID NO: 2883:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2883:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60  
TTTTTTTTTT TTTTTT 77

(2) INFORMATION FOR SEQ ID NO: 2884:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2884:

ACGGTGTGCT TGATGCACTT GGAAGTGTGA GTTTGGGTGT GACTTTGCTT TGGCTTGCTT 60  
GCTGAATGTT TTGACTATGC ATTGCGTATA TGACTTGnAG CGCG 104

(2) INFORMATION FOR SEQ ID NO: 2885:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2885:

AGCAACGTGT CTGTCAACGT GGTGTCATTG GAAAAGGCGT CATGTATTGn CCGGTGGGAT 60  
TTACGTGTAG TCACACATGT GCCCAATTAT TGTTTTGAGG CCAACTTGAG TAGGTTGATG 120  
GTTATGT 127

(2) INFORMATION FOR SEQ ID NO: 2886:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2886:

TGAGCGAGTG CTGTGTGAGC GCGAGGTTGT GAGAGTTAGA ACCTTGAG C 51

(2) INFORMATION FOR SEQ ID NO: 2887:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2887:

10 TTGAAACCGC GAACCTGAGT TCTGGTTAAC TACAGTCTGG TATACACATT GAGGGAAACT 60  
TCG 63

(2) INFORMATION FOR SEQ ID NO: 2888:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2888:

25 AGTAnCATAC nCAACTATCT CAGCATACAA TATTGGnCAC CTCGCAGCTT 50

(2) INFORMATION FOR SEQ ID NO: 2889:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2889:

AAAnATAATC CCGGTTTTAT CCCCTACCT AATTAGTGGG AAAAGTACCA ATTGCCAATT 60  
GGTAAAATAG GTTGCCATAA CGGCCTCCCA AAAGTAAATT CCCTTTTTTG GTTTA 115

40

(2) INFORMATION FOR SEQ ID NO: 2890:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2890:

AATCGGTCCG TTATACTCTT CATAATATTG TGGCGCAACC ATTTCACTT TATCTTTTCT 60  
TATAAATAGC ATCATCGCAA TAnTAAAGAA TAATATCGGA ATGATTAAAG TAACGATAAG 120

55



## (2) INFORMATION FOR SEQ ID NO: 2891:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2891:

AACACAACAA GTTGTTAAAG ATGCATTTTT ATCACAACAT AAATCTATTG GACGTAAAGC 60  
 TCAAGAAGCA TACTTATCAT ATCGTTTAGA ACAAGAGTAT AGTAAAGATG ATATCTTCCA 120  
 AGTATATCTA AACAAAATTT ACTATTCTGA TGGCGTAACA GGTATTAAAG CTGCTGCTAA 180  
 GTATTACTTT AATAAAGATT TAAAAGATTT AAACCTAGCG GAAGAAGCTT ATTTAGCCGG 240  
 TTTACCTCAG GTTCCAAACA ACTATAATAT TTATGATCAT CCAAAGCTG CTGAAGATCG 300  
 TAAAnCACT GTTTTATACT TAATGCATTA TCATAAACGC ATTACAGATA AACAGTGGGA 360  
 AGATGCTAAG AAAATCGATT TAAAAGCGAA CTTAGTAAAT 400

## (2) INFORMATION FOR SEQ ID NO: 2892:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2892:

CCTAATTAAA CCTCCATCCA TCCTTTTGAA GGGGGATCTT TAATAAnCC GGAAAGTTTG 60  
 GGGGAAAAAT CCTCCATCCT TTGAAGGGGG GGGCTTTCCA ATGGCCTTTA AGAATGGCCT 120  
 TTTCCAAGCC AACTTTTAAT TCCCCCGGT 149

## (2) INFORMATION FOR SEQ ID NO: 2893:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2893:

GCCCCAAGTA TTCTTGTAAG TATTATGATA CTCGGTnCTT TTTATGATTT ATGTTAATTT 60

TTATGTTAGT

130

## (2) INFORMATION FOR SEQ ID NO: 2894:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2894:

GATGAGACCT GAATTGATTG CAACCCAAAT CGGCATATGC AAATTGCATT AAAGTTGGTT 60  
 CAACG 65

## (2) INFORMATION FOR SEQ ID NO: 2895:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2895:

CGCACAAACAC ATTTAGCGAC TCAGATGTCG CGCGAATGGA CCGATATGGC GTGTCTACAC 60  
 ATTGTTCATAT TGTACGAATA GATGAGAAAT TnCAAAGACC GA 102

## (2) INFORMATION FOR SEQ ID NO: 2896:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2896:

ATTAAGTGAT GGGCTAATGT TTACGCCCCA ACCAAAGGTT TCCAAAGAGC CCTGTGTTGGG 60  
 CCTGTGTTG 69

## (2) INFORMATION FOR SEQ ID NO: 2897:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2897:

ATTGAATTAA TGTCCCAACC AAACGAATGG TTGCCCTTTT TCCATCCAAA GGGGGCTAAT 60  
 TGGGAAGGGT ATTGGTTCCC 80

(2) INFORMATION FOR SEQ ID NO: 2898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2898:

CAAATCCTGG AGATGAGCGT AACCAAAAT AACGTTGAGA AAATGACCAC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2899:

ATCGTGAACC TCTCATCAA TCACTCATGT GAGTGAATTG GATGACCTGA A 51

(2) INFORMATION FOR SEQ ID NO: 2900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2900:

AGCTTTCAGG GCTATATCAG ACCCACGCAT TCATCCACGT GAATGAAACA CG 52

(2) INFORMATION FOR SEQ ID NO: 2901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GGTACTGACA GAGGGACAAG GTGGAAAGGn TGCCAATGTA AGAATACGGT

50

(2) INFORMATION FOR SEQ ID NO: 2902:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2902:

TGTCTGGAAT TCAGGTGAAT TGATGCGGAG ATTTAGGTGA TTAAGGAGTG TTGATTATGA  
AGATGACCAC TT

60

72

(2) INFORMATION FOR SEQ ID NO: 2903:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2903:

CATGCCAAAG CAGTAGGCAA GCCGCTTAGC AAGCCAAAAA CGTCAGCCCA

50

(2) INFORMATION FOR SEQ ID NO: 2904:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2904:

TTGATGTTAC CTGATCGCAA TCTTGACCAC CTGGCAGGGT CTCATTGTTG GGTATCGA

58

(2) INFORMATION FOR SEQ ID NO: 2905:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2905:

GCGGTCTAT

69

## (2) INFORMATION FOR SEQ ID NO: 2906:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2906:

ATTCCATTAG GTTCAATTAA AAATTAACGG GGTATGGTT CCGGTAATTC GGG

## (2) INFORMATION FOR SEQ ID NO: 2907:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2907:

AAAGCTAAGA AAGGAGGATT AGCTGGTAGT GGAGGAATGT TAAGTGAGGC TGGTGAT

## (2) INFORMATION FOR SEQ ID NO: 2908:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 86 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2908:

GGGAATGGCG CATGAACGTG CACATCAAAT GACACTGCAG GAAATCAATT AGCACGGATA

TGGCATAAAG ACAATGGTAA AAGTGG

## (2) INFORMATION FOR SEQ ID NO: 2909:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2909:

## (2) INFORMATION FOR SEQ ID NO: 2910:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2910:

GAATTTGTTTC CGAGGTATCG AGGACTACGC TTATAAGGTG CTTACAGATA CATTTAnCAT 60  
 TAATGGCGTG TGCTGCTGTA TGGGTTATAC TGTTACAGG TTTAAGAGA 109

## (2) INFORMATION FOR SEQ ID NO: 2911:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2911:

TTGTCCCCAT AGGGAGAAAT AATTCGCCT GGGCAAACC AAATCCACGA GCTTCTAAGG 60

## (2) INFORMATION FOR SEQ ID NO: 2912:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2912:

TAGATGTATC CAGCTGACAT TAGCTATTGG TAAGGTAACG GCTTACCAGG CAACG 55

## (2) INFORMATION FOR SEQ ID NO: 2913:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2913:

GCCATGAGGC CCACCCATCC ATGTTTATGG ATGGTGGATT GGGGAATTAC TTGTTTCAAA 60

TCA

123

## (2) INFORMATION FOR SEQ ID NO: 2914:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2914:

ATCCGTAATT CTGGCCTACC AAGGGTTTAG GCCAATGGGC CATTCTTTTA TTTAACCC 58

## (2) INFORMATION FOR SEQ ID NO: 2915:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2915:

TGGTGGCACA GTGGTAGGCT TTTTACGGTn TGCnGGCGAG AGTTCTGTAG 50

## (2) INFORMATION FOR SEQ ID NO: 2916:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2916:

CTGTTACGCT ATGCCCCCA GTTGTATGTT GAGTGAATC GTGTTTTTCG ACCTGCCTTT 60  
GCTTTTTT 68

## (2) INFORMATION FOR SEQ ID NO: 2917:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2917:

GGAAA

65

(2) INFORMATION FOR SEQ ID NO: 2918:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2918:

AAATTCCAAT CCTGGGAATG GGATTCCATG GTnTTCGGAA AAATCCGCCA CCCCCAAAAA 60  
ATAAATGGGT CCCTTCCCTT GGAAATATTA CCTTTACCAG G 101

(2) INFORMATION FOR SEQ ID NO: 2919:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2919:

TAATAAATCC ATGACCACCG TCACGACGAT CTGACTGATA AACTAATGAC ATATGACTGG 60  
TGACACACC GTATG 75

(2) INFORMATION FOR SEQ ID NO: 2920:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2920:

CTTGGATTGA CCATCATTA TTTTGGTCAC TCTAAGTTGT ACTGTCCGTT GTACAA 56

(2) INFORMATION FOR SEQ ID NO: 2921:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



GCTCATTGCT TGTATATTAA TCCCTGAAAT TGACCGTGTA TATCCCGTCG ATCTATCTTG 60  
TCCTG 65

5 (2) INFORMATION FOR SEQ ID NO: 2922:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
10      (C) STRANDEDNESS: double  
        (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2922:

GCAATATTCT AATCTGTATG TTACAGCACA TGGATATAGC ACATCCGGGC 50

(2) INFORMATION FOR SEQ ID NO: 2923:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
25      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2923:

30 TGTGATTTAA CAGGATTACA CAGGTGTACC AGCCGATAGT TGATTAAGCT TCTT 54

(2) INFORMATION FOR SEQ ID NO: 2924:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
35      (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
        (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2924:

ATCCTGGGAA GTGCTGAAAA ACCACTnCAC TAAAGGCATA GGAnCCACAC 50

(2) INFORMATION FOR SEQ ID NO: 2925:

- 45 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 52 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
50      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2925:

## (2) INFORMATION FOR SEQ ID NO: 2926:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2926:

TTGGTCACAT TTATTCTCGT GTTGTGCCGT TCTTCTTCAG TACTAAAGAC AAGGTGATTG 60  
 GG 62

## (2) INFORMATION FOR SEQ ID NO: 2927:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2927:

CAAAAGGCTA TCCCACCTGA TTTGCAAAAG GAACTGGACT GCAAGGGAAG TCTCAG 56

## (2) INFORMATION FOR SEQ ID NO: 2928:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2928:

TGATCTTGCT ATTTAGTTGC GGCTTGGATT CATTTGGCAT GGTAAAGATT AAATTAGATG 60  
 CTTCAATTCAT TCAAGATTTC TTCATGTTAG CATTCCTTAC GACAATCGGT CTTGGTGAT 120  
 CATTGAAATT ATTTAAATTA GGTGGCAAAG TCTTGCTATT ATACTTTATG TTTTGTGCTA 180  
 TCATTCAGT CATTCAAAC ATAGTTGGTG TATCACTAGC AAAAGTATTA AATATTAAAC 240  
 CTTTGTTAGG ATTAACAGCA GGTTCATGT CTATGGAAGG CGGTCATGGT AATGCTGCTG 300  
 CTTATGGTAA GACAATTCAA GATTTAGGTA TTGATTCGGC ACTGACAGCG GCTCTTGCGAG 360  
 CTGCAACTTT AGGTCTTGTA TTTGGAGGGC TATCGGTGGT 400

## (2) INFORMATION FOR SEQ ID NO: 2929:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2929:

10 CTGAACCGAT GGCGCACTTT GCTACGCCAC CTACAGCAGA TCCCA<sub>n</sub>GGGG GG<sub>n</sub>GAAGCTT 60  
 ATACTGAAGC TCTACGTTCA ACATTTTTCC ATTGGGGATT CCATGCTTGG GCTGTTTATG 120  
 GTGTTGTTGC GTTACGTTTG GCATATTCGC AATTCCGTAA AGGTGAACCA GGTTTATTAT 180  
 15 CTAGAACTTT ACGTCCTCTT TTAGGTGATA AAGTAGAAGG TCCTATTGGG ATTTTTATTG 240  
 ACGTTTTATC TGTATTGCG ACAATCGTTG GGGTAGCCGT TTCGTTAGGT ATGGGTGCTC 300  
 TACAAATTAA TGGTGGTTTA CATTACTTGT TCAATGTTCC AAACAATACG TTTGTACAAG 360  
 20 CGATTATCAT CATTGTTGTT ACTATCTTAT TTATAGCAAG 400

## (2) INFORMATION FOR SEQ ID NO: 2930:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2930:

ATGTAGATCT ATATGATGAC TTTTACAAG ATCCATCATC TGTACCAGAA GATTTAAAGT 60  
 35 CTTATTCAGC ACAATTAAGA ATGATGACTC AATTGTACCA GCTTTAAAAA GTACAAGTAG 120  
 TC<sub>n</sub>AATAGC GACGGCACAA TTAAGCGTGT CATGCGTTTA ATTGATAATA TTCGCCAATA 180  
 40 CGGGCATCTT AAAGCCGATA TTTATCCTGT AAATCCTCCA AAAAGGAAAC ATGTACCTAA 240  
 ATTAGAGATT GAAGACTTTG ATTTAGATCA ACAGACTTTG GAAGGTATAT CAGCAGGAAT 300  
 TGTTCAGAT CACTTTGCCG ACATTTATGA TAATGCCTAT GA<sub>n</sub>GCAATTT TAAGAATGGA 360  
 45 AAAACGTTAC AAAGG<sub>n</sub>CCAT TGCATTTGAG TATAC<sub>n</sub>TAT 400

## (2) INFORMATION FOR SEQ ID NO: 2931:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

GGTTATACAA TCTAGAATCG CATGATAATT TAATGCTACA AATCGATAGT ACAATATATC 60  
TACCGTGAAT AACTGTGCAA ATAGTGACGT TGTAGCCGCC ATACGCATTT CATTTTCATC 120  
5 AGTTCTGCCA TAAATCAATG CATAGTCTGC AATTTGAGCC ACTGGATTAT TAGCTGTACT 180  
AGATATAGTT ATGATGGGAA TACTGTAATG TGTGGCCACC TGTGCAATTG ACTGCAATTC 240  
10 ACTATGGACT ACCTTGGATT CGTCACAAAA ATCATGCAAT CTCTATCATC ATGCGTCGCA 300  
AATGTTGACA CAAGTGAAAT GCGTTTCCAT GTAATAACCT GACATTTGAA GCCATACGAG 360  
ATAACTTTGG AAAAAGATCA CCAATAGnCC AACTCGATGG 400

(2) INFORMATION FOR SEQ ID NO: 2932:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 392 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2932:

25 CTTTCAGTAG CAGCTACAAT TGTCTTTAAC ATTTAAGTTT AAAGCTGTAT GTGTCAACCG 60  
CAAATACCGA TAGCCATTCA CTAATGAAGT TTCAACTAAT TTAGTACGAT CTGACAATAA 120  
30 CTTTTTGTA TCTTGGGCTG CTTTCAGCTGA TACAGCAATA TTTCTCATTG TTTTAACAGC 180  
TTCTTCAGGA TATAAACCAG CAGCAGTTTC ACCAGATAAC ATTACTGCAT CTGTACCATC 240  
ATAGATTGCG TTGGCAACGT CACTAGCTTC TGCACGTGTA GCACGTGGGT TACGTTGCAT 300  
35 AGAATCTAAC ATTTGTGTAG CTGTAATAAC TGGTTTACCT AATTTGTnAC ATTGTCTGAT 360  
TAAATCTTTT TGAACCATTG GGACTTTnTC AG 392

(2) INFORMATION FOR SEQ ID NO: 2933:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2933:

50 TGA CTATGGT ATCGCATGTT GTGTATCAGC GATGACAATT GGTAACAAA TGCAATTCTT 60  
CGGTGCACGT GCGAACTTAG CTAAAACATT ACTTTACGCT ATCAATGGTG GTAAAGATGA 120  
AAAATCTGGT GCACAAGTTG GTCCAAACTT CGAAGTATTA ACAGCGAGTA TTAGAATATG 180

ATTAAATGTT ATTCACTACA TGCACGATAA ATACAGCTAT GAACGTAATT GAAATGGCAT 300  
TACATGATAC AnAAATTGTA CGTACAATGG CAACAGGTAT CGCTGGTTTA TCAGTAGCAG 360  
5 CGGACTCATT ATCTGCATTh AATATGCACA AGTTnAAACC 400

(2) INFORMATION FOR SEQ ID NO: 2934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2934:

AAAATATGCC ATGACTGGCA TGACAAGAAT TGGACGTTAG AAGCATCTCA AACTGGTACG 60  
20 TTCAGAGGTC GTAACThTAA CTTCAATGGT GAAGGATTCT CACGTCAAAC ATTTAAAGTA 120  
AATGCCGTTA GTCAAAAAGA CTACGACAAA TGGTGAAAG AAGTTAAAGG TAAGAnAACG 180  
TTAGATCAAG ATACATTTGA TAAACAATTA TTACCAAGCA CACCTAATAA AGCTTTAGAA 240  
25 TTTAATGGTA CACATATGGC GTTTGTTGAT CCAGCAGCCG ATCCAGAATA CATCTTCTAT 300  
GCATATAAAC GTTTCAATTT CGGATTGAAG GTCCCAAACT TCACTAGTGA GGAAAATATG 360  
30 TTTAAGGTGT ATCAGACAAA CCCTTAATAC CTGCTCGTGA 400

(2) INFORMATION FOR SEQ ID NO: 2935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2935:

ATGGAGTATA CAACTACTTC GGCATTGGCG CTTACGACAA CAATCCTAAC TACGCAATGA 60  
45 CGTTTGCAAG GAATAAAGGT TrGACATCTC CAGCAAAAGC AATCATGGGC GGTGCTAGCT 120  
TCGTAAGAAA GGATTACATC AATAAAGGTC AAAACACATT GTACCGAATT AGATGGAATC 180  
CTAAGAATCC AGCTACCCAC CAATACGCTA CTGCTATAGA GGGTGCCAAC ATCAAGCAAG 240  
50 TACAATCGCT AAGTTATATA AACAAATCGG CTTAAAAGGT ATCTACTTCA CAAGGGGTAA 300  
ATATAAATAA AGAGGTGTGT AAATGTACCA AATAAAAGAT GTGAAACGAG AATTAAAAAT 360  
GATGGTGTTG ACTTAGGTGA CATTTGGCTG TCGTTTTACA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2936:

```

10 AAACAATACA AACAAAAGAA AGTCAACCAA GGATGGATTG CTATTTTAAT CCTTG GTTGA      60
    CTCTTATTTT ATTTAAATTG TAGAACCTAG AAAATAAAGT TTAATTAAAA GCACCAATCA      120
15 TTTCTACTTT GAAATCTAAG GTTCTAAAA TAGCAATGAC TTTCTTTATA TCGGTTGTAA      180
    TTGCAGAATC AGCCTGAACG AAAAATCGAT ACATACCTAA TTGTGTTTTT AAAGGACGAG      240
    ACTCAATCCA GGGTAAATTA ATATTAAACA AAGCAAATGT ATTAAGCACA CTTGCTAACA      300
20 ACCCGGGTTA TCATGCATTG GTGTAATTAA AAACATCAAT GGTGTCGCAT TTTGATCAAA      360
    TGCTGCTGAT TTTTATAAC TAAAAACGTG TCAGGTATGT      400
  
```

(2) INFORMATION FOR SEQ ID NO: 2937:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2937:

```

35 TTATTATCTT GATACATTGA GTGTATATTC CATTTTCCAT GAGGCGTTAA ATAACGCATA      60
    CCAAAGCATC TGTACCACCT TTAATTTTCT TATCTCTATT CCCAAATACC ATTGGCGGCA      120
    ATGTCGGTTT ATATACTGGT AAGCTCTCCC CAAATTGTTG GAAAACTTCG TGATCCACAT      180
40 AATAACTTTG GACGTCCTGT TAATGTTCTA AAAGGTACTA GACGTTCTAT ATTCGTTGTA      240
    AATGGTGGA AATCGTCGAC CTTGTTTATT TGAACCGGGG AATACTGCTG TCGGTATTAC      300
    TTCTCGTGGT TGTGGAAGTT ATATTTAAAA ACGGAAATTT TCTCAGCAGC GntTTCGTTA      360
45 GGAAATATCT TTAAACGGGC ATTCCAGTTT GTTCnTCGGG      400
  
```

(2) INFORMATION FOR SEQ ID NO: 2938:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2938:

	TATCTCTTAA AGCCGGTGAT GGTGGTAATG GTATTACCGC ATACAGAAGA GAAAAATATG	60
5	TACCATTTGG TGGACCAGCT GGCGGTGACG GTGGTAAAGG TGCTTCAGTC GTATTTGAAG	120
	TGGATGAAGG TTTAAGAACG TTATTAGATT TTAGATATCA ACGTCATTTT AAAGCAAGCA	180
	AAGGTGAAAA TGGCCAAAGT AGTAATATGC ATGGTAAAAA TGCGGAAGAT TTAGTATTAA	240
10	AAGTTCCACC TGGTACAATT ATTAAAAATG TTGAAACAGA CGAGGTTTAG CAGATCTTGT	300
	TGAAGATGGT CAAAGAGCTG TAGTAGCGAG GCGGTCGAG GTGGCCnAGG TAATTCACGT	360
15	TTTGCAACAC CTAGGAAACC CTGGCACCTG GACTTCATGG	400

(2) INFORMATION FOR SEQ ID NO: 2939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2939:

	CTAACCTCGA GTTCGTATTA TGCCCACCAC ATGTCTGCTG GCTTGTCGTA AATATTAACA	60
30	GATTTCAAAG TTTGACAAGC TTTTGGAAA CCTTCTTCTA CTGACATAAT AGGATCTTCA	120
	TGTTCAATAC TTAATACATA ATCATATCCA TTAATAATAA GTTGACTIONTAT GATATCTGCC	180
	CATACATATG GACTATGTCC TAAGCCAACT GTACGGAATG TCATGCTCTT GTCGCAACGT	240
35	TACCATATGG TTGCATATCA GTTAGACCAT ACATATTTAC ATTTTCTTGG ATTAATATAC	300
	GTATCTTTAG CATGGAAGTG ATGAATTGCA TTTGCTTGGn CTAATATGCG AATCGCAGCC	360
40	AATTGGGTCA ATAnCnTGGC CACC	384

(2) INFORMATION FOR SEQ ID NO: 2940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2940:

	TTTCATATTT TTCTATTAAT GATTCATATT GTAGGGTGAT TGCAATGTCA TCTAAGCCAT	60
55	TTACAAGTTT ATTCTTCCAA GTTTCATCAA TTTCAAATG GAAACGCTTG TCTGGTGATG	120

CACTTTTTTC TAAAACGATA GGCAACATCG CATTTTTAGT GCAATTCATA TAAAATATGT 240  
 CACTGAAACT TCCTGCAATA ATAATATGAA AACCATAGTC CTTAAGAGCC CAAGCAGCAT 300  
 5 GTTCACGACT TGAACCACAT CCAAAATTAT CTCCAGTnAT TAAATnGGAG GCCCCTTTAT 360  
 ATTGTGGTTT GTTAGGGTTG AATCAGGGTT TnTnGGAACC 400

(2) INFORMATION FOR SEQ ID NO: 2941:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 409 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2941:

20 ATCATAATCC ATCGTGCGTC CAAGAAGTAC TTGATTATTT AAAGTTTGTA TTGTGAATCC 60  
 TGTGCACATT GTTCTCACTC CTCTGTACCT TCATTTACTT TAATCACTTT CAAATAAAGC 120  
 TGTTCACATT AACATACTA TAAAAAATCA ATTATACAAG CAATTAATTG ATATTCATTC 180  
 25 TCAATAACTG TGGTATGATA TGTAAGGAAA TCATGACTTA TGTGTGAGTG AACGATCATC 240  
 TATACATCCG TTCACTTCAT CTCATGACTT TCTATATTTA ATTTTACAA GGgAGTGACA 300  
 TCTGTGAATa ACACACAATC TTCACCACGC gTaaTaTtAT TaTTGCGATT ATGTTGTCTG 360  
 30 CATAACATAT GGTTGTTGCA CAATCATTAT TAnTATAGGA CCTCCGTTG 409

(2) INFORMATION FOR SEQ ID NO: 2942:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2942:

45 ATGAAGTGTC AAAAGGTTTA AAAACATCTG AAAGGGGTTT GCACATGTTT TAAACTTTAA 60  
 AAATAAAGGT GGATGTCCAA AATGTCGACC AGCAATCAAC TATTATTTAA ACATGGTTTA 120  
 TCCACATGAT CATGAAGATG AAAGAGAATC AAGATTTGCT AACGAACGTT ACCATGCGAA 180  
 50 TATTCAAAAT GATGGTACAT TTTCTGTTAT ACCTCAAATG CGTGGGGGTG TTACAGATGC 240  
 AGACCAACTG ATTCGTCTAG GAGAAGTGGC TAAGAAATAT CATGTGCCAC TAGTTAAAGT 300  
 GACAGGTTCA CAACGTGTTG GTTTGTATGG AGTTAAAAA GAAGATTACC AAATATATGG 360



## (2) INFORMATION FOR SEQ ID NO: 2943:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2943:

```

ACCTGGAAAT GTATGTGCCA TCTCTTTAAG CCAATCAGTA TCTTGAATAC CTTTCGTTCC      60
AACTATGCAA TAATTAATCC CTGCGGCAAA GTAGTCCATG ATTGTGACTT CGTACGAATG      120
CCACCACCTA CTTCAATATC TTTGGTTGTT AATCTCCTCA ATGACTTAAT ATAATCAAAC      180
TCTCGGGCAT GCTGTGCCTT AGCACTCATC AAGTCGACGA TATGAATACG ATTCACACAT      240
TCAAATTGAC TATAGTAAGC AATACTTTCT TCAGCCGAGC GTGGACATTT TTTCTTCACT      300
ATCATATTTA CCCTCTGTTA ACCTCACACT TGTTGACCCA ATCAAATCAA TCGCTGGGCC      360
ATAATTCAAT CATTtATAA ATCCCCCTTG TATTGGCCTG      400

```

## (2) INFORMATION FOR SEQ ID NO: 2944:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2944:

```

AACAAAAGGG GTCTATCGTC AATCGTTTCT TGAATAGTGT TGAAAAAATC GGAAATAAAT      60
TGCCAGATCC TAGCGTCTTA TTCTTTTTAA TGTGTGTGGG CTTAGCCATT ATGACATGGG      120
TTATCTCATT ATTTAATGTA TCTGTTAAGC ATCCAGGTAC GCATCAAACC ATTTATATTA      180
AAAATATAAT TAGCCATGAT GGATTTCGA TGATAATGAA TGATACGATT AAAAAATTCT      240
CAGAGTTCCT AGCATTAGGC TTAGTACTAG CAGTGATGAT TGGTATTGGT GTTGCAGAGA      300
AAACAGGATA CTTCGATAAG TTAATGATTT CTGTTGTGAA TCGCGCACCA CGTTTCTAAA      360
TTTACCGCTA TAATATTAAT GGGnATTTTA GGGAGTCAGA      400

```

## (2) INFORMATION FOR SEQ ID NO: 2945:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2945:

5 ATTTTACAAG TAACGGTGCA TCACCAGATT CTAATTTAAT GTCATGCTCA GCAGCATTTT 60  
 GATAACCCAA CTTTTCAAAG TAGTCAAAAC AATGGTCTAC AACAACCGTA CTATACTCTT 120  
 GTGCTTTGGC CGCTCTTCTA CTGCTTGAAC CAAGCCACGA CCTAATTTTT GTCCACGTAA 180  
 10 TTCAGGATGA ACTGATAAAG AGGCAATCGC CAAACCATAA TACGTCTTAT CATCACTATT 240  
 AATTTCTACT TCAATTAATA AAACGTGTCC AACGACATCG TTATTTTCAT TTTTCGCTAT 300  
 TACTTCTAAT TCAAAATTAT AGCAAGGAGA TTTTCTTAAA TGGTTTACTT TCGGCACGTG 360  
 15 CCTGGCCAAC TCGTTTTTCAG GATTATCATC CAAACTTTCC 400

## (2) INFORMATION FOR SEQ ID NO: 2946:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2946:

GGAAATAATT ACTTGAGCTA GATAAGTTGA CAGCTGTGCA ATTATTTTCA GCAGCTAATT 60  
 30 GTAAAATTCG CTCTAATCTT GCTGATGAAT GTTCAGGCCC TTGACCCTCA TATGCATGAG 120  
 GTAAGAATAA TGTTAATCCT GAACGTTCTC CCCATTTTGA GCGAGAACTG AATAAGAAGT 180  
 TGTCAAAAAT CATTTGTGAC ATATTTGGCA AAATCACCAT ATTGTGCTTC CCAAATATTG 240  
 35 AAGCTTTTTT TGTTTTCCAC ATTATAGCCG TATTCAAAAC CAACTACTGC TGCTTCTGAA 300  
 GCGGAGAATT GTGTATATCA AATGTCGCTT TTTGAnCAGG AGCATGATGT AAAGGTGTAT 360  
 40 ATGTTnCACc nGTTTGCTCA TCATGTnACA CGGCAGCCGT 400

## (2) INFORMATION FOR SEQ ID NO: 2947:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2947:

50 AAGTGGCATA AAAAAATCAC ATGACGATAC ATTGTCGTCA TATGACTTTA AATATTATTC 60

55

TTCAATTGTG TCACCGATTT TTAATACATC TTCCACTTTT TCAATTCTAT TTTTGTAAAT 180  
 TTGTGAAATG TGAAGCAACG CATCTTTACC TGGGAATAGG CCTACAAACG CACCGTATTT 240  
 TTCAATACGT TTAACAGTGG CTTGGATAAG TTTGACCTAC TTCCGCTTCA CGTGTAATTT 300  
 CCTCAATGAT TTCACGAGCA CGATTATCA TAGCTTGATC AACAGCACCC ATAAAGATAG 360  
 TACCATCCTG GnCCATATCh AATTTAACAC CnGGnTCCTC 400

(2) INFORMATION FOR SEQ ID NO: 2948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2948:

TTTTTCAAGT TTTGCTGAAG GCTTTACACA AGGCTATTTA ACAATGGATG CCATTGCAGC 60  
 AATTGCTTTT TCAATGATTG TTGTTAATGC AGTAAACTA ACAGGCATTA CTAAAACAAA 120  
 TCAAATATTC AAACAAACTT TGA CTGCTGG TTTAATTGCA GCCGTAGCTT TAATTTTCAT 180  
 ATATATTTCA TTAGGTTATA TTGGTAATCA TATGCCAGTA AGTGACATGA CGTTAGATCA 240  
 ATTGAAATCC AAAGATCGAA ACATTGGGAC ATATTTATTA ACGACAATGG CTTCAACAGG 300  
 ATTTGGTCAT CCGGAAAATA TTATTGGGCA TCATTGTGGC GCTGGCATGC TAACTACAGC 360  
 ATGCGGGCTA TGGTGCA GTT CCTGAATATT CCATAGATCG 400

(2) INFORMATION FOR SEQ ID NO: 2949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2949:

CATGGCTTCA GATTGTTTGA ATTGAATGGA CAATTTTGGn TTCTGTCCAA AATTCTTACA 60  
 AAATCTTCTA CCGATAAACT ATCAAGTTCA ACTCTAATCG GAAAAACGAC CTTGCAATTC 120  
 TGGTATCAAG TCACTCGGCT TAGATACATG GnAAGCTCCA GCACCTATAA ACAGCATATG 180  
 TTCAGTATTC ACAGTACCAT ATTTGGTTTG AATAACGCTA CCTTCAAGTA TAGGTAAAT 240  
 ATCTCTTTGA ACACCTTGTC TTGAGACATC TTGACCACTA TTATGATTAT TCGTCGCAAC 300

GTTAGCGCTT TCTTGATCAn TTAGTTCATC CGCATAACTA

400

(2) INFORMATION FOR SEQ ID NO: 2950:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2950:

15	TTGACTTTGT AACTAAACTA CTCACTCGAC CGACTCAACT GTTTAAATGT TTCAGATGGT	60
	TTAACTCTAA ATACTACGTA TAAATCACCA GCAGGTCCTC CATTACAGCC TGGAGAGCCT	120
	TCACCAGCTA ATCTAATTTG TTGTTTCATTG TCGACACCTT CAGGTACTTT CACTTCTAAT	180
20	TTAACTGTTT TATTTTCAGT ACCTTTTCCG TGACATGTTG GACAAGCTTC TTCAAATTCT	240
	TGACCACTTC CATTACATTT AGGACAAACT TGTTTCAGTAC GAACTCTACC TAAAATTGTG	300
	TTTTGTTCTA CAGCTACATG ACCAGCGCCA TTACAGTAAC TACAAGTCTT TTTACTTGTT	360
25	CCAGGCTTTG CACCATCACC ATGACATGTT TCGCATGTnA	400

(2) INFORMATION FOR SEQ ID NO: 2951:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2951:

	CAATGATTTT AAAAGATGCA ATAAAACCAA ACTTAGTACA ATCAATTGAA GGGACACCTG	60
40	CATTAGTTCA TGGTGGACCA TTTGCGAATA TCGCACACGG TTGTAACTCA ATTTTAGCAA	120
	CTGAAACAGC ACGTGATTTA GCTGATATCG TTGTAACGGA AGCTGGATTT GGTTCAGACT	180
	TAGGCGCTGA AAAATTCATG GACATTAAAG CGCGTGAACA GGATTGATC CGGCAGCTGT	240
45	CGTTGTTGTT GCGACAATTC GTGCGTTAAA AATGCATGGT GGTGTAGCGA AAGATAATTT	300
	AAAAGAAGAA AATGTAGAAG CAGTAAAAAG CAGGAATGGT TAATTTAGAG CGTCATGTTA	360
50	ATAATATTAA CAATTCCGTG TAGAnCCGGT TGTTGCCATA	400

(2) INFORMATION FOR SEQ ID NO: 2952:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2952:

TCAAGTAGCA AAAGAAACAG GTGCTTCAGT TATCGGTATT GATATTGGTC CACAAGCCGT	60
10 TGACCTAGGG CGCAGAATCG TTAACGTCTT AGCACCAAAT GAAGATATAA CAATTACGGA	120
TCAAAAGGTA TCTGAACTTA AAGATATCAA AGATGTGACG CATATCATAT TCAGCCGACA	180
ATTCCCTTTAA AGTACAGCAT TTTAGAAGAA TTATATGATT TAACAAATGA AAATGTCCGT	240
15 AGTTGCAATG CGCTTTGGTG ATGGCATCAA AGCAATATTT AATTATCCGA AGAAACAGCG	300
GAAGATAAGT GGGCCATGTG TGAATAAACA TATGAGACCA CAGCAAATTT TTGATATAGC	360
ACTTnATnAA AnAGCCGGCT ATAAAGTnGG TATTACGGAT	400

20

(2) INFORMATION FOR SEQ ID NO: 2953:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2953:

CGCAATTCAC AATAACATTA AATAATTTTT GGTCTCATAT TTTCAAAAAA CATACTGTTA	60
TTATCCCATG GgTTAAAAA TATCATTAGT ATATAAACGA AACACTTTAC GATAAATGAT	120
35 ATCTGCAAGC CAAGCTGTTA CAAATGGTAC AACAAAGAAC GCTACTACAA TTAGTAAGAC	180
ACTCAACCAA GCAGAATCAA CCTCCATAAA TTTAAATGCA TTAATCGGTC CTACCATTCC	240
TATAAAACCA AATCCAGCTG ACTCTTTCGT TCCATGAATA CCTACTAATG CTGATACCAA	300
40 ACCTGATACA ATGGCTGTCTG TAnGGGCGGG GnGCATAAGA ATTGGATATT TCACCATATT	360
AGGTATCATC ATTTTAACGC CTCCAAAGAA GACCGGATAA	400

45

(2) INFORMATION FOR SEQ ID NO: 2954:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2954:

AACACTTTAA TGGAGATTTA GCAGGCACTG TTACACTGAC AGCAGGTTTA GGTGGTATGG 120  
 GTGGTGCGCA ACCGTTAGCA ATTACTATGA ATCATGGGGT AGCAATTTGC GTGGATGTTG 180  
 5 ATGAAACACG TGTTGATAAG CGAATTGATA CGAAATACTG TGATGTTAAA ACAGCTGATT 240  
 TAGATGAAGC ATTAAAATTA GCAGAAGAGG CGAAAGAACG TGGGAGAAGG ATTATCAATC 300  
 10 GGGTTAATTT GGAAATGCTG TAGACATCCC ATCCAAGCGG ATTCTAGGAA AAAGGGTTTT 360  
 AAAATTGGAC ATTAATTACT GGnCCCAAAC CAAGTGCCCC 400

## (2) INFORMATION FOR SEQ ID NO: 2955:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2955:

TTCAGAATAC GAGCAATGTC AGTTGCAGTG TTTAATAAAT TTTGTTGCT ATTTTGTAGG 60  
 25 CATCTTCTAA AGTGCTAGGT GAAGAGATTA TAGAATAGGC ACTATCAATA CCGAAATCGT 120  
 AAACATGTTG ATAATTTTCG CCTAGACTGC CACAAATCGC GATGACAGGA ATATGATATT 180  
 30 GTTTTGCAAG TAACGCAACG CCTACGGGTG TTTTACCAA GATGGTCTGA TAATCCATGC 240  
 GTCCTTCTCC AGTAATAACG AGGTCTGCAT CTTTAATTCT TTGATGAAA TCTGTAATGT 300  
 CAAAGACGAC ATCAATACCT TTTGTTAAAG TTGTCTCACA AAACGnTAAT AATGCTGCGG 360  
 35 CCATACCGnC AGTGCACCAG AACCTGGTAT TTGGTTnACG 400

## (2) INFORMATION FOR SEQ ID NO: 2956:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2956:

AATACGTCCT TTATATAATG TTAATAACCA GTTAAACAAT TTCACACCAG TTGAATACC 60  
 50 AATCAGCATT GTTGAAATTG AGAAGAATGA GTTGATTAAC GCACCATTAC CCATTGTGAA 120  
 GAAATGGTGA ACCCAAATA AGAACTAAG GAACGCGATA CCGGCAGTTG CCCATACCAT 180  
 ACTTTGATGT CCGAATAAAC GCTTACGAGC GAATGTCGGG GATAATTTCT GAGTAAATAC 240

CCAAAGCATT GGGCATACCG CCATGTGGCA CTGTGGAAGA ATGCTGTGTC CAATATTCCG 360  
 nTCATTGGTn CATTAAATGGC TAACGCTAAC GGTTTAAAGG 400

(2) INFORMATION FOR SEQ ID NO: 2957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2957:

TAGTAATTAA TACGATGTCA GCACCTACTG ATTTTGCTTT GTCTGCTAAT AATCTTAAAT 60  
 GTTCCGTGGA CCTGAACCAG AGATAATTAC AAATACATCA TTCGACTTAA TCGCAGGTGT 120  
 CGTTGATTCT CCAACAACAT GTGCCTGTTT GCCGAGCTGA TTTAAGCGCA TTGCAAAACT 180  
 ATTCGCCACG AATCCTGGAA CGTCCTTTGC CAGCTACAAA TATATGTTCA GCATGTAGTA 240  
 TTTTGGGATG CAAAAGTTGG AAAACTCCAT CCGnTTCAAC ATGTGACAAA GTCATCTTTG 300  
 AATTCATCTA GAnTTAATTG ATAGTCACTA AnTTTAGCCA TATTACTTAC CTTCGGTTGC 360  
 CAGCGCGACC ATTGTTTCGC AGCTTCTTAC TGGG 394

(2) INFORMATION FOR SEQ ID NO: 2958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2958:

AATTATTCTA CCTATAATTA AAAATGCTGG CAAAGGTGTA ATGATGATGA GTAATGAACC 60  
 TACAACATTT AATATCAATC CTACATAAGT AATTTTGACG CGACCAAATT TATCAGCAAC 120  
 ATCACCAGCA CCTACGATAA ACAAACCAGC AAATAAGGCA GATAAGCTAA CAGCGATTAT 180  
 TTATCGTTCC AACGTCCTA CTATATGTTG ATTGTAATGG GACAACAAGA TTAACAAGTG 240  
 ACTGCGCGAA TAGCCAAAAG GTAATAACCC CTAAAACGAT ACCCAAAnGC AATCGGTTGT 300  
 TCACCTCTTA AATTGTTTTG ATGTGTCCnT GGATTAGGAT AAGCCTCCTA TGTTTAGGAA 360  
 AAACAATTTT TAATATGGTA TATTAAGGAn ACATTTTCCTT 400

(2) INFORMATION FOR SEQ ID NO: 2959:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2959:

10 CTTCTTTCTC AACATCAAAG AACATATGGT TTTGTTTCAA ATATTCTTTT ACTAGCGCGA 60  
 TATGTTTCGTC TGATCTACCA GTTAACTTCA TATATTTAAG AGATTCATCA TCAACTGGGA 120  
 AGAATCCGCA AGTTGCTCCA TACTCTGGTG CCATGTTTGC AATTGTAGCA CGGTCTGCTA 180  
 15 GTGGTAAATG TTGTACACCT GGACCAAAGA ACTCCACAAA TTTACCAACA ACACCTTTTT 240  
 TACGTGGCTC TTGAGTTACT CTTAACGCTA AATCAGTTGC TGTTCGCGCT TGTGGTAATG 300  
 AATTTACTAG TCGTACACCA TTAACCTCTG GAATTGGGGA AATAGGAGGG TTGTCCAGGC 360  
 20 ATTCCAGCTT CAGTTTCAAT ACCACCAACA nCCCTCCTAG 400

## (2) INFORMATION FOR SEQ ID NO: 2960:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2960:

ACGTCAAATG TAATCACAAT CGGAAAGTAT CGTGACAATG CATATATAAC AGGGAGGGTT 60  
 35 TAAATATGAG TTAATAAGGG GATTTTTAGA TTTAGGTGCA CTGTTTATTT TACCGGTTGT 120  
 CATATTCTTG CTGGCCTAT TCTTTAGGCA GAAAATTGGA GCGGCATTTA GGTCTGGTTT 180  
 AACAATAGGT GTGGCTTTTG TAGGGATTTT CTTAGTCATC GATTTATTAG TTAAAAATTT 240  
 40 AGGGCCAGCA GCACAAGCGA TGGTTAAAAA TTTAGGCGTC AnTCTGAATG TGGATTGATG 300  
 TAGGTTGGCC AGCAACATCA TCTATCGCTT GGGCATCATC TGThCGChCC ATTTTATTAT 360  
 TCCACTCGGG ATTCATAGTT 380

45

## (2) INFORMATION FOR SEQ ID NO: 2961:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55



GGCCATTGGT CGAACTTACG AAGAATCATT GTTAAAAGCA ATTCGATCAC TTGAGTATGG 60  
 TGTGCATCAC TTAGGATTAC CAAATGGTGA AAGCnTCGAT CTTGATTATA TTAAAGAACG 120  
 5 TATTTACACAC CAAGATGATG GACGATTATT TTTCATCGGC GAACAATTAG AAGAGGCACA 180  
 ACAGTAGAAG AAATTCATAA TATGACTCAG ATTGATTACT TCTTCTTACA CAAGTTCCAA 240  
 10 AACATTATTG ATATTGAGCA TCAATTAAAA GAGCATCAAG GTGATTTAGA ATATCTTAAA 300  
 TATGChAAAAG ATTATGGnTT TAGTGGTAAA ACAATAGCGC ATCGCCTTAA TATGACGG 358

## (2) INFORMATION FOR SEQ ID NO: 2962:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 364 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2962:

TTTGGGCATC ATTAGGAAAA TTCTTTGAGC AACTTTAGTG TCTACTGGGT AATACAATTT 60  
 25 TATCACCATG TTTTCTAAT AAATCTTTTG CGAATCGATT TTATCTTCTT CTAATAATGA 120  
 AATACCAATT TCTTTACCTT GCGCTTTTAA GAAAGTATAA GCCATACCTC CGCCGATGAT 180  
 AATTTTATCA GCTATGTTAA CTAAGTTTTT GATGACATTA ATTTTGTCAG ATACTTTTGN 240  
 30 GnCACCATAA ATAGCAACAA CTGGTTTATG TGGATCGTTA ACTACGCCGC CAATAAACTT 300  
 AATTTCTTTA TCCATTAAGA ATCCAGCTGC AGTTTCTAAA TGTGTAGAAA TACCAACATT 360  
 35 ATn 364

## (2) INFORMATION FOR SEQ ID NO: 2963:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2963:

GTTGATTTCT TGAAAGATAA TAAAAAATTC AAAGAAATGG GATCTAGGAT TCCTAAAGGT 60  
 GTCTTACTTG TTGGACCTCC AGGTACTGTT AGAAACATTA CTTGCTAGAG CGGTTGCAGG 120  
 50 TGAAGCTGGC GCACCATTCT TCTCTATTAG TGGTTCAGAC TTTGTAGAGA TGTTTGTGG 180  
 TGTGGGTGCG AGCCGTGTTT GTGACTTATT CGATAATGCT AAGAAAAACG CGCCTTGTAT 240

TCATGATGAA CGTGGAACAA ACCCTAAACC AnTATTAGTT GAAngGATGG TTTnCGGTGG 360  
 AAAATGAAGG TG 372

(2) INFORMATION FOR SEQ ID NO: 2964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2964:

TTAGCAGAAC GCCCACAAAA CCTATCTCTT GCTGTAAAAG AATTTGTGAA nCTGCTGGCT 60  
 TAAAACGTGT TGGCATAATT GCAGCTTTAG GAGCTACAGT TATGTTAGGT TTAAGTACAA 120  
 TTAAAAAATT ATGCCGTAAA TAGAGCAAGA CATAACAAT AATTTAGGAG TCTGGAACAA 180  
 TAATCAATGT TCTAGGCTCC TAAATGTTAT ATTGGCAGTT CTGAAACATT TATAAATCTT 240  
 TGATTATGAA CTCACAACAG TGCTCTATGC TTTTATAGAT TTTAATAAAT TAGCCATTTT 300  
 AATTGCACTT ACTGCTGCTT CACACCCTTT ATTGCCAGCT TTCGnACCTG CnCCTTCCAC 360  
 AGCTGGGCAA TACTGCCAGC CG 382

(2) INFORMATION FOR SEQ ID NO: 2965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2965:

GGGAATCATA CAATCATTAC CAATAAACAT GTTACTTATC ACATGAAAGT CGGTGATGAA 60  
 ATCAAAGCAC ATCCTAATGG TTTTATAAT AACGGTGGTG GACTTTATAA AGTTACTAAG 120  
 ATTGTAGATT ATCCTGGTAA AGAAGATATT GCGGTCGTAC AAGTTGAAGA AAAATCAACG 180  
 CAACCAAAG GTAGAAAATT CAAAGATTTC ACTAGCAAAT TTAATATAGC ATCAGAAGCT 240  
 AAAGAAAATG AACCTATATC AGTCATTGGT TATCCAAATC CTAATGGAAA TAAACTACAA 300  
 ATGTATGAAT CAACTGGTAA AGTACTATCA GTGAATGGAA ATATAGTGAC ATCTGATGCG 360  
 GTTGTCCAAC CTGGCAGCTC TGGTTCACCT ATATTAAATA 400

(2) INFORMATION FOR SEQ ID NO: 2966:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2966:

10 TGGGGATTCA CAGGCTAATA CATTTGACTT TATTAGCTGG TGGCGGTAAC GCGCTGAAC 60  
 TTAAATGCG ATTCAAAGTG CTGCAATTAT AAGTGCATT CCATTCTCCT TTGTCGTCAT 120  
 ACTCATGATG GTAAGTTTCT ACAAGGATGC GAACCAGGAA CGTAAATTCC TAGGTTTAAAC 180  
 15 ATTGACTCCG AATAACATC GCTTACAAGA ATATATCAAG AGTCAACAAG AAGTTATGAA 240  
 TCTGACATTC TTGAAAAGCG TCAGTCACGT GAAATATAGA GAAAAAAGAT AACTAATAAA 300  
 GTTTAGTTAA GTATTTTAAAT AACAAAGTAGT ATGTCATTCT AGTAGCTAGA ACGGTnATAC 360  
 20 TACTTGnTG TTTTGTGGA AATTGAGTAT TTCAAAGGTT 400

## (2) INFORMATION FOR SEQ ID NO: 2967:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2967:

ACGAGGAATT AGTGAAGTAC AATATTATCG GTGGTTTTGA TTTAGGTGTT GTTTCAGACG 60  
 35 ACTTTAAAAA TCACATGTTA ATAGCTGTAA CTGAATTAAG AACAAAAGAT GAAATCGATA 120  
 CATTTGTAGA AAAGGCTGGT GAGTTAAATG ACTAGTAAAT CAAGTCCATT AATTTTGTAA 180  
 AGATCTCGTG AAGGCAGATA TGCATATTCA TTACCAGAAA GTGATATTAA AACAAATTCT 240  
 40 GTTGAGTCAT TGTTAGATGA TAAATTTATT CGTAAAAACA AAGCGGAGTT TCCTGnAGTT 300  
 GCTGGAAC TA GACTTnGTAC GTCATTAATC CTGGACCTTT CCAAATAAAA AATTCCGGnG 360  
 GTAGACACCG GGTTTAACCC ATGGGGT 387

45

## (2) INFORMATION FOR SEQ ID NO: 2968:

## (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 806 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

AACAAAGTGCA AGTGAGTCAA CATCAGAAAG TCGGTCAACA TCACTCAGTG ACTCAACAAG 60  
 TACAAGTAAC TCAGGATCAG CAAGTACGTC AACATCGcTC AgTAACTCAG CAAGCGCAAG 120  
 5 TGAATCCGAT TTGTCGTCAA CATCTTTAAG TGATTCAACA TCTGCGTCAA TGCAAAGCAG 180  
 TGAATCCGAT TCACAAAGCA CATCAGCATC ATTAAGTGAT TCGCTAAGTA CATCAACTTC 240  
 10 AAACCGCATG TCGACCATTG CAAGTTTATC TACATCGGTA AGTACATCAG AGTCTGGCTC 300  
 AACATCAGAA AGTACAAGTG AATCCGATTC AACATCAACA TCATTAAGCG ATTCACAAAG 360  
 CACATCAAGA AGTACAAGTG CATCAGGATC AGCAAGTACA TCAACATCAA CAAGTGACTC 420  
 15 TCGTAGTACA TCAGCTTCAA CTAGTACTTC GATGCGTACA AGTACTAGTG ATTCACAAAG 480  
 TATGTCGCTT TCGACAAGTA CATCAACAAG TATGAGTGAT TCAACGTCAT TATCTGATAG 540  
 TGTTAGTGAT TCAACATCAG ACTCAACAAG TGCAGTACA TCTGGTTCGA TGAGTGTGTC 600  
 20 TATATCGTTA AGTGATTGCA CAAGTACATC AACATCGGCT AGTGAAGTAA TGAGCGCAAG 660  
 CATATCTGAT TCACAAAGTA TGTCAGAATC TGTAAATGAT TCAGAAAGTG TAAGTGAATC 720  
 TAATTCTGAA AGTGACTCTA AATCGATGAG TGGCTCAACA AGTGTCAAGT ATTCTGGCTC 780  
 25 ATTGAGCGTC TCAACGTCAT TAAGAA 806

## (2) INFORMATION FOR SEQ ID NO: 2969:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2969:

ACCATCTACT CCGTTAATAG TTACACTGTT ATCATTGGTG TTTGGACTTT CAGCCCTTGC 60  
 40 ATCTAAAAAT ATAAGCTGAT TAAATCTGT TATTACTTCT TCCTTGTAAC CATCTATGAT 120  
 TTTTACAAAA GATTGCATTA ATTAGTCAAA CCTCCCATAT AATTATTTGC ATTTGCTCTA 180  
 45 TGCCCACTTT GTTTTGACAA TATTTTCT AAACCTCTAA TTGCATCATT AGAACCTAAG 240  
 GATTATCCTG AGAAGAAACA GTTGAATCA ACGCATCTGT TAATTnATTn CCTTTATCAC 300  
 TTAACATAAC AATTGGTTC AACAAATTn CAACTGTAGAA GTATCATTAT T 351

## 50 (2) INFORMATION FOR SEQ ID NO: 2970:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2970:

AGTGCTTGAT GAATTTTGAC CACAAATTC AATGTATCAG GCGTTTCTTT TATCCATTTT 60  
 AATATATTTT TTTCCGGTTG TATCGCATAG TATGTCGCAT CTAATTCGAC AACCGGAAAA 120  
 TGTCCAGCAT ATGTTTAAAG TTTATCGGTT TGGCGTTCTA AATCTTCATA TAATGAATAG 180  
 TGATCACCCC AACCTGTTAA TCCGATGTTT ATCATATATA TCACCAATGT CATCATACCA 240  
 TATAACTTTT ATCATAATCA TTTCAGCGAA CTTTAGTTTG ATGTTTTTGC TTGATTAAAA 300  
 TCTTTTCGGC GAnCCTCAGC TTGATGTTTT TCGTTGATTA AATGGTAAAT AGnnACGCA 359

## (2) INFORMATION FOR SEQ ID NO: 2971:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2971:

CAGACGGTCA AGAATCTTAT ACTTATCAAA ATTTATACTG TGAAGCGAGT CTATTGGCTA 60  
 AAAGACTCAA GGCTTATCAA CAATCTCGTG TTGGGCTATA CATAGATAAT TCGATTCAAT 120  
 CGATCATTTT AATACATGCA TGTTGGTTGG CAAATATTGA AATTGCGATG ATTAATACAA 180  
 GGTGACACC TAATGAGATG ACGAATCAGA TGAAGTCAAT CGATGTACAA TTGATTTTTT 240  
 GTACCTTGCC ACTGGAATTA CAGGGTTTCA AATTGTATCG CTGGGTGATA TTGAATTCGC 300  
 TGGAGGGATA TTACAnCGAn CAGTTGTTGG GCAACACAAT GGGTATCCAT TTGAACCATC 360  
 GGATGnAACT TTGTGCCGAA GGTCGCCTCC ACATnTAATG 400

## (2) INFORMATION FOR SEQ ID NO: 2972:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2972:

TCAACCGCTT TACAGCCAAC CGGCGACGCT GACATGGATC GCCTGGCCCA TGCCCACGCC 60  
 TTGGCGCCAT CATTATTAAT TGCTGCAGTT ACGGTATCTT TAATTGCGTT AAATAAACCT 120

AAATCACCGA AATGTTATTC GCTTAACGTT TTGTTGTTGT TATTTTAAAA TAAATTTGAT 240  
 GCAATTAGTT TGTTTATCCG CACAACATCT TATAATGTAC TTAAGTGTAT TTAAAGAGA 300  
 5 AAAGAAATAC AGTTAGGCAT TCAAACTGT ATTTAACACA ATTAAGTTGC CTGAATTCGT 360  
 ATTTAAGTCT TATTGAACCT TTTnAGATA An 392

(2) INFORMATION FOR SEQ ID NO: 2973:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2973:

20 ATTGCAATGA TAGCAATCGG AATCGCACCT GCTAAAATAA ACGTTGTGCC ATCCGTCGCA 60  
 TTTGTACCAC GAATCACAAT GTCACCAAGC GTAGGTGCTC CTATAAATGA TCCAACGGCA 120  
 ACAACACCTA TCGCAACAAC CAAGGCAATA CGAATGCCAC CGATAATAAC CGAAACAGAT 180  
 25 AACGGTAATT CAATCATTCT TAGCACTTGA TTGCGTGTCA TTCCCATACC TTTGCCAGCA 240  
 TCCTTAATAT TCGCATCAAC ACTAGCTATA CCAGTATAAG TGTTTTTATA ATTGGAAGTA 300  
 ACGCATATAA AAACACTGTT AAAGTACTGT TCTGAnCTAG CCTGACTACA TTAAATAGTn 360  
 30 ACATTGCATG ACTGGACTGn TGGATATATT GCATGGATnC 400

(2) INFORMATION FOR SEQ ID NO: 2974:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2974:

GTATTCCTTA GGTAATGCAA CTTTAAATCC TTTAATATCT TTACCAATTT CAGATGTAAA 60  
 45 GTCTACATCA TCAACTGGTG CACTTGTAGA GTCATTAACA TCTGCACCAG AAATAGCTTC 120  
 TAATACGATT GCATTATCTT TTACATTTCT AGTCAATGGA CCAATTTGGT CTAATGAAGA 180  
 TGCAAAAGCA ACTAATCCAA ATCGAGATAC ACGACCGTAT GTTGGTTTCA TACCGACAAC 240  
 50 GCCACAATAT GGCAGCCGGT TGTCTAATTG AACCACCTGT GTCTGGAACC TAAGCTAAAT 300  
 GGTACTAAGC CAGCTGCAAC TGCTGCTGCA GATTCCACCT GAnGGAACCA CCTGGGCACG 360

## (2) INFORMATION FOR SEQ ID NO: 2975:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2975:

GAGATCGCGG GTTCGATTCC CGTCGAGACC GTACAAATGC CTATCCAAGA GATAGTTTTG 60  
 TnTTGCGTTT AATATTATAT TAATAAAAGA TATATGGACG AATGATAATC ATATTGATTT 120  
 ATCTGTTTCGT CCATTTTCTT TAAAATGTAT GAACCTCAAG TAACTTAGTG GTTGGATATG 180  
 AAAGATAAAC GTnGACAATA AAATCTTTAT TAGACGTACA AACATATGCT ACTGTCAACA 240  
 TATTTCTTCG TTGTGATATG CCACCAGTCC TCCATAACAT CAATTGTTAA AGTAACGAAT 300  
 AACGAATAAT GATATTTnAT TTCTGAGCCA TGACGTGCCA CTAGAAGTTG CCCATTATCC 360  
 T 361

## (2) INFORMATION FOR SEQ ID NO: 2976:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2976:

TGCTGCTTCT GAAGCGGAGT AATTGTGTAT ATCAAATGTC GCTTTTTGAT CAGGAACATG 60  
 ATGTAAAGGT GTATATGTTT CACCTGTTTG CTCATCATGT AACACGGCAT GCCTATGACT 120  
 GAATGTACCA CGTTCACTAT CTTGACCAGT TAAGCGAATC GGTGTACCAT CTTGTAAAAT 180  
 TGTCGCAAAT GCAAGTnGTT CTGCTTGTC CCAATCAACT AAACCATCTT CTTTATTAAA 240  
 CGGCTCATGA CGCTTCTCAA GAACTTTGTT TAACTTTTTn CAAAATGTTA AAGCCATCCG 300  
 GATATGTTAA CAATGCATCA TTATTTCTTT CAAGTGATCC AAAAGTAAAG GnTTGT 356

## (2) INFORMATION FOR SEQ ID NO: 2977:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2977:

CTTTAGAGCG ACACCTAGTC ACTGCAGCAA GCTATTTCTT TATTTGCTAT GCTATAnATC 60  
 5 GTTAATTACT AGACCTATTG CTGGTAGATT GATGGATGAT AAAAATGAAA ATATTATTGT 120  
 CTACCCAGCA TTTATCATGC TTTTCCTTTC ATTTGTATGC TTAATTTCAA GCTATCAAAG 180  
 CTGGTTAATA TTAATTGCTG GTGCTTGCCCT AGGTTTAGGG TATGGAAATT TATCATCTGC 240  
 10 AATGCAATCT ATTGCGATAA AAGTCTCACC CCCGATTAAA TATGGTATCG CGACATCTAC 300  
 TTTTACGTT GGTCTAGATG CCAGGTGTCG GCTTCGGTCC AGCATTCCTT GGGTTAnTTA 360  
 15 CGCAGnGTTT T 371

## (2) INFORMATION FOR SEQ ID NO: 2978:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2978:

TTGTAATTTT ATGATTACAC CTCAATTGTT CTTGTTGTTA AAACCTCAATA TTTAATTGTC 60  
 TGCGCTCAAT AATTGTGTTGT TTAAGTTGCT CAATATGATT TGATTGGAAT TCTTCCAATA 120  
 30 ATGCTTTTGC TATTTCAAAT GCTACGACAT GTTCGCAGAC GATACTTGCT GCAGGAACAG 180  
 CACAACTATC AGAACGTTCA ATTGTTGCTT TAAAGTCTTC TTTAGTATTA ATGTCTACTG 240  
 AATTTAATGG nTTATATAAC GTTGGAATTG GnTTCATTAC ACCATTACGA TAATTGGCAT 300  
 35 CCATTGACAT ACCGCCTCTA ACCACCTAAG TGATTAGAnC ACCATAATAC CAATTCACTA 360  
 TATAT 365

## (2) INFORMATION FOR SEQ ID NO: 2979:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2979:

TGATTATATA AATCTAACCA GCCAAGTTTC GTCTGCGGTG AGACATTGAC ATTAATTGCT 60  
 GCAGATAATG ATTAAACAAC ATGTGTGGCA TGTGATTCAT TAACGATGAC AATATCATGT 120



TGGCGATGGG TAACATTGTT AACATTGCTT CATTTAAAAC GATATCGAAT TGATTGTCAT 240  
 CAAAGGGCAA TTAAACAGCA TTCGCTTGTT GAACTTGAAT ATATGATTCA nGACCTGCTG 300  
 5 CGGAAATGTT TTCCGTGCTT TTTCTAAGCC TTChTATTAT ATCAACGCCT GAnGTGACAC 360  
 CAnAGTGTGA GCCAGATAAA TAGAGGTGTG CACAGATACA 400

## (2) INFORMATION FOR SEQ ID NO: 2980:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2980:

TTTCTGCTTT TGATAATCTT TCATCAATGC AAAAGCTACA TTGGACAGTC CTATAATGGA 60  
 AATAATGTTT ACAATTGCCA TTAAGCCCAT AAATAAGTCT GCCGTATTCC ATACTGTTTC 120  
 TGTTTTTACA ACTGCACCGA CAAAGACAAG TACTACAACA AGACATCTAA AGATAAATAA 180  
 25 TATTACACGG TTTGTTGATA AAAATTCAAT ATTAGATTGA CCGTAATAGT AATTACCTAC 240  
 AACAGATGAA AATGCAAACA GTGnAACGCT TATTGGTTAA GAAAATACCT CCAGCAGAAC 300  
 CTAAATGCTC CTTAAGTGCC GATTGGGTAA CTGCAACACC nTGGAGGGCG TTTATCACCA 360  
 30 AATTTnCGTC CCGAATATAG TAAA 384

## (2) INFORMATION FOR SEQ ID NO: 2981:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2981:

AATTCTAACG ATATCACCAT TTTTACAACC ACGTTCTCTA AGCGCATCAT CAATACCCAT 60  
 45 CGAACGCATT TGACGAGCAA ATCGACGTAC TGCTGGATCA CTGTTAAAGT CAGTCATTTT 120  
 AAACATTCTT TCAATAGCAT TACCACTTAC CACATAAGCA CCATCATCAT CTCTTGGAAG 180  
 TTGTAAATTT ATCTTGTGAC GGTGTATGTT TATATAATAC TCGGTTAATG CCAACTGACT 240  
 50 CCTCTTCTTC AACTGTGGAG TCAACATCTT TATATTCTTC TGAATTTATC TGCTTATTGC 300  
 ATATGAATAA TTGnnCAATG ATTATCACGC GTTATTGTTG GAAACTGGGA TTAAGTGGCA 360

## (2) INFORMATION FOR SEQ ID NO: 2982:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2982:

CCTCAACCGC TTTACAGCCA ACCGGCGAGC GCTGnACATG GATCGCCTGG CCCATGCCCCA 60  
 CGCCTTGGGC nCATCATTAT TAATTGCTGC AGTTACGGTA TCTTTAATTG CGTTAAATAA 120  
 ACCTTCCATT GAAAACACTC CTTAAATTTT AAATTTGAAG ATAACAAAAA CGTGCGTACT 180  
 TTnTGAAATC ACCGAAATGT TATTCGCTTA ACGTTTTGTT GTTGTTATTT TAAATAAAT 240  
 TTGATGCAAT TAGTTTGT TT ATCCGCACAA CATCTTATAA TGTA CTTAAC TGTATTTTAA 300  
 AGAGAAAAGA AATACAGTTA GGCATTCCAA AACTGTGATT TTAACACAAT TAAGTTGGCC 360  
 TGAATTC CGT ATTTGAAGTC CTAATGGAA 389

## (2) INFORMATION FOR SEQ ID NO: 2983:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2983:

ATATTCCTAT GACAATGTTT AGGCAACGAT TCCAAGGATT AAGAAAAGAT CAACCGGTAT 60  
 ACTTATGTGA TGCCAATGGG ATTGCTAGCT ATAGAGCCGC TCGTATTTTG AAAAAGAATG 120  
 GATATACAGA TATCTATATG TTAAAAGGCG GCTATAAAAA ATGGACTGGA AAAATAAAGT 180  
 CTAAAAAATA GTTTTTGTAA ATTTAATATA CGATTTAATA AAATCTGAGT GTTAATTGAT 240  
 CATCAATAAC AATACTCAGA TTTTAATTTT TTAACAAAGT CTGTTACTAT ATTTCTCTAG 300  
 CTTCACTGAT CATTAAACCT TAGTTTCAGC ATAATTAAGG AAGGTCCGnC CCATTTCCAT 360  
 CGnGnTCCAT TACCGCCAC 379

## (2) INFORMATION FOR SEQ ID NO: 2984:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2984:

5 ATGCTGAAAA TATGGTGCCG TTTATATGAA TCAATTTGAA TCCGAACATA ATCCGGATAC 60  
 ATATTTTTCAT ACATTGGGAC CCGAATTGAC TTCAGCATTa CAGCAAATTG ATTATTTTGT 120  
 GGCTGGTATT GGCTCTGGCG GTACATTTAC AGGTACGCAC GTTATTTAAA GCAACATCAC 180  
 10 GTGCAATGTT ATGCCGTTGA GCCAGAAGGG TCCGTGTTAA ATGGAGGGCC AGCTCATGCA 240  
 CATGACACTG AAGTATCGGT TCTGAGAAAT GGCCGATATT TTTAGAGAGA CGCTTGTAGA 300  
 TGGGnTATTT ACGATTAAGA TChAGATGCC TTTCCGAATG TCAAAGTTTG CTATAATGAn 360  
 15 GGTGTAGTAA GCAG 374

## (2) INFORMATION FOR SEQ ID NO: 2985:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 464 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2985:

GGAGCCACCA TTGGAGCAnG TTACGGTGGA AAAGATACGG nAAGGTTnGT ATGACTGTAn 60  
 30 GTCTTGATA GAGTAACAAA CCTAATTTGT TAACTCTAGG CCCCATATGT CGCAGTACCA 120  
 TCTGCATGTG TTGTTAcATT GTATGCATTT GTTTTACTTG GCTTCTTGtA TGTCGGGCGA 180  
 GCTCCGTATG ACACTTGACC GTTTGCATGT GTTGTTACGT TGTATGCATT TGTTTTGCTT 240  
 35 GGCTTGTTTT GTGTTGGGCG AGCGCCATAT GATACTTGGC CGTTTCCATG TGTTGTTACG 300  
 TTATATGCGT TTGTTTTGCT TGGCTTGTTT TGTGTCCGAC GAGCTCCGTA TGATACTTGG 360  
 CCGTTTGCAT GTGTTGTTAC ATTGTATGCA TTCGTTTCGC TTGGCCTCCT GTATGTCCGA 420  
 40 CGAGCTCCGT ATGATACTTG ACCATTGCAT GGGTGGTACG TnnG 464

## (2) INFORMATION FOR SEQ ID NO: 2986:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2986:

AACTATTATA TTAACATACA ATGTAGGGAT GTGATGCGCG TGAAGTTTAG GGATAAAGAT 120  
 AATCGTCAAG TTAATTTGAC ATTAAAAAG GATAATGAGA TAGCAGATGG CAATCATGTG 180  
 5 CTAGCTATTC CAACGTTTAA AAATCAATTG CTTTTTACCA AACATAATTT ACGGGGGATT 240  
 GAATTTCTCG GTGGTAAAAG GGAACGCGGG GAAAAAGTAGT GCTGGAAGCA GTTACACGTG 300  
 AATTATATGA AGAAACAGGC GCCAAATTGA AAAATGnTTA TTACATAGCA CAATGTnCC 359

10 (2) INFORMATION FOR SEQ ID NO: 2987:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2987:

TAGAATTCTT CTAATGAATG AGCTTCTTTA GAATGATAAC CATAACGAAT TCCGTCAAAA 60  
 CGAGAAAGGT TTGACGAAGC TTCTGATGAT GCAATCACGT AATATGATGG AATACCAAAT 120  
 25 TTAGTATTTG GCAATGATAC TTCCTCAACG ACAGCACCTA AAGATTTTAA AGTTTCTACA 180  
 GCGTTTTGAA CTGCTTCTTT TACGTCATCA GCTACACCTT CACCTAAGTA TTCTTTAGGT 240  
 AATGCAACTT TTAATCCTTT AATATCTTTT ACCAATTTCA GATGTAAAGT CTACATCATC 300  
 30 AACTGGTGCA CTTGTAGAGT CATTAAACATC TGCACCAGAA ATAGCTTCTT AATACGGTTG 360  
 CATTATCTTT TACAnTTCGG GTCATGGnCC CATTTTGGTC 400

35 (2) INFORMATION FOR SEQ ID NO: 2988:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2988:

45 ATTCATTCAT AATTATCAAT CCTTTGTGTT AAATTACTAT ATAAATAGTG TACGnATTTT 60  
 CGAAATTTGT GATCATAAGT TTATTCAATG CTAAACAATA AGGTTGAGAC ATAATCGTAT 120  
 CTCAACCTTG AAATTATTAT ACGTTGACGT CACTAGTCAT TCAGTTTTCT TAATGCTGCT 180  
 50 ACAATCTCTT TTTTAGTATC TTGTACTTCA GAAGCTTGCT TAATCACTTT TGCAGGTGTA 240  
 CCAGCAACAA CTGCACCAGC TGGTACATCT TGTGTCACAA TCGnGCCACT GGCAACAATA 300

nGATTATAAC CGTGGAG

377

## (2) INFORMATION FOR SEQ ID NO: 2989:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2989:

15	CCAGGnACCT GGACACGCCG GGTCTTATCA TCAATAATAG TAGCATGACA AATCTACTAT	60
	TTTTTCGCTA ATAAGTGGAT GTAATGCTAA TAATGTTGCT GTAGGGAAAC AGCCAGGATT	120
	AGAAATGAGC TTCGTTCCAT TGTTATCAAA CGATTGCCAT TCTGAAATGC TGTAAATAGT	180
20	CATGATTCAA ATCATCTTGT GCCTGCAGCA GTTTCCTTGT AATATGCTTC ATATATTTCA	240
	CGnTCTTAA TTCTAAATGC GCCAGATAAA TCGATAACAT GAATACCTTT TTCTACTAAG	300
	GGAGGGATAC ATGTTTTACT TACGGGTGCT GGTGTCGCAA AGAAAATTAC ATCAAn	356

## (2) INFORMATION FOR SEQ ID NO: 2990:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2990:

35	TCATTTTCCA AGTGAGACTC TGCTCTTGCT TTGGCTAATT TAGCTCTTTC AACATCAATT	60
	TCTCTTGCAg TTTCTGCAGT CTGAACAATG ATTGAAACTT TATCTTTTCT AACTTCAACA	120
40	AAGCCATCGC TTACAGCAAT ATATTCAGTT CCATCGTGGA AATTTCACCTT TTACAAAGCC	180
	TGTTTTTAAA GCAGCTACAG TTGGGAATAT GTCCACTCAT GACACCTATC TCACCAGCTG	240
	TTGTTTGCAT AACAAACGAGT TCAACATTAT CACGATTGTA AACAGAACCA TTAGGAGTGA	300
45	CAATATCTAG GTTTAAATGT CCATTATCCA TTCnCCnGA ATTGGnTGA	349

## (2) INFORMATION FOR SEQ ID NO: 2991:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2991:

5 ATGGCCACGT TCATGCCAAT AGCTGTCGTA GTCGCATTTT CACGTTCTAG TATTGCATTT 60  
 TTTAAATGCG ATGTGTGCTC TACATAACGG CAAATTTTAA GTTTATGAAT CAACATATCA 120  
 ATTGCTTCGT TTCGAGACAT GTCGTGGATC AGTAATTATC ATAGTTTGTT GATCAAAAAC 180  
 10 ATGAGAAGGT TTATTGAGAT GTGAATGTTT CGCGGTGTTA TCTACATTGT CAACCTCTGT 240  
 ATCATGTTGT GTAATATCTG TATCATGAAG TTGCGGTTGC GCTGGTGCAT CTACTGCTAT 300  
 AACTGGTGTA TTGCGTTTTA ATAATAGTAC AGTAGTnCAT TGTnGACAAG ACTnACCGAC 360  
 15 TTA 363

## (2) INFORMATION FOR SEQ ID NO: 2992:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2992:

AAGTTTATTT TAAATTCGT AATAAAAATA ATAACTCAT CGAACGATTT AATGGTCTAG 60  
 30 GTTCCATAT CAACTATGAG TACATTAAAT TCAAATTCGA ATCACGTAAC GTAAAAGATC 120  
 AAACAATCCC TGAATAAAAC ACCAAGCAAA TACCCTACAG TACATCATTA GCATGTATTG 180  
 TGGGTTTTTC TACTTTTTGT AAATATTGAn AATTATnAGT AGTTGTTTTT TACTATTAGG 240  
 35 GCAGAAATGCT TTACAATAAC ATGCAAGTGT CAATTAAGGG GAGCACTTGC ATAAATAGTA 300  
 TAGGnGAGTG AGTAGTCCTG GCCATTTCTT GGAATTCCTT AATCGGCAC 349

## (2) INFORMATION FOR SEQ ID NO: 2993:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2993:

50 TTTGTGCAAT AAGCGCTTTT TGTTGTTTTG CTTTTGTTGC TAATTCATCT TTCGCAACAT 60  
 CTTTAATTGT TGTATCTGCA GTAATACCTT GAATATCAGC AACTGCTTGA TCTTTAATTT 120  
 GCGTAACATC ATTAGTTGTT TGTGCATTTA AGATATCTTG ATACGCTTTT TCTTTAGCTT 180

TTGCTTGATT TTGAGTTGTC ACAGCTTGAT CAACATCATT TTTAGCATTG ATTTAACCGC 300  
 TGTGCTGGTT GCGGCTTGAA TTGAATCTTC CAGGCTTCGC TGA CTACACA TACACAGTGA 360  
 5 GnGnAATATT TCGGCTGAAC GCGTGCATGT GAA nGCTCT 399

## (2) INFORMATION FOR SEQ ID NO: 2994:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2994:

AATGACAGGA ATCGTCGTTG CCTTTACTAA TTGACCAGTT AATTCAAAGT TAGGTCCGGA 60  
 20 CATTTTGCCA TCTTTAGCAA TATCAGTATA TATAATGCCG CCAAGAGGTA TATCCGATAA 120  
 CCGTCTCACA AACTAAATAA ATTTAACTCT GTGTCCTCTT CCCATCCGTT CACTTTAATA 180  
 TCTTCTCCAT AGGCATCAAC AGATAAATAA ATGCGACCTG GAAATGTATG TGCCATCTCT 240  
 25 TTAAGCCAAT CAGTATCTTG AATACCTTTC GTTCCAATA TGCAATAATT AATCCCTGCG 300  
 GCAAAGTAGT CCATGATTTG TGACTT 326

## (2) INFORMATION FOR SEQ ID NO: 2995:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2995:

CTAATGCCGA TGAGCAAAAC ACAAGCATTG GAAATTATTA AAAAAGTTAG GTACGTATAC 60  
 AACATTGATT TTGATAAACC GAAGTTAGAA ATGTGGATTG ATGTATTAAG TCAAAATGGA 120  
 45 GATTATCAAC CAACTGTAAA AGCGGTAGAT GTTTATATCA ACAGTAACAA CCCGTACCCG 180  
 CCTAACTTAC CAGCAATCAT GCGTAAGGAA CCTAAAAAG TATCTATCGA GCCAGTAGAT 240  
 AACGAAACCG CTACACACCA TGGGAAAATG CAGAATGACC CGAATTGTCA GACAAGGAAA 300  
 50 ATAGCGCTAG ATAGTTCATG AATAGTTGGC AGATTGGGGC GAACGATGAT ACG nCATTCG 360  
 ATTGAAGTCA TATCGTCGTA CTTAACACCG GACGTT nGAA 400

## (2) INFORMATION FOR SEQ ID NO: 2996:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2996:

10 GAATGTAAGT GTCCCTTAAG CATAGTGCTC CCACCTTAAA TTTTGTTACA TACTTTCATG 60  
 GAATGTACGA GAAATTACAT CTAATTGTTG TTCACGTGTT AATTTAATGA AGTTAACAGC 120  
 GTAACCAGAT ACACGGATGT TAACTGTGGG ATATTCTTCT GGATGTTCCA TTGCATCTAT 180  
 15 TAATGTTTCA CGGTAAATA CGTTAATATT TAAGTGGTGA CCACATTGCA TTGCGTAACC 240  
 ATCTAACATA CTAGTTAAGT ACGGTTTGAT CTCTGGnTCT TTACCTAATG ATTTGGnACG 300  
 ATACTGATGT ATTGAAATAC CATCCTTACA GCATCGTAAG GGGTCCTAGC CACAGAACTT 360  
 20 ATGAAGAAAT GCACCTTTTn GGCACnGGCA TGCATGGGGT 400

## (2) INFORMATION FOR SEQ ID NO: 2997:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2997:

ATGATATTAA CCTGTTTACA AGATGGTTGA TACTTGCGCA TGA<sup>n</sup>ATTTGA ATCTTCAACA 60  
 35 CCATATTATT ATGGTACATA CGAACTGAA AATGAATCCA TAGTTACTGA CAAAGAAAAA 120  
 ATCTTAGTAT TAGGCTCTGG ACCAATTCGA ATCGGCCAAG GTGTAGAATT TGACTATGCG 180  
 ACAGTTCACG CCGTTTGGGC AATTCAAAAA GCAGGGTACG AGGCGATAAT TGTGAATAAC 240  
 40 AATCCAGAnA CAGTTTCAAC AGATTCTCAA TTTCTGACAA ATTATACTTT GAACCTTTAA 300  
 CTGAnGAGGA TGTGATGAAT ATCATTAAAT TTGGA 335

## (2) INFORMATION FOR SEQ ID NO: 2998:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2998:

55



GCAGTAACTA ACTTTTGTAC AAAAGGATCA TTTTATCAA CATAATGTGG TGGTTGGACT 120  
 TTACCTAATT TCACTTCAAA GcATTGTTGA ATCTCATTG CAAAACGATC CATAGCTTTT 180  
 5 TCAAATTCAA ATCCTTCTGG GTAGCGTAAt TGATACCGAA AAGACCTGCG TTTTCATTAT 240  
 CATATGTAAT AACACCAATG TTAGTTGTCA CGTCACCCAT GgACATCTGT ATGGgAATTT 300  
 CATTCCCAnc TTTTTCACCA AAATCnGGAA TTGAAATAAG TGAGCGATTA CGAAATGGCG 360  
 10 ACAAACGCCT GTGGCATTGA TnGAGCAAGA TTnAAGG 397

## (2) INFORMATION FOR SEQ ID NO: 2999:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2999:

AAAGCTGTGT TGGTAAAGAG TTTGTGCGAT TTGGTACGCA ATACACGACA CGACTTGGCA 60  
 25 TTCGTTTAGA AAAAACATTT GAATACATCG ATACACCTCA TAAATTCAAA ATGGGTGTAT 120  
 CAGGCTGCCC AAGAAGTTGT GTTGAATCAG GTGTTAAAGA TTTTGGTATT ATCTCAGTTG 180  
 AAAATGGGAT TCCAAATCTA TATCGGTGGT AATGGTGGTA CAGAAGTTGA AAAAGCTGAA 240  
 30 TTTTAAACAA CTGTAGAAAC AGAAGATGAA GTAATCAAAT TATGTGGTGC TTTGATGCAA 300  
 TATTGAnCGC GAAACAGGTA TATATGCnGG AAAGAACCAG CGCCCAGGTT AAGAAGACCT 360  
 GGATTTGAAA ATGTnAAAAG AAGTCCTTAC CTGGGCCCCCG 400

## (2) INFORMATION FOR SEQ ID NO: 3000:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3000:

AACGGTAGTA TTACAGAAAG CTCTACTTAT GGTGATAATG ATACACCAGC GCCACCAACT 60  
 GACGAATTAG GTGGTAGTTG GACACTATGG AAAAATTTAG CGCGACAAAG TCCTGAATTT 120  
 50 GGTAATCCTG ATAAGTTTTG CCAAAATATT CCTAAAAAAA GTTGGTTTGT TTCAGCAACT 180  
 TCTACAACAA ACAATAAAGA GATTATCGAT ACAATAGAAA GTATTTGTAA ACGTGACCCA 240

AGTTTTACAA TCAATCGTCA GCmACAGTTT aaAGACCAaC CTGrAAATGA AaTATCTACA 360  
 TGGATTTATG CCTTATATyC AGATGTAAaC GGCGATTATA TTAAAAAGCC AATTACAGAA 420  
 5 TGTAGTGGTA ATGAAATATG CCAAGnATGG CTGTATCnCT TnGGTGTATC AACTGACAAG 480  
 ATTGAAGACT TAGCAAAACA TGCCTC 506

(2) INFORMATION FOR SEQ ID NO: 3001:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 353 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3001:

20 ATTGATGGCA TCGAAAACT TTAATAAGAC AACAAAGTTGA TGAGATATAT GTATATAGGT 60  
 TTGGCATGGA TTTCGATTGC AGTTAATTAG AATAGCTCAA TGCTATAAAT GTAAGTAGTT 120  
 GATATGAAGA AACTAATGAA CTAAATGCAA GTATTGTCTA AAACAATCAT TTTATTGAAA 180  
 25 TTTAGTAGAG CTGAAATTAA TATAACGTCG TTAATTGAAT AACGCTTATG TTATAAGAGC 240  
 ACTCATACCA nACCATAATC ATCTATAGnT ATAACAATTC ACGTATAAGG GGCTGTGTTT 300  
 GGCATAGCCC TTAGGTATAC ACCTAATTCC CATTAAAATA GTAGGGGnTT AAA 353  
 30

(2) INFORMATION FOR SEQ ID NO: 3002:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3002:

CAACAAAATG TCTATATGGT AAGTGGTAAA ACGAAAAATG ATGAAGACTA TTCATCAACT 60  
 ATTTTATATA ACAACGAAAA AGAATTACAA AAAATTACTG ATGCTGCTAA AAAGCAAAAC 120  
 45 GGTGTAAAAT TAACGATTAA AGAAGAAGAA AAACAAAGTG TCTTTGTGAG TATACTTTCA 180  
 ACATTAAATC CAGTTGTAGT CATAGCGTTA TTATTTCTTC TCTTCCTAAG CCAAGCACAA 240  
 GGTGGCGGTA GTGGCGGTCG TATGATGAAC TTTGGTAAAT CTAAAGCAAA AATGTACGGT 300  
 50 GATnAATAAA CGTCGTGTTT GTTTCTCTGA TGTAGCCAGG GGCCAGATGn AGGAAAACCA 360  
 AGGnTTAATT GGAAATTGTT GGTTCCTTGG AAAGGTAATG 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3003:

10	ATAACATCGG CACAGCAGCT AAAATAACCA TACCCAAAAT GAnTGTATCT TTAAACGTGC	60
	ACCGTAAAGn CTTCCGACTA GCCATGTATA AGCTTTGGCA GCAGATAATT GCTTCGTTGT	120
15	AATGAGTAAT CCTTGGACAA GCGCAATAAA CAACGTTTGC ATCGAAATAC CGATGATTAT	180
	GAGTGTTGTC GGGCGTATTT GTCCTTTCGT TTGAAACACT AATAGTATCA TCATTGCAAC	240
	TGCGCCACCT AATACTGCAA ATAGTGGAGT AAATGTATTG TTAAAGGCTG AAAATGCAAT	300
20	AAAGACAACA GCACTTAAGC TAGCACCACC TGTGATACCG CTAATATCAG GTGAGGCCAA	360
	TGGnnTTTTT TTATACATTT TGGCAACATT TAACCACTTC	400

(2) INFORMATION FOR SEQ ID NO: 3004:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3004:

35	CTAATAACAA ATGCGATGAT GATTAATACT AATTTACCTG CTGCTAATAC AGAATCTCCA	60
	AGGAATGAGA AGAATGGTTG ACGTTCAACT TCATTGTTTT TAAGACTGTA GATAATATCT	120
	TCTTTCTCTT CAACACTTAC TGGATTCAAC AAGCATGACA CAATAATCGC GTTAACGGAT	180
40	ATTTAGTGGA ATTGCCGTTA GTACCAGTTC TCCTGGTACC ATTTGTACAT ACGCACCTAC	240
	AATAGCTCCC GATACAGAGC TCCATTGACA TCATTGCGAT TGTTAATACA CGCATTTCAT	300
	TnCAGACGTT TTAGTTGCTC ACTTGGATAC GGGCTAAngC TTnCGTGAAT TGCC	354

(2) INFORMATION FOR SEQ ID NO: 3005:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGTCAGCTTA TTGAACAAGG GACACGTGAA TCAGTCTTGC ATCATCCAGA ACATGTTTAT 60  
 ACGAGATTTA TTATCAACGA AGAAGAAGAT TAATGATCAT TTAAACATG TGATGAGGGG 120  
 5 TGATGTACAT GATTAAAATT AAAGATGTTG AAAAGTCATA TCAAAGCGCA CATGTTTTTA 180  
 AGCGTCGTCG AACACCTATC GTGAAAGGTG TGTCAITTTGA GTGTCCAATC GGTGCGACGA 240  
 TTGCGATTAT CGGAGAAAGT GGTACGGnTA AATCGACGTT TGAGTCCTAT GATATTAGGT 300  
 10 ATTGAGGAAC CGGATAAAGG TTGTGTACCC TTAAATGATC CACCGATGCn TAAGAGGAAG 360  
 TGAGCCGCCA CChATTGG 378

(2) INFORMATION FOR SEQ ID NO: 3006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3006:

ACnTTAGTTG GCCAAGCCTT TATCCGGAAT TATTGGGCCT TAAAGCCCCC TTAGGCGGTT 60  
 TTTTAAGTCT GATGTGAAAg CCCCGGCTCA ACCGTGGAGG GTCATTGGAA ACTGGAAAAC 120  
 TTGAGTGCAG AAGAGGAAAG TGGAATTCCA TGTGTAGCGG TGAAATGCGC AGAGATATGG 180  
 30 AGGAACACCA GTGGCGAAGG CGACTTTCTG GTCTGTAACT GACGCTGATG TGCGAAAGCG 240  
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300  
 GTTAGGGGGT TTCCGCCCCT TAGTGCTGCC AnTAACGCAT TAAGCACTCC GCCTGGGGAG 360  
 TACGACCGCA AGGTTGAAAC TCAAAGGAAT TGACGGGGaC CCGCACAAGC GGTGGAGCAT 420  
 GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC TTGACATCCT TTGACAACTC 480  
 40 TAGAGATAGA GCCCTTncTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCTCAGC 540  
 TCGTGTCTGT AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC 600  
 ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG 660  
 45 ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA 720  
 AAGGGCAGCG AAACCGCGAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT 780  
 AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG 840  
 50 GTGAATACGT TCCCGGGTCT TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC 900  
 CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG 960

TATATTCGGA ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT 1080  
 GAATGTTTTAT TTAACATTCA AAAAAATGGG CCTATAGCTC AGCTGGTTAG AGCGCACGCC 1140  
 5 TGATAAGCGT GAGGTCGGTG GTTCGAGTCC ACTTAGGCCC ACCATTATTT GTACATTGAA 1200  
 AACTAGATAA GTAAGTAAAA TATAGATTTT ACCAAGCAA ACCGAGTGAA TAAAGAGTTT 1260  
 TAAATAAGCT TGAATTCATA AGAAATAATC GCTAGTGTTT GAAAGAACAC TCACAAGATT 1320  
 10 AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG CAGACAATGA GTTAAATTAT 1380  
 TTTAAAGCAG AGTTTACTTA TGTAAATGAG CATTTAAAT AATGAAAACG AAGCCGTATG 1440  
 TGAGCGTTTG ACTTATAAGn ATGnnnGATA TGTTGAATAT CCATATCTAA AGCTAGATCT 1500  
 15 AAACTTTGTT CAAAATCTTC AATCGTCTGT TTCGGTAAAT GATACATTAA ATCTAAACTG 1560  
 ATTGATTTAA TACCTGCGTT TTTAGCATTT AACACCGAAG TGTAATATC TTCAGTATTG 1620  
 20 TGCCTTCTAC CTAAACAGA CAATAACTCC GGCTTGAATG TTTGAACGCC CATTGAAATC 1680  
 CTTTTACTC CATATTTCTC TAATAGTTGG ACTTTCTCTT TAGTTAACTC ATCAGGATTT 1740  
 GCTTCAAATG TATACTCGCC TGTGATTGTA AACGTATCAC GTATT 1785

25 (2) INFORMATION FOR SEQ ID NO: 3007:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3007:

TGCAAAAAAC ACAATAACGA TAAATGTTCC CATGATCCT ACAGCATCGC GAACATTTTA 60  
 CCTAAGTCTT TTGTATTTT AATTTCTTTG CTTAAATCC CATAAACTAA TCCAGGTACT 120  
 40 AAAAATACGA CAAGAATAAT TAATCCGACA CCGTTAATTA ATGGCGATCG TCTAGTAAGC 180  
 TGCCTGTTTT AGCATTTCTT AAAAAGCTAT GTCAGGAATG GCTGTAATAA TTAATAAAAT 240  
 AATTGnGCTA TGAAGTATA TTTGCCATTT TAAAnATGT GCTCTTTGTC AGAATATGTG 300  
 45 AGATGTnCTC ATGGCATCAT GCATTAACT GCATCATATT TTCCTAATCT AGGATAATGA 360

(2) INFORMATION FOR SEQ ID NO: 3008:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3008:

TTGCCTTCAA ACACATACTT GTAGTCGGAT GATCACCTGT TCCAAAAGnC ATACCTGGGT 60  
 5 CGAGCTCAAT GCAAAGCTCT TCATCCGCTT CTTTAGCATA TGTTTCCCAA CTAGGAACTA 120  
 TTGTGAACTT CTTGACGCT CGGGAATGGA TGGAAATAGT TTTTCCATTC ATTTTCCCAA 180  
 TCCGTCTCTG CAATAATTTG CTCACTGAAT TGAACGTTAT GTTGATCAAG TTCATCTAAA 240  
 10 TTTAATAACT CATCTTTGAA TTTGCTGTCG CAACTGTATC ATCATAAGTG CATTTTCAGTA 300  
 AAATAGGCTT nGCAAnCTTA CTCCCTTATC TGGGATAAAG CCTCGGTTTT 350

## (2) INFORMATION FOR SEQ ID NO: 3009:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3009:

25 TCTTATATCA CCAGGAATTA ACACTGCCTT TTGACCACTT TCTTCAATCA CTTGGCGTAC 60  
 TTCTTGTGCA TCTTGTTCTT CACTCGGAAG ATAGTTAATC GCTACATCTG CACCTTCTTT 120  
 AGCATACGCA ATTGCTGCTG CACGCCCTAT TGCTGAGTCA CCACCTGTGA CTAAtATTTT 180  
 30 ATAGCCTTGT AAGCGTTGAT GACCTTGGTA AGACGTTTCG CCACAATCGG GTGCTGGCGT 240  
 CATTTTCAGAT TGTAACCCG GTACCTCTTG TTCTTGTTTT TCaTAATCCG TTGTTTTAAA 300  
 TTTTGTTcNA GGaTCTkGAG CkGCCAtTTT TtGACaYcTc CGTATnCGCT TAATGGGTAT 360  
 35 CATTTACCCC AATCTTCCTA AGG 383

## (2) INFORMATION FOR SEQ ID NO: 3010:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 388 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3010:

50 TAATTCAACG GGAATTTTCC CTTTGAAGTT AACATAACGG TAGGCTGCTT TAACAGCTTC 60  
 ATCATCGGGC GCTTCGACAT CTTCTAATTC ATATGCAATG CCCAATGTTT TCCACTTATG 120  
 AACACCTAAC TGATGATATG GCAGAATTTT AACTTTTCG ACGTTATCAA GAGAATTAAT 180

TGTCGAATCC ATACCAGGTG GTTTCATATC TGACAGTTTG CGCGCGAAGT TAAAGGATGT 300  
 GTGTATTAGG GCTTTCCTGG TCCATCCAAA TAnGGTTGGT CCATTAAATCC ATAAGGTTTT 360  
 5 AnAATCnAAA TAATAATCCA GTCCGGTA 388

(2) INFORMATION FOR SEQ ID NO: 3011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3011:

ACTGCTGTAA CGTCAGTTGA TCTTTTCATT CTTGGTTTAA TTTCTGAGAC GTTACTTGGT 60  
 20 TGnGcAnGc CACCAATTGC CATACCGACA GATTGGAAGA ACAATGCATC AGTTCACCA 120  
 ACACCAAAGA TGTCACCAAG TACAACGAAA CCTACATATC CAACTGTAGA TACAATTAAA 180  
 ATACCCATTG CTTTTTTAAA TTCAGGATTA TCTGATTGAC GThCATTITT AGCTTTAAGT 240  
 25 GAAGTAAGTG CTACACCAAG AACTAATAAT ATCATGGCGA TTAAACCAAA GATAATTTGA 300  
 GTCATTGAAG ACCATTACCC TAAAAGATA ACGCTGGAAT AATGGTGTAC CCAACTAATT 360  
 GGCATACCTG GTAGGAAACT GGGCATAGGT ATTTGGATAC 400

(2) INFORMATION FOR SEQ ID NO: 3012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3012:

TTATCGGATT CGTTAATACT GGCGGTTTAC GCAATAGTTT AGATGTAGAT GATAACAATG 60  
 TGCCTATTAA ATTTAAAGAA GAGTTCGAAC CTAGAAAGTT TGTTTTCACT AACGGCGAAA 120  
 45 TTAAATACAA TAGCAATTTT GAAAAAGAAG ACGTACCGAA TGCATCAAAC CAACAAAGTG 180  
 CGTCAGATTT AAGTGATGAG GAACTTCGCG GAATGGTTGC GAGTATGCAA ATGCAGGTGG 240  
 CACAGTAAAC GTATTAACAA TGGGATTAGC TCAACCAAAC GCTATGTTAA CACCACAGTT 300  
 50 GACTGACTGG AACTACCAA ACCAGTACTG AGGGGnCGTT AATAATGAGT GTTTCCACTT 360  
 AAGCATAAAC TTTTGTGGT CTTAAACGGC ATTAGTGTGC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3013:

GGCTGTAATG AAAATCCAAA AGCCAAGCTT ATTTAATTCG CCTTCATGTG TGC GTGAATC 60  
 AATAGTGT TT GTATCATGAC TCATGACTTA CAGCCTCCCT TTCTTTAATA CGCGCTTCTC 120  
 TTAATCTAGC TTCAGTTTCT GCAACTTCAG CAGCAGGGAT ATGATATCCG TGATCGATTT 180  
 GGAAACTGCG ATAAATCATA GTACCAAAAA TACCGAATAA ACAAATTAAT GCTGGAATTA 240  
 CAGTTTCGAA AATTAAGAAG AAACCGCCGA TAGTCATAAA GATACCAATC CAGAATCCAA 300  
 CAGGAGTAAT GGTTTGGCAT ATGGATGGCC TTGGnAATAA TGGGTTGnCC TAAGTAATGG 360  
 CCGACCAAGG TCCTTTCCAn ATCCACCAA 389

(2) INFORMATION FOR SEQ ID NO: 3014:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3014:

AATCGCTTCG GTTAACTGTT CTAACCATTG GTAATAAACA TGTGTATGAT CAAGCTGAGC 60  
 TTAAATTTTT TGTGCCTCTT GTGTTTCAGC TTCAGTTAAA TCACTGCTTT CAAGTAATGG 120  
 ATTGATAATA GCTTGAGCAT CTTTTACTGC TTCGACATTG ATGTCAATTT CACGCTGGAA 180  
 TTTTTTAGTG AAAAAGTTTC GGAAAAAGAT GAAAAAGTCT TTCTCGGCGA TAAAATGTGT 240  
 TTGCGGCTCC TCTCGTAAAT TGTGGTTAAC AATATCAAAT TCCTGCAATT CCTAACGCAG 300  
 CACTCATACT nGTTGnCAT TGCAATGATG ACGCATTAC AGGGCAACTG CTCAACACAT 360  
 GGGCATAAAG TTCCCACTC ATAGGCAACA ATCATGGCGG 400

(2) INFORMATION FOR SEQ ID NO: 3015:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3015:

nCCTATCTCT GGTGAGAGT CTTTGAGCTG AAAAAATGTGA CACACAAAAT TGCAATGGnA 60  
 5 TCAACAAATG TTTCCCATTG TGGATGGTCT TGAATAAGTA TTTGGTGTTC AACTTGGTGA 120  
 TTTGCCATGA CTAATACCAT GTCATTTGTA CTTGTATCGC CATCAACAGT AATCATATTA 180  
 AATGTATGGT CAGTCGAAGA TTTTAATAAT TGATGAAGTG TATTCGATTC AATCGATGCA 240  
 10 TCGGTTGTTA TAAAAGCAAG CATGGTAGCC ATATTTGGGT GAATCATACC TGAACCTTTG 300  
 GTGCTACCAC CAATTGTAAC GGTTTACCAT CGATTTTAGT GATACAGCGA TATGTTTTGT 360  
 ACAGGTATCA GTGTTAAAA 379

## (2) INFORMATION FOR SEQ ID NO: 3016:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3016:

CATATAAATT GCTAACGTGC CACCATTAC TAAGGAATTG ACATCCACTT CATTTTCTTC 60  
 TGAATCTTTA AAGTGACCTG TAGAAAATGT CACACTTTTA GCAACTGTAC GCATTGTCAA 120  
 30 ACCTGTCTGC ATAGTAGCAA CTGCTGCGCT CGCTGATGTC ACCCCTGGTA CAATTTCAAA 180  
 CGCAATATGA TGTTCAITTA GTATGTCGAC TTCTTCTTGC ACACGACCAA ATATCGCTGG 240  
 ATCGCCAACT TTAAGTCTAA CAACCTTGTT ATATCGACGC GTGCTTCCAC GATACAGTCA 300  
 35 TTATTTTTCT GCGGAAAAT GTTTGGAAAC GGCTTTTACC AACAnGGTAA TTCAGAGGCA 360  
 ATCGCAATGn AAATTACGGn TCACnAACGG TCATTGGATG 400

## (2) INFORMATION FOR SEQ ID NO: 3017:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3017:

CCTTTTTCTC TTCTTCATA TCTGCAAACG TGCATCAATT TTAGGATCTA AATCTCCAAA 60  
 TGCTTCTGCA ACTGGTTCAG AGCGTTCATA ATACATACGA ACTTTTGGAT ATAACGCTTT 120

TCATTTAACT GTTCATCAGT ATATTTATCA TATGCTTTTG TTGCTTGTTT TAATTCTGCT 240  
 TTAACACCAT CATCTTTTTT CGATGTCTTT GAATCATCCT TCTTACTATC GTCGTTCCCC 300  
 5 ACATGCAGCA 310

(2) INFORMATION FOR SEQ ID NO: 3018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3018:

TCGCTTTGTA AATTCTGGAA CAAAGnCAGT CATGACAACA ATTCGTGTTG CACGTGCATA 60  
 20 TACTAAAAGA AATAAAATTA TAAATTTGTC TGGATCTTAT CATGGCCATT CTGATTTAGT 120  
 ATTGGTTGCA GCAGGTAGCG GCCCATCTCA GCTCGGTTCT CCAGACTCAG CTGGTGTTC 180  
 AGAAAGCGTC GCACGTGGAA GTCATTACTG TACCTTTCAA TGATATTAAC GCCTATAAAG 240  
 25 AAGCAATTGG AATTTTGGGG TGATGAAATT GCCGCAGTAT TAGTAGAACC AATTGTTGGT 300  
 GAACTTTGGG AATGGnnAAT GCCTCAACCT GGGATTTTTA GGAAGAGGGT 350

(2) INFORMATION FOR SEQ ID NO: 3019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3019:

ATATCATGTG CCAGTGAAAG CGGCACTGGn CGGATATGGC GCACATATGG ACATTATGAA 60  
 AGAGTACCAA TTAATCATTT TAGCGCCACA AGTTGCGTCT AACTATGAAG ATATTAAGCA 120  
 AGATACAGAT AGATTAGGTA TTAAATTAGC GArGACTCAA GGTGCTGAAT ATATCAAATT 180  
 45 GACACGrGAT GGCCAAGCAG CCCTTGATTT CGTTCAACAA CAATTTGAAA ATTAAGAATA 240  
 GGAGTTTTTC ATATGACTAA AACATTACCT GAAGGATTTT ATTTTGGTG GAGCAACAGC 300  
 AGCATATCAA GCAGGAAGGT GCGACCAAAT TACGGGATGG GTTAAAGGTC GCGTGCATTG 360  
 50 GGGATACGGT ATTTTAGGAA GGAAACTTA TTTGGTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3020:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3020:

10 ACGTTCGTCT TACGTTTAAC GCCATACGGT GTATTAGCAA TTATGGnCCA ACACATTATC 60  
 GACAAGTGAC TTTGGCGCCA TTTGGACTTT AGGAAAAATT CTTAATCGCA TCGTACGCTG 120  
 CATTAAATTAC GATGTATATC ATTCACTTAA TTATTTTAAG CCTGTTAGGT ATTAGCCCAA 180  
 15 TTCGCTATGT TAAAAAGACT TTGGAAGTAT TAATCTTTGC ATTCACATCA CGCTCAAGCG 240  
 CGGGTGCCTT ACCAATGAAT GTACCAACAC CAACCAGACG TCTAGGCGTG CCAGAAGGTA 300  
 ATGnCAATTT CGCTGCGACA TTTGGAATGG CGATTGGACC AAATGGGTGG GCAAGnAATT 360  
 20 A 361

## (2) INFORMATION FOR SEQ ID NO: 3021:

- (i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3021:

CAATGACCAT GACCAGTTGA TTTGGAACAA TGATTGACAT TGGAGCTATG CATCAAGTTT 60  
 35 GTCTTTAAGA CTAATAAACC CACGAACCAT GTTAACCCCG TGGTGACCA TCACCAATTG 120  
 nCTCGATCTA ATTCAGTTAA TTCAGATTCA TGTTTTTTAA ACGTTTCTTC TAAATTTAAT 180  
 AAACGTGnCT TTCATATCAT TCACTTTCAT TTGTGnCCAC CTCATAAATG TATATTATCA 240  
 40 TATTCACTCT TATTAAAGTA TGACTGTTGT TGGTGCTAAA AATGCTCCAA ATATTCGGTT 300  
 TATTAGGCAC GATAGTTATA GAAAAACCTG ACAGTCTAAA GATGTCATAT AATCAC 356

## (2) INFORMATION FOR SEQ ID NO: 3022:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3022:

55

GTGTTTGGTC CAATATCCAT ACCTTCTTGG nTCTGCTGGA ATTGAATCAG ATGGTACTAC 120  
 AGTGATTTTG GCATCATTAG nAAAAATTCTT TAGTCAACTT TAGTGTCTAC TGGTAATACA 180  
 5 ATTTTATCAC CATGTTTTTC TAATAAATCT TTTGCGAGTC GGATTTTATC TTCTTCTAAT 240  
 AATGAAATAC CAATTTCTTT ACCTTGCGCT TTTAAGAAAG TATAAGCCAT ACCTCCGCCG 300  
 ATGATAATTT TATCAGCTAT GTTAACTAAT AA 332

10 (2) INFORMATION FOR SEQ ID NO: 3023:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 311 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3023:

AAAGGTATTC CACAAGAATT AGCTTTGCAA AAATGCCAAA GCAAACAGAA GATGGnACAA 60  
 TTTAAAGTgn CCTACAATCA TGAATGAGGA GGACGCGTAA GATGAGCATT CGCTACGAAT 120  
 25 CGGTTGAGAA TTTATTA ACT TTAATAAAAG ACAAAAAAAT CAAACCATCT GATGTTGTTA 180  
 AAGATATATA TGATGCAATT GAAGAGACTG ATCCAACAAT TAAGTCTTTC TAGCGCTGGA 240  
 TAAAGAnAAT GCAATCAAAA AAGCGCAAGA ATTGGATGAA TTACAGGCAA AAGATCAAAT 300  
 30 GGATGGCCAA T 311

(2) INFORMATION FOR SEQ ID NO: 3024:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3024:

ATTAGACATT ACAAGGTGCA GTACGTGCAA CATATTAGAC ATATTGAATT AAGTGGTCAT 60  
 45 GnAAGGTATT GACAGTTAAA AAAGTTGAAC AATTAGAAGA AATCGAGGGC TTAATATTAC 120  
 CTGGTGGCGA GTCTACAACG TTACGTCGAT TAATGAATTT ATATGGATTT AAAGAGGCTT 180  
 TACAAAATTC AACTTTACCT ATGTTTGGTA CATGCGCnGA TTAATAGTTC TAGCGCAAGA 240  
 50 TATAGTTGGT GAAGAAGGAT ACCTTAACAA GTTGAATATT ACTGTACAAC GAAACTCATT 300  
 CGGTAGACAA GTTGACAGC 319

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3025:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60  
 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTCGAATAA AGGTAGCATA 120  
 TGTAAATTGTT TGTGTTTACG TATTTCTGGT GGTAAGTTCC GTGAAACCCA ATGTCTATAT 180  
 TCCCATTTAA TACGCTATTT ATAAATGTGT CATGTTCTAA TAAGCTCGGT ATGACATGTG 240  
 TATCATTTTG TAAAATGAAC GTTTGGATAA GnGGGAGTAA CATGTGGGAT ACGTCACTCT 300  
 CATCAAGCCA TG TAGATACH 320

## (2) INFORMATION FOR SEQ ID NO: 3026:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3026:

TCTCAACAAA TGCATCCAGT ACTTAAATTG GCATTATAGT AATTTAAGnA CAATATATCA 60  
 ATATTTCTCC TTATCCAGCA ACAGCAAATT TATTGGTAAG GTGTACGATT GAACCTTTAG 120  
 TCAATGAAGC AGGTACATTT GGATTGGCCA GGTGGATTTA CTTCAACTGA GCGCTTTGTG 180  
 AGAATGGGCA TTTATGAAAG CAAACATTGC TCAAAACAAT GATAAAGAAA TGGATTTAAT 240  
 GAATGCATTT TATTTATTAG ATGCGGTAAA TATACCGATT GGAATTGTAC GTCCGCATGA 300  
 TGCTGACAAT CACTATACGA TGTATCCA 328

## (2) INFORMATION FOR SEQ ID NO: 3027:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3027:

ATTGAAAATA TGTGTTCTnT GTAAAATTTT AATCGTTCGC CACGATGCTG TTGATAAAAA 120  
 TTCAAAACT GGAGTTGATC TTCTAGTTCA ACATAATCAT CGTAATTAGA CATGTAACTT 180  
 5 TTGATTAAGA TTTCAAGTAC ATGATCTTCG ATAGTATTGn TTTTAACTTG TTGTTGAGCC 240  
 GCTATATCTT CCATCGTGGA ATTGTTCAAG CAATTTTGTA TAAGTAATAT AAGTTCGATT 300  
 TAATGAATGT AGGTTTCATT AT 322

10 (2) INFORMATION FOR SEQ ID NO: 3028:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3028:

CAAGAATCTT ATACTTATCA AAATTTATAC TGTGAAGCGA GTCTATTGGC TAAAAGACTC 60  
 AAGGCTTATC AACAACTCTG TGTGGGGCTA TACATAGATA ATTCGATTCA ATCGATCATT 120  
 25 TTAATACATG CATGTTGGTT GGCAAATATT GAAATTGCGA TGATTAATAC AAGGnTGACA 180  
 CCTAATGAGA TGACGAATCA GATGAAGTCA ATCGATGTAC AATTGATTTT CTGTACCTTG 240  
 CCACTGGAAT TACGAGGGTT TCAAATTGTA TCGCTGGATG ATATTGAATT CGCCnCCGG 300  
 30 GCnTATTACA ACG 313

(2) INFORMATION FOR SEQ ID NO: 3029:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3029:

CTTCCAAAGA AAAGACCACA GTTTTTGACG CATCAATATG GTGCAATTTT AGAGACACTG 60  
 45 TAGTTGCAGA AGATGGTTCA GTTGACTTTT GAAGACAATC GTTATACAGA AACACGCGTG 120  
 CCGCTTATCC AATTAATCAC ATTGACAATA TTGTAGTACC ATCTAAAGCA GCACATCCAA 180  
 ATACAATTAT TTTCTTAACT GCGGATGCAT TTGGTGTAT TCCACCGATT TCAAAGTTAA 240  
 50 ATAAGACCAG CAATGTATCA TTTCTTGAGT GGTTCACTTC TAAATAGCTG GnCAGAGCGT 300  
 GGTGTGACAG ACCTGACCAT CATCTCAACA TGTTGnGCA CCGTCTTCCG TACATnACT 360

## (2) INFORMATION FOR SEQ ID NO: 3030:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3030:

TGATGGATTG GCTAGCAGGT GTTTACATTA ACTCATTAAA TGTATTTCAC TACATGCACG 60  
 ATAAATACAG CTATGAACGT ATTGAAATGG CATTACATGA TACAGAAATT GTACGTACAA 120  
 TGGCAACAGG TATCGCTGGT TTATCAGTAG CAGCTGACTC ATTATCTGCA ATTAAATATG 180  
 CACAAGTTAA ACCAATTCGT AACGAnGAAG GTCTTGTAAGT AGACTTTGAn ATCGAGGCGA 240  
 CTTCCCTAAA TACGGTAACA ATGACGACCG TGTAAGATGAT ATTGCAGTTG ATTTAGTAGA 300  
 CGCTTCATGA CTAATTACGT GGTCATTAAA CATATCGTGA TTCAGACCTT CCATGGGnGT 360  
 ATTACCATTA CTTCAACGTG GTnTCGGGTA GAAACTGGGT 400

## (2) INFORMATION FOR SEQ ID NO: 3031:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3031:

nGCGTTTAAT CACATCTTTT TGATAATGTT CCCTTACCAT TTCTTCATGT GCATCTGCAT 60  
 AGTCTTTTCC AAATGGCAAA CTAAACTGAT ATGCAACTTT TAAATAGGCA TCTATATGCG 120  
 ACTCGTCAAC GATGGCAATT TCAACGTCnA GTTACGCGGA CAAATTGGCA AGCGCATCAC 180  
 TTTCTATGGC ATACAATTCC ATAATACCTA GTTCAAAATT CATATCTTTA AAACATAGCC 240  
 ATCCAATGGA TTATCAAGTT GTTCATTTTC CGGGAAAACCT nAAACGCATA AATGATTTGG 300  
 AACCTTGATT TGTATGTGA 319

## (2) INFORMATION FOR SEQ ID NO: 3032:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3032:

5 AAGAAGTGGC AATTATGATT GATGCTCTAG CTGACAAAGG GAAAAAAGCA TTAGAAGCAT 60  
 TATCTAAAAA GTCACAAGAA GAAATTGATC ATATTGTTCA TCAAATGAGC TTAGCAGCTG 120  
 TTGATCAACA TATGGTGCTA GCAAATTAG CACATGAAGA AACTGGAAGA GGTATATACG 180  
 10 AAGATAAAGC GATTAAAAAT TTATACGCTT CTGAATATAT ATGGAATTCA ATAAAAGACA 240  
 ATAAGACAGT AGGGATTATT GGTGAAGATA AAGAAAAAGG ATTAACGTAT GTAGCGGAAC 300  
 CAATTGGTGT TATTTGTGGT GTTACCGCCC AACCACCAA TCCCTACGTC CGACCACCTA 360  
 15 TTTTAAAGC CGATGGATTT GCCATTTAAG ACnGGGAATC 400

## (2) INFORMATION FOR SEQ ID NO: 3033:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3033:

TAGCGGTAAT CGAAATTGGG GACTAAATTT CGCAAAAGCG GGTGCGACGA TATCAGAAGA 60  
 30 GTATAATGTC CCTTTATTAA TGAAGTTTGA GTTACATGGA AAAACAAAG ACGTTATTGA 120  
 ATTTAAGAAC AAGGTGGGTA ATTTTAATGA AAACCATGGA AGAGAAAAAG TACAATCATA 180  
 TTGAATTAAT TAATGAGGTC ACTAAACGAG AGAAGATGGA TTCTTTAGTT TAGAAAAnGA 240  
 35 CCnGAGCTTT AGTAGCTTAT TTAGAGGAGT AAAnGACAAA ACATCTTCTT CGACACTGAA 300  
 TCG 303

## (2) INFORMATION FOR SEQ ID NO: 3034:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3034:

50 CTnCGCTATT TTGTAGGACA TCtTCTAAAG TGCTAGGnGA AGAGATTATA GAATAGGCAC 60  
 TATCAATACC GAAATCGTAA ACATGTTGAT AATTTTCGCC TAGACTGCCA CAAATCGCGA 120  
 TGACAGGAAT ATGATATTGT TTTGCAGCTA ACGCAACGCC TGACGGGTGT TTTACCAAAG 180



TGATGAAAAT CTGTAATGTC AAAGACGGAC ATCAATGACT TTTGTTGAAA GTTGTCTCAC 300  
 AAAACGnTAA TGAATGCTGC GGCCCATGAC CGGCCAGCTG 340

(2) INFORMATION FOR SEQ ID NO: 3035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3035:

AAAGAACATG GTGTAGCAAT AGTCTCTGGA GGTGGAAGCG GACATGAACC TGCGCATGCC 60  
 GGTTTTGTG CAGAAGGTAT GCTAGATGCA GCGGTTTGTG GCGAGTATTT ACATCACCTA 120  
 CACCTGATAA AATATTAGAA GCTATTAAAG CAGTAGATAC TGGTGATGGT GTATTACTAG 180  
 TTGTAAAAAA CTATGCAGGT GACGTGATGA ATTTGAAAT GGCACAAGAG CTTCCAGAAA 240  
 TGGAAGGTAT AAATGTTCAA ACTGTTATTG TTCGTGnCGn CATTGCTGTG ACAAACGnGT 300  
 ACA . 303

(2) INFORMATION FOR SEQ ID NO: 3036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3036:

GGGGAAAGTA AATTAACAGC TGTGTAGAAT AATTAAGGTT TTAATTTATA TAGAACAAC 60  
 TATTGTAAAC TTTTCATTC TTAAAGTTTA CAATGGTGCT ATAATAATGG TCATGAAATA 120  
 CGAAAGGAAG GAAAAAATGA CnACAAAACA GTTAGTATAT ACAGCTTTAA TGACAGCGAT 180  
 TATCGCTAGT TTAnGATTGG TACCGGTAAT TCCACTACCA TTGnCTTCAG TACCAATTGT 240  
 ACTTCAAAAC AGTGGTATTT CTTAGCAGGG GCGATTTTAG GACGTAAATA TGGCACATTA 300  
 AGTGTTATCG TCTTT 315

(2) INFORMATION FOR SEQ ID NO: 3037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3037:

5 GCACCAATTG ACGAAGGAAT ACCGAATCCC ATTGTTCTTA AACCACCGCT TGTAACCCAT 60  
 TGTCGGTGAT TTTTAAATGG ATAAAATTGA GCTGCCCACA TTTGATGTTG TCCCACGTCT 120  
 GTAGTAACAA TTGCTTCACC ATTTGTAATT TTGCCGATAT ATTCGATTGT TTGTTGTGGC 180  
 10 TTACAAAATA CTTGATCTTC TTCACCAAGT TTAAATGGGT GTTCTGCTT ATTATTTTGA 240  
 CAATGTTTAA CCCAGTCACT GTGTTCTATA GTCTCAACAT TTTTATCATT TAAACCTCC 300  
 AAAAAACCTT TACAnGCCnG CAAAAAACC 330

## (2) INFORMATION FOR SEQ ID NO: 3038:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3038:

25 GTGAGTCCAC ATAATAACTT TGACGTCCTG TTAATGTTCT AAAAGGTACT AGACGTTCTA 60  
 TATTCGTTGT AAATGGTGAA TATCGTCGAC CTTGTTTATT TGAACCTGGG AATCTGCTG 120  
 30 TCGGTATTAC TTCTCGTGGT TGTGAAGTTA TATTTAAAAA CGAAATTTTC TCAGCAGCGC 180  
 TGTCGCTAGA AATATCTTTT AACGGCATT CAGTTTGTTC TTCGAGATCT TCATATGGAT 240  
 TTTTGTGnAT AATTnACCAT TCGTAGCAGA TGGAATACT TGAGTATnGG CATCAGCGAC 300  
 35 ATTGACGTGC TGTATCAATA CGTGGACGAT TCGC 334

## (2) INFORMATION FOR SEQ ID NO: 3039:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3039:

45 GGTCTGATCG TGGTGAATGA AAAAGGTTCT TCTCTGTAAT GAATTATCTC TTACCGATGC 60  
 50 AAGATATTAT GAGCATGCAT TGCTCAGCAA ACGTTGGTGA AAAAGGCGAT GTTGCAATTAT 120  
 TCTTTGGTCT ATCTGGCACT GGTAACAA CTTTATCGG CTGACCCACA CCGTAAACTA 180

ATGCAAAAGC AATTAATCTT TCCAAAGAAA AAGAnCCACA GntTTTTTGA CGCATTCAAA 300  
 TATGGTGCA<sub>n</sub> TTTTAGAGAA CACTGTA 327

(2) INFORMATION FOR SEQ ID NO: 3040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3040:

GTGATATTCA CGAnCGTTAT TTTCAATATT TGATAAGTAG AAAnTATGAC GATCTTCATG 60  
 AACAGCATCT TGTTCCTTCGT CAAATTCAAC GTCATCAAAA CGTTTGAAGA ATGTTTCATA 120  
 TGCATCAACA GATACTTCAG TACGGTTATT TAATAATGCT TTATGTGCAG CTGGATCTA 180  
 AATGATCTTT GTAGCCTTCA ACTnAATGTC GCACTATAAA ATTCACCAAC TGAACCTGAG 240  
 CCATAACTGA ATAAACCGAT TGTTTCCACC AGCTTGTGAA TCTCGATTTT CAAGTGAATG 300  
 ATATT 305

(2) INFORMATION FOR SEQ ID NO: 3041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3041:

GTTGTGTACC TTAAATGATC AACCGATGCA TAAGAAGAAA GTGAGACGTC ATCAAATTGG 60  
 TGCTGTATTT CAAGATTATA CGTCATCATT ACATCCATTT CAGACTGTTA GAGAAATCTT 120  
 ATTTGAAGTG ATGTGTCAAT GTGATGGACA ACCTAAAGAA GTTATGGGAA GTCCAAGCAA 180  
 TTACATTGTT GGAAGAAGTC GGTCTATCTA AGGCATACAT GGATAAATAT CCTAATATGT 240  
 TATCAGGTGG AGAGGCGCAA CGTGnTGCAT nTGCGCGTGC AATATGTATT GAACCCnGAA 300  
 ATATATTTTG TTTGGAT 317

(2) INFORMATION FOR SEQ ID NO: 3042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3042:

5 AATCTTCGAA AAATAATGCA ATGCAGATTC CGAAAAAAC AATATGATAG AAACACCTCA 60  
 ATTAAATACA ACGGCTAATG ATACATCTGA TATTAGTGCA AACACAAACA GTGCGAATGT 120  
 AGATAGCACA ACAAACCAA TGTCTACACA AACGAGCAAT ACCACTACAA CAGAGCCAGC 180  
 10 TTCAACAAAT GAAACACCTC AACCGACGGC nATTAATAAT CAAGCAACTG CTGCAAAAT 240  
 GCAAGTTCAA ACTGTTTCCTC AAGAAGCnAT TCTCAAGTAG GTTATTAAAA CACGGATGGT 300  
 GCTAATAGCT TnGCAACAAC GTGGGCTTTA AAATTCTCCA ACTTTAGTTT T 351

## (2) INFORMATION FOR SEQ ID NO: 3043:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3043:

25 ACGnCCTTAC TGGnTACTTG GTTGATAAGT GTTAATCCAA ATGACGTCCT GCTACGTACA 60  
 GCTTTACGAA TATTTAATGC ACGTGTGATA TTTTGAGAAA ATACACCGCC TGGCTAAACC 120  
 30 ATACTCAGAA TCATTAGCTA TATCAATTGC TTCTTGATCG TCCTTCACTT TAATCACTGT 180  
 TAACACTGGT CCAATATTT CTTCTTGTGC TAATTTGTGA TGATTGTCTG GCACnCAATT 240  
 AATGTCGGCT CAAAGAAGAA CCCTTTATCT AATCCATTTT CAGTTAAGCG ATGACCGCCT 300  
 35 GCTAAAATTT GTGCATCCG 319

## (2) INFORMATION FOR SEQ ID NO: 3044:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3044:

45 GTCATATAAT CTAACATTTG TGTTATCTGT TAATTAAGTG GnTTTTACCT TAATTTGTTA 60  
 CATTGnTCTG TATTAAATCT TTTTGTAACC ATTGGTTACT TTTTCAGGTG GAATTTCAAC 120  
 50 ACCCATGTCA CCACGTGnCA ACCATTAAAC CATCAGACAC TTCAAGAATT TCCGCAATAT 180

AAATTCACGA ATTTCTAAAA CATCACTAGG TACGACGTAC GAAACTTGCT GCAATGAAGT 300  
 CAACATTTTC TTTAATACCG AAACGGATAT CTTCAGCATC TT 342

(2) INFORMATION FOR SEQ ID NO: 3045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3045:

TAATATCATG TTGTGCTTTT AGTGCTTCGG CAATTGTGTT TGTACTTACT GACCCAAACA 60  
 ATTTACCACC TTCACCAGTT TTTGCTGATA CTTCAACTTC AATGTTTGAT AACGTTTCTT 120  
 TTAATGCTTT ACATCTTCAA TTTCTTGTTG GCGTTCTTGT TTTGCACGTT TTTTCTGTAA 180  
 CTCTAATTGT TTAAGGTTAC CTGGTGTTGC TTCTACAGCA TAATTCTTTT TCAATAAGAA 240  
 GTTATTTGGC ATAACCTACT GGTACTTCTT TAACTTCACC TTTTTTACCT TTACCTTTAC 300  
 CTTTAACAnC TGTGTAAAAA TTACTTTCAT GCAGnTCACT CCTACTTAAA TGTTCCGTAA 360  
 TGCCTGTTGT AATGTGCCAA CGCCnCTCGA CGTGACACCT 400

(2) INFORMATION FOR SEQ ID NO: 3046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3046:

AATCACTGTT TCATTACTTG TTCCAAATCT GnATTCAAAC TATTGTTCAA AGATTCTAAT 60  
 TCCGCTTTAT TTTTATCTTT AATCGCTTTT GTCATCGCAG CATCTTTAGn CATCGACTTn 120  
 CTGTTGCAAT AGTTTAATTT TAGAACCCGC ATCTTTACTA GCCAATTTCT CTTCATAAGC 180  
 AATTAATGAC TTCGTTAATT GCGAAAGTGT ATCTTTTGA TTATCATTCG CTTTTGCATC 240  
 TTCAAGCTTT CTCACATCTG CATTTGACAG CATTACTTGC ACTATTATCT TCAAGCGATA 300  
 ATTTCT 306

(2) INFORMATION FOR SEQ ID NO: 3047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3047:

ATGGATCATA TTAGCACGTA AAAGAAAATT CTGTTTCATTA TGAAGAAGTG CCAGAnGTTG	60
AATTTAAACG CACATATGTA TGTGAAGATA TGTCTAAATG TATTTGTTTA TACAACGCAC	120
CTGATGAAGA AGCGGTAnTC GCGCGCGCAA AGCAGTTGAT ACACCGATTG ATGGCATCGA	180
AAAACCTTTAA TAAGACAACA AGTTGATGAG ATATATGTAT ATAGGTTTGG CATGGATTTC	240
GATTGCAnTT ATTAGAATAG CTCAATGCTA TAAATGTAAG TAGTTGATAT TGAGGAACTA	300
ATGAAC	306

(2) INFORMATION FOR SEQ ID NO: 3048:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 287 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3048:

GACAGGCTAC GAGATATTTT AAACAAATTT ACATCAAATC CAGTATTAGG TGTtATTGCA	60
GGTATCGTTG TAACTATTTT AATACAAAGT AGTTCAGGTA CGACATTATC ACAATCGGAC	120
TGGTAACnCT GGATTTATGA CATTGAAACA AGCCATTGGA GTGATAATGG GTGCTAATAT	180
CGGAACAnCG GTAACtGCAT TTATTATCGG TATAGATTTA GGCGAATATG CAATGCCAAT	240
TTTAGCATTa GGTGCATTCT TGAATCTTTT TCTTTAAACG CTCTAAA	287

(2) INFORMATION FOR SEQ ID NO: 3049:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3049:

CATATAAATA GCGnTACATC GCGCCATTCT TGATCTGnAC ATATCTTTCT TAGGTCCAAC	60
CGTGAATGAT TACGTCCATG ATAACGTACA AACGCAATTT CATTTGTGAT TCGATTGACT	120
AAAGGTACAC TGCCATCTTT CACTTGTGGT TCATCAACTA CTGCATGAAT GATTTGATGT	180

55

AATTCTACAC ACATTGGAAA GCTTGTAATG CTGTCTTACA TACAAATATA TTGATATTTG 300  
 TGCATGCAGT CAACCAGGCG GAAATGACCA TACCATGCTA ATTTTCTGGT AnGAAGGCCT 360  
 5 ACATATCTAA A 371

## (2) INFORMATION FOR SEQ ID NO: 3050:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3050:

CGCCAAATAA AGATAATACA CGTATTGGTG AAGATATAAC TGTAAGTCA CATATCTTAA 60  
 20 TTGATGGCGA AACAAAGCCG ATTACGAAAA CAGCAACATA TAAAGTAGTA AGAACTGTAC 120  
 CGAAACATGT CTTTGAAACA GCCAGAGGTG TTTTATACCC AGGTGTTTCA GATATGTATG 180  
 ATGCGAAACA nTATGTTAGG CCAGTAAATA ATTCTTGTCG ACAnATGCGC AACATTGAAT 240  
 25 TTCCAATTTG TTGGAnCATA TGGGCTAACA AGGTGTTTAG GCATATCTAC TCGTCTTATT 300  
 GGGTGCAAT GTAATGGCAA GCA 323

## (2) INFORMATION FOR SEQ ID NO: 3051:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3051:

CCGnACCAAT CGGTTTACAG TTCATTGGTA AACCATTTCG ATGAAAAAAC GTTATATCGT 60  
 GTCGCTTATC AATATGAAAC ACAATACAAT TTACATGACG TTTATGAAAA ATTATAAGGA 120  
 GTGGAAATCA TGCATTTTGA AACAGTTATA GACTTGnGTT CACGTAGAGT TAAAAACGGA 180  
 45 CTCAAAAATG TTTCTCCATC ACCAGCGCAT TnGAGCAGA ACCTAACTCA AATACGAATG 240  
 GTATCGCTTA GCATATCCAG TGCTTACCAG TTGTTAATAA GCGTGCGTAG ACGGGCATGC 300  
 GTGCTGCAAT GCCTAAATAG GAACG 325

## (2) INFORMATION FOR SEQ ID NO: 3052:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3052:

CTTTTAATCG CTTGAAACT ATAGGTAAGA CAATACAAGT AGCTACAAAG CCATATATTA	60
CTGTTAATTG ACCTATGAAA AAATATCCGC TAACGGGTGC CGTCAATCCT GCGATAGCAA	120
TACCAATAAA AAGTACAGTC CACGAAGGAT AAACATTTTC AAGTGAAAAA TCTTTTAAAT	180
ATTTTATTGA AAAAATAATC ATATGCGTCA TAATCCCAC AAGGCATAAA ATCCAAATAG	240
GCGTATTAAG CTATTGTAAA GTTTGTTACT AAAAAATGTT TTAAATAGTG TnCTAAAAAG	300
CCGGCATGAA AATGTGTGAC CTGATGAACT GAGGCTGTTA TTGTCTTCAC TTATTAAATT	360
TGTCTAGTCT AAAGGTGATC CAATCAGAAG CAAGTCCGCA	400

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(2) INFORMATION FOR SEQ ID NO: 3053:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3053:

AATGAGATGC GAAGGATGAT CAGAGAAAAA GTCTCTCAAT CAGGTGTGAA AGTCAGATGG	60
TTATCACAAC TTTGGCGTAC GTTTTCGATA TAATGCACTA GGTGATTAA ATACGAGCAA	120
TATTGTTTCT TCAAAAGAAA GTTTCGGTAT TACTGAAGTG TGAAATCTGT CTCTATGCAT	180
GCCGGATCGA CATTAGCATT ACTAATCCAG AGAAAGCAAA AGGTATTGTG TATACACCAG	240
AACATTGCCA GCGAAAAGTA AATGGTCACA GCTGTAGAnC AAGGTATTTA TAATGGGGGC	300
GGTAAAGCAG AAGGCCCTTA TGTAGCATTT CnTAAAGnTG GGAAAAGGTA AAGCAGCATT	360
ATCGGTG	367

45

(2) INFORMATION FOR SEQ ID NO: 3054:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 382 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3054:

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TnATTTATCT nAGCTCATGA CATGATGGCT GTTCACATTG CAAGGCGTTG ATGATnAAAT 120  
 AAGGAAAGGC ATTAGGAAAA AGCCACAGGG AAAACATTTT AGCAGCAGGT TCTTGGAATC 180  
 5 ATATATTCAA GTTCAACAAG CGAATGCTGT TAAATTGCCC TTTGGATGAC AATCAATTCG 240  
 ATATCGTTTT AAATGAAGCA ATGTTAACAA TGTTACCCAT CGCCATAAAG GAAAAAGCAT 300  
 TACGCGAGTA CTACCGAGTC TAAAGCCTGG GGGTATCTGT TAACACATGA TATTGTCATC 360  
 10 GTTAATGAAT CACATGCCAC AC 382

(2) INFORMATION FOR SEQ ID NO: 3055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3055:

CTTAAGATTA GGTGTGCTTA ATTAGTACTG GCTGGAACG ATAAAGGCAT ATTGCAAAAA 60  
 25 ATAGAACATC CATATCCATT AAATGTATTT ACGCTAAATA TTGnCGACTT ATATTTTTTAG 120  
 ACATAGAGAA GAGACAAGAC AATTTTAAAC GATGCAACGA CAGTTAGGCT GAGGCAGTTA 180  
 AAACAAATAT TTGATACACA TGTTGnCAGA TAAAGTCAG TGTTCCCATC AAATGChAAT 240  
 30 TTTGTACTAC TAAAGCTCA GCAGCGCAAC AATTAGGACA ATACGTATAT GAACAAGGGA 300  
 TTAAACCTC GCTTTT 316

(2) INFORMATION FOR SEQ ID NO: 3056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3056:

GTTCACCATC CGTTTATTTT AATGAAAAA TCGACAAAAA TGGTCGTGAA AACTATGATG 60  
 CAACAATTAT TCCAAACCGT GGTGCATGGT TAGAATATGA AACAGATGCT AAAGATGTTG 120  
 TATACGTACG TATTGATAGA ACACGTAAAC TACCATTAAC AGTATTGTTA CGTGCATTAG 180  
 50 GGTTCCTCAAG CGACCAAGAA ATTGTTGACC TTAAAGTGAC AATGAATATT ACGTATACTT 240  
 AGAGAAAGAC nGCACTGAAA AACTGACCA GCGTATTAGA ATCATGACGT TACGTCCAGT 300

CTTAGCAGCG TGGGnCGTAT

380

## (2) INFORMATION FOR SEQ ID NO: 3057:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3057:

15	TATGTGATGG ACTTAAAAAA ACGAACTCAA TTAATACAAT GGGCTCAAGA AAAAGAAGAA	60
	CGATTTATTA TAGAAGATGA TTATGATTCC GAGTTTAGAT ATTTGGCAA ACCCATTTCCA	120
	GCAATTC AAG GTCTATATTC AAGAGGAGAA AAAGTGATTT ATATCAGTAC ATTTTGCAAA	180
20	GTCTATTTTT CCTAGCTGTT CGAGTTGGCA TATATGGTGT TACCCTATTC TATnATGGAA	240
	AAAATATCAT TTCTnCAAAA TCCACCATTG GAAGGGCAAC ACTGGTAACC TGTTTCATAT	300
	GGCAAAACCT TATTGGCAAC GTTTnAT	327

## (2) INFORMATION FOR SEQ ID NO: 3058:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3058:

35	CGAAAAAGGA GAATGAAACA TGAGGTAATA CAACATTACA TGCAACAACA ATTTATGCGT	60
	GTAAGACATA ATGGAAAGCA GCTATGGCTG GAGATGGGCA AGTAACGCTT GGTTCACAA	120
40	GTCATCATGA AACAAACGGC AAGAAAAGTG CGACGTTTAT ATGAAGTAAA TGTTAGCTGG	180
	TTTCGCAGTA TGTAGCAGAT GCGTTTACTT ATTTGAAAAA TTCGAAACAA nATTACAACA	240
	GTTTAGTGGT AACTTAGAAA GAGCnGCTGT TGAATTGGCA CAAG	284

## (2) INFORMATION FOR SEQ ID NO: 3059:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AAAGAAGCGG ATGAAGAGCT TTGCATTGAG CTCGACCCAG GTATGGCTTT TGGAACAGGT 60  
 GATCATCCGA CTACAAGTAT GTGTTTGAAG GCAATAGAAA CATATGTATT GCCACAGCAT 120  
 5 TCAGTAATTG ATGTTGGTAC TGGCTCAGGT ATATTAAGTA TTGCAAGTCA TCTAATCGGT 180  
 GTAAAACGTA TTAAAGCGTT GGATATTGAT GnaATGGCAG TGAGTGTAGC TAGAAGAnAA 240  
 CTCAGAAGA nATCATTGTG AACGTTGAAT TGGAAGCTGT TCCAGGTTAA CATATTGGAA 300  
 10 AG 302

(2) INFORMATION FOR SEQ ID NO: 3060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3060:

TTTTTAAnGA CACATTGnGC TGTGTTTAAT GCATGAAAGG AACCACTGAC ATGCATnAAA 60  
 25 TCTTTGAATG GTTCTTTATC AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA 120  
 TATAATTCAA AAAGGGTCGA GGATATGAAA TCACATCTTC GACCCTTTAT TTACTATTTT 180  
 AATTCAGCCA CACGCAAACG GTTATTTGCT CTCTCTAAAG CTCTTTCGGC TCTATGGAAT 240  
 30 ATCAGTATTG TCGTCAATCA TTTTCCAAGT GAGACTCTGC TCTTGCTTTG GCTAATTTAG 300  
 CTCTTTCAAC ATCAATTTCT CTTGCAGTTC 330

(2) INFORMATION FOR SEQ ID NO: 3061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3061:

CGATCAATCA ATATAATTCA CGGCGCAAAA CGTTTATTTA GCATGTTCTT GCAGACTCTG 60  
 AAAGTGGCAT TAAACCTTCC ATTAAGATTT TTACCATTTCT AGGCATTAAAT ACCATTACTG 120  
 CAGCCATTGA CATTCTTAAA TTAATGATGT CTCCAGGTTT GTAACCTGCT AACACACCAA 180  
 50 TACCTAAmCC TAAAATTAAG CCGACAAATA TAGACTCTCC AAATGCGCCA AAACGTTTTT 240  
 GAATTGnTTC AGGATCAGCA TCTAACTnAT TCAGACCGGG TACTTTTTGT AACAAATTTAA 300

## (2) INFORMATION FOR SEQ ID NO: 3062:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3062:

TATAAAATCA ATGATTTTAA CAAATAAAAA CGTACCGCAA ATACTGCAAA TAACAGCAAA 60  
 TACTAGTTTT AATAAAATAT GACCGGTTGG AAAGAACAAT AAAGCAATTA AAATACCTAG 120  
 TTTAGCCCAT TCCATCGTTC CAGCTGTAGT CGGACTAACA AACTTATTTT GCATCATTTG 180  
 TTGGCATTAT CAAGCCTGCT GAAAGCCAAC GAACTTCCAG CAATTAAAAT ACTCATCGTC 240  
 CTTGGTATTC GGGCTTGGAG AATAAAATGA TTCCGCTGGT GACTCAGTTG AAATGTAGTG 300  
 AAATCTTTGA ATTGGATAGT TnCACTGCAC ACCTGATGGn AnCAACGGAA 350

## (2) INFORMATION FOR SEQ ID NO: 3063:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3063:

TTAGTGATTT TAACGTGTAT CGGTAATTTT AAATAAATGT TTAATGCTTT TGAAAATACA 60  
 GTTCTAACCG AAGACGTCGG GTACACTGAA TCACCGGAAA CGCCAAGGTC TTTTATTAAA 120  
 CCTTGTTTAC TATATTGCAT ATACTGTGGA TGCTGTCGCA ACACATTGAT TTGATAAGGA 180  
 TGTGTTGGTA ATAAAATAAA ATCTTTGGGT ATCTCTGATA TATCTATGTC TGCTAATTGG 240  
 ATACnACACT TTCTCAACCT GGATCCTTCC TTTTACCTnC CACCATAGCC GCGTGGAnCA 300  
 GGAAACCATC CTGGGATGCA CCAGCCAAAA TAAATGCCAA TT 342

## (2) INFORMATION FOR SEQ ID NO: 3064:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GTCCAGCTCC AGAACCAAAC TTAACAGTAT TATGGTCAGT ACGTTTACCT GACAACTTCA 60  
 AAACATACTG TGCAAAAATG AGTATTAAAA CAAGTTCTAT CCAATATGAA AATGATGACA 120  
 5 TTATGCGTGA AAGCTATGGC GATGACTATG GTATCGCnTG TTGTGTATCA GCGATGACAA 180  
 TTGGTAAACA AATGCAATTC TTCGGTGCAC GTGCGAACTT AGCnAAAACC TTACTTTACG 240  
 CTATCCATGG TGGTAAGATT GAAAATCTGG TGCACAAGTG GGCCCAACCT CCGAGGGATT 300  
 10 nACCAGCGGA GTAATT 316

(2) INFORMATION FOR SEQ ID NO: 3065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3065:

TGATTGCGTG GATCAGCAAC TTCAAAGATT AACAAATAAT ATTACTTGGG CAGATAACCG 60  
 25 CGCTGCAAAA TATGCAACAG TAATAAATGA AGTGCATGAT GGGCAATGCG ATTTACCAGC 120  
 GnACAAGCAC AnCGGTTTCA TCCTATGTCG CCATTAGCGA AGATTTTTTG ATGAAACATG 180  
 ATGGCCAGAT GTATTTCCAC GTACTGCTAA GTTTGCAGAT ATTAAAACAT ACATTTCTAT 240  
 30 CATTATTGAT ACATATATCA TTGATTATTC CATGGCTTCC GcNACAGGGA TGTTAATTAG 300  
 AACATAGATT GGAGTGAGGC AT 322

(2) INFORMATION FOR SEQ ID NO: 3066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3066:

TATAAAGAAT CCTGCCTTAC CTAAGAACAC TTGTCTTGTC GTTAAGACTG ACTCTAGACT 60  
 CTTATGTTTA TTATCAACCG TTAATAAACT TACCATCAAG AGTGCACCTA CCCATACTGA 120  
 CAGTGCAGTA TAGAATGGTG TCATACCTGA ACCATAATCC TTAAGTGGGA AAACATCAAC 180  
 50 AGTCTTCTTA TTAATAGATT GCAATAATAC CCGCTGCTTT TTCAAATCAT TCTAnTGGTC 240  
 GATTAATTGT CGACGCATCA TCTGTCAAT TCTTGAAATT TATTCGCTTT TCAACTTTCA 300

CACGCTGACA TAC

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## (2) INFORMATION FOR SEQ ID NO: 3067:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3067:

TTCAGAGTTC GGAACATAAG GCGCTACAAT GTTGTGTTGC CAGTAGTTGA CTGAATATGC 60  
 GTTTGTAACA AGCTTTTTTC GATTCTAGTC AACAGTAATT AAATTTATGA TATGGGCAAT 120  
 ACTTTGTAAT ACTAATATTA AATGGCGACT TTATTTCACT ATGTTATAAG AGTGCCATTT 180  
 GTTGATAAAG GnATACTAAA GGGTATCGTT TGGAATTTTA GTAAC TAGAT ATGTTCCGGT 240  
 ATAGACCGnA TTGTGGATAC GTAAATTTAA TGChATGAAT TTTAAATGA AAACATGACA 300  
 TTAAATGAAT C 311

## (2) INFORMATION FOR SEQ ID NO: 3068:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3068:

TATGATTATC TAGTAAGTAA ATTGCTGACG CGCCGAATAC CGCAAAGAAT ATAAAGCAAA 60  
 CTAACGCCGG GACAAAAAGT ACACCTAGGA ATAAATTCTT TAATCGTACG TCCTTTTGAC 120  
 ACACGTGCAA TAAhATACCT ACAAATGGGT GCCCAGGnTA TCCACCATGG CCCAGTAAAA 180  
 GATTGTCCAA TTTTGTAACC ATTGGGAATT TTTGACCACC TGTCGGAATG CGTAAACTCA 240  
 TACTTAAAGA AATTGTCATT ATAATTACCT AGACC 275

## (2) INFORMATION FOR SEQ ID NO: 3069:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AAATGGGTTT TGTGACATTA ACGTCTACAA AAGATGGTTC AGAAGAAACA CACGAGGCTG 60  
 ATGGTGTATT CATCTATATT GGTATGAAAC CATTAAACAGC GCCATTTAAA GACTTAGGTA 120  
 5 TTACAAATGA TGTGTTGTTAT ATTGTAACAA AAGATGATAT GACAACATCA GTACCAGGTA 180  
 TTTTTCAGC AGGAGATGTT CGCGACAAAG GTTTACGCCA AATTGTCACT GCTACTGGCG 240  
 ATGGTAGTAT TGCAGCnCAA GTGCAGGGAA TATATTGACA TTAACGATCA GCCTAAnTCC 300  
 10 GAGCnGATTA GATGTGAGCG G 321

## (2) INFORMATION FOR SEQ ID NO: 3070:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3070:

GTTTGACCTG CATATTTGAC AGTCATAACC TTTGTATCAC CATTATATTA ATATCAAAAT 60  
 25 CTGGAACGT GTTATTTGAG nTGACATTTA ACTTCGACG ATTATCAGCT GTTGAACCTG 120  
 ATGTATACGT TGCGCAACCC ATAACATCT GTGTTACAAT GCACCAAACG CACCTCCACC 180  
 30 AGCTACATTA GATGGGCAGC TTCGCCTTGC AGCTGATTGG TTTAGATGAT TGTGATACGA 240  
 TCCAATTTGA AGCCAAATnG TACTTAAGCA CAATCCTACT GCGGACCGTT TAACCCTGTT 300  
 TCACCTATAC ACTGnTGAAA GGCAAACCGT ACCACTCACC ATTTCCATGC CTTCCATATT 360  
 35 TGGTTACCAA ATTTACTTTT CCCnGAAAAA TGAAACTCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3071:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3071:

TGGCCATTTG TCATTGCATT TTTACCGTGG GTGTTGATTA TTATTCCTTA CTTACTATTT 60  
 50 AAATCGGATA CACTAAATAT TATTCATACG GGTGATAATA TTGCACGAGG TCTAGGTGTA 120  
 AGGTTAAnCA GAGAACGTTT AATATTATTC TTTATCGCAG TGATGTTATC ATCTGCTGCT 180  
 GTAGCATAGC AGGTTCAATT TCGTTTATCG GATTAATGGG TCCGCATATT GCCAnACGTA 240

## (2) INFORMATION FOR SEQ ID NO: 3072:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3072:

GACTCCCTGC AGGTCGACGT CTAGAGGATC CCCCCACAGC AATTCACCTA TACATGTAAC 60  
 AGTGTGAAAT AATAACGTCA CAACGGCATA ATACACATTG CAACGTCCCA ACAACATATC 120  
 ATAGAATCGT AACGGCATGA CATCAACACC AAACCTGGGC TATAACACCA TAACAGCGCA 180  
 ACGCCACATC ATAGGCACTA CATCAAGTCG CATCGTAGCA CCAGCACATC AAAGTAACAT 240  
 GGGCATCAAC ATCAAACCGG TCTATAACAC CATAACACCG GCAATGCCAC ATTCATAGGC 300  
 ACTACATCAA GTCGGCATC 319

## (2) INFORMATION FOR SEQ ID NO: 3073:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3073:

ATATACGCTT ATCAGCTGGA GCTCAATAGA TGGAGGATGA TTATGGGGCT ACCGGTTCTG 60  
 TCTATAGCAC TGGTCTATCA GCTATGTGGA TTACAATCGG TTTAACATTA GGTGCTTATA 120  
 TAAATTACTT TGTGTGCTT CCTAGACTTC GTGTTTATAC CGAATTAGCT GGAGATGCAA 180  
 TTACATTACC AGATTTCTTT AAAAATCGTT TAAACGATAA AAATAATGTG TTAAAGATTA 240  
 TTTCTGGATT GATTATCGTA GTATTCTTTA CATTATATAC nn 282

## (2) INFORMATION FOR SEQ ID NO: 3074:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3074:



AATCGAnAAA TCATGGATGT ACTTGAATCA AATGCAAACA GCGAAGTGTh TTGAATTGCA 120  
 TGGTAGCGTT ATAGACGAGC CAGTAGAAAT TCAATCAATT AAAGTATATG TTCCTAACGA 180  
 5 TGATGAAGGT CGTACGACAA CTGTAATTGG TAATGCTTTC CCTGACTCAG AAGTTAAATG 240  
 CATTACACCA GCAGATATCA TkGCTTCAAT GAGTTACTTC TTAACTTAT TAAGCGGtAT 300  
 TGGGtATACA GATGATATTG GACCATTaGG TAACCGTCGT TTACGTTcTG tAGGkGGaAT 360  
 10 TACTACmAAA CCaATTCCGT ATCgGTTTAT CCAAGA 396

## (2) INFORMATION FOR SEQ ID NO: 3075:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3075:

ACCTACATTT GCAGTTGTCG GTGTATAACC GGCTGGTGTT GAAAACTCTA CACTATAAGT 60  
 25 TCCATTGCTT AAACCAGTGA ACTGATATTT ACCATTTTCA TCTGTTGTCG TACGATCTAA 120  
 TTCTTTACCG TTAATATCTT TAAGAATGAC ATAAACACCT TTAATCCCTT TTTCATTGGC 180  
 ATCTTGTTTA CCATCTTTAT TTGTATCTCC CATACATAGT CACCTAGATT ATATTChTTT 240  
 30 GGGCGCCATA GCAGTTGATG AGCATTACACA TTGAAAACT ATTGACCACT ATATTAGTTT 300  
 GCAGTGCTAA GnATAACATT TCCATACGTG ACATACTGAT AGACTGTGAG TGATGTATGC 360  
 35 GCTGnTGCTC ATAACG 376

## (2) INFORMATION FOR SEQ ID NO: 3076:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3076:

TTACATCACC AATTAGACGT TATCCTGATT TAACAGTTCA TCGTTTAATC CGTAAGTATT 60  
 50 TAATTGAGAA ATCAATGGAT AACAAAGAAG TGAAGCGTTG GGAAGACAAA TTGCCTGAGT 120  
 TAGCTGAACA TACTTCTAAA CGTGAACGTC GTGCTATTGA GGCAGAACGT GATACTGATG 180  
 AATTGAAAAA AGCAGAATAT ATGATTCAAC ATATTGGTGA TGAATTTGAA GGTAATGTCA 240

AAAnGcNnGA TATACGTTTG AGGCGCAATG C

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(2) INFORMATION FOR SEQ ID NO: 3077:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3077:

AATCATATGC ATCGATTTC AGCAACAGCA ACCATTTCATC CTATGTCCCA TTAGCAAATT 60  
 TTTTGGATGA AACATGAATG GCAAGATGTA TTTCAACGTA CTGCTAATTT GCAGATATTA 120  
 AAACATACnT TTCTATCATT ATTGATACAT ATATCATGAT TATTCATGGC TTCCGCAACA 180  
 GGATGTTTAT TTAGAAACAT TAGATTGGGA TGTTGAGGCA TAGAACTGCT GGGTATTTC 240  
 AAGGAAATGT TGCCGGAATT ATTCCAACAA CTATTGATGT AAGTATGAAA GAACGTATGC 300  
 AACATAATGG GCTAATAAAG TACACCGTnT GTTAATGGTG CnATG 345

(2) INFORMATION FOR SEQ ID NO: 3078:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3078:

GATTATCAAG CGATTGATCA AGTATCATCA TTGTTGAAAG AAAAATATGG CATTGCACAT 60  
 TCAACGTTGC AAATTGAAAA CTTGCAATTG AATCCATTAG ATGAGCCATA CTTGACAAA 120  
 TTAACATAAA TAAACATTG TAGCGCCTAA AACATTAATC TATGTCATAG GCGCACGTTT 180  
 CGTTTTATAC TTATGTTGCA TCATTTAAAT GATTTTCGTC AATTTCTTTG ATGCTATCTA 240  
 CATCTAACAC GAGGTAACT TGC GTTGATT TTGATAAAGT GATCATAGCT TTTAGTACTT 300  
 GAGGATTTTT ATTGTTGCTG TTACGAATGT GGT CATGTTT AATGCGGGAC AGTAATTTAA 360  
 GTTGTTTTTT TACAATTGAG AGTGTGATAT TTCGATTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3079:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3079:

5 AAACGTTTAA TATACACTTT TACACGTCGC CTTCAATTGAA GCGAATTGCC ATAACCTTCA 60  
 CATTATATAT AGTTCTTTCC ATATAAATGT CCAAATTTT AGAACAACGC AATAATAAC 120  
 CATCCACCTA ACTTATCAAA AATTAAAGTG GATGGTTTTT CATTTTCATT TATATTTATA 180  
 10 TTAGTGTTAA TCCAATCATA GATTATCTA TATGCACTGC TCTATACaTT TCCTCaTTTA 240  
 ATTTGcYTTA CTTTCATTTA TATCATTATC AGAACACTTG GCGTGTCATC GnTATTATTT 300  
 CGCATCTTTG AnACGTTTA 319

15 (2) INFORMATION FOR SEQ ID NO: 3080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3080:

TCAAATGCAT CTAGGnCACA TTATTCTATT TGGGCATTCT TAGTGCTGTT CTTATTTGCG 60  
 GCTTTAACGT CATCTATTTT TTTATTAGAA TTAAATGTTT CTAAC TTCAC GAAGAATGAC 120  
 30 AATACAAAAC GTAAAAAAGT CGCAGTGATC GGTAGTATTT TAGTATTTAT CATTAGTATT 180  
 CCAGCAACCT TATCnTTTGG TATCCTAAAA GATGTAAGAT CGGTGCGGGA ACGATTTTGT 240  
 ATAATAAGGA TTCCACCGTT CGAATGTAAT GAAGCCATAA GCGGG 285

35 (2) INFORMATION FOR SEQ ID NO: 3081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3081:

ATCATAGCGT TTCTCCTAAA AATTACGATT AATCAAAGTA TGCCATTATT TAACTTTAGT 60  
 TTCTTCAGAA TTATTTGCCC CATTATCATG TTTTCTTCT TTATTAACAG CATTTTATC 120  
 50 ATTTTAAACA AGATACAATT TACCAATTAA TGGGCGGTGT GCGTGCTGGT ATGGGTTATA 180  
 CTGGTTCACA CGATTAAAGA GAATTACGCG AAGAAGCACA ATTTACACGT ATGGGTCCTG 240

CATTCTAATT AAGATAAAGG AGAACGACAA ATATGGGAAA TGGCAAAGGA CCAAGAGTTA 360  
 ATCCTTGTCT TAGGACTTTG GTAGGCCATT ACACCCATTA 400

(2) INFORMATION FOR SEQ ID NO: 3082:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3082:

TGAATTTGCT CCAAATAAAA ATACAATTGC CATTAATAATC ACCAGATATT ACAAGTGGCA 60  
 ACATGTTAGA AACACCGTTC ATTAAGTGTT TATAGAATGC TTTACCTGGG CTTATTTCTT 120  
 GACTGTCATT TGAGTTACCT GGCAACAAAA GGTTTACGAC TTGTATCTAA TGAATACCAT 180  
 CTGCTACTGG TnCTTCTACG ACATTTTTTAC CATCGAnGCG GTCCGTCTCA ACATGTACAT 240  
 CAGCAGCA 248

(2) INFORMATION FOR SEQ ID NO: 3083:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3083:

TACTAAAGGT TTAAATCAAA AATGGCTAGG TATCGTATTT GCGATTTTAA TTACAATTAC 60  
 ATTTGCATTT GTATTTAACA CAGTGCAATC TAATACAATT GCGGAGTCGT TAAATACGCA 120  
 ATATAATATT AGTCCAGTAA TCACAGGTAT TATTTTAGCA ATCGTAACAG CTATTATTAT 180  
 ATTTGGTGGT GTACGTAGTA TTGCTACGTA TCCTCGTTAA TGTACCGATA TGGCTATCAT 240  
 TACATGGTAT GGTTTAGTAA TAATGCTATT AATTTAGACC AATTGTCCnA TGATAGGACG 300  
 ATATAAAAGG CATTGGnACG ACAAGnACTG GTGCGCTGAG GGCTCGGTCT CCAGGACAAC 360  
 GGGGTATC 368

(2) INFORMATION FOR SEQ ID NO: 3084:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3084:

5 TTGGACTTTA TAAAGTTACT AAGTTGTAGA TTATCCTGGT AAAGAAGATA TTGCGGTTGT 60  
 ACAAGTTGAA GAAAAATCAA CACAACCAAA AGGTAGAAAA TTCAAAGATT TCACTAGTAA 120  
 ATTTAATATA GCATCAGAAG CTAAAGAAAA TGAACCTATA TCAGTCATTG GTTATCCAAA 180  
 10 TCCTAATGGA ATAACTACAA ATGTATGAAT CAACTGGTAA AGTATTATCA GTGAATGGGA 240  
 TATAGTGnAT CGGATn 256

(2) INFORMATION FOR SEQ ID NO: 3085:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3085:

25 ATATGCATAT GCTTCTTTAG GTGAACGAAT ATCTGGTTCA GATACGATTT CAATTAGCGG 60  
 TGTACCTTGA CGGTTCAAGT CAACTAATGA ATACTCCACC TTTATGTGTT GACTTACCAG 120  
 CATCTTCTTC CATGTGAAGA CGAGTAATAC CGATTCGnTT TGTTCACCG TCGACTTCGA 180  
 30 TATCGATATA TCCCATTTCA CCAATTGGGT TGATCAATTG AGAATTTGAT AGCTTTGGGA 240  
 TATCGGGATA GAATAGTCTA CGGTCAACTA GATCnGGTGC GAnTCCATAT TTAGTGCCAT 300  
 GCAGCACGCA T 311

35 (2) INFORMATION FOR SEQ ID NO: 3086:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 40

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3086:

ATGTAAATGA TCATCCTTCA TAATAACAAC GATTACTGAT CTTGATCATG ATTTTGAACA 60  
 ATAACAACCTG CTTTATTAAT ACCTTGTATA CGCTCGAGnC ATGCCAACCT CTGACAACCTC 120  
 50 AATCCTAAAC CCTCGAATCT TAACTTGTTT GTCCTTTCGA TATAAATAAT CTATGTTGCC 180  
 ATCGGGTAAC AAACGAACGA TATCACCCT TCCTATACAT CAGCTGATTT ATATTTGAAT 240

55

## (2) INFORMATION FOR SEQ ID NO: 3087:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3087:

GTAAAGATTT CAATTCATCA TCTTTAAATA AACTTAATGG TAATTnGTTA TACCnAATAA 60  
 AGCCTTCTGG ACACTTCCTT TAGACCGACG ACCGTCCTTAG CTAATGTCGA TTTCCCTGAC 120  
 CCTGATTCAC CGACAATGCC TAATGTTTCG CCTTTTCTAA TAGCCAAGTT AATATCATAA 180  
 CTGCTCGGTA TGGGCTGCCC CTCGGTGATG TGTAATCCAC GCTCCACGCG ATCGATTTTA 240  
 ATAAAATATC ATGGTT 256

## (2) INFORMATION FOR SEQ ID NO: 3088:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3088:

AAGGTTATTT GAATGATCAA GGTATCCACA AAAGAGGTGC TGAAATAGAT CGACTCGTTA 60  
 AAGGATGTAC AGGTGTTAAA CGTACAAC TGACAGCATCC AGGGGGTATT ATTGTAGTAC 120  
 CTGATTACAT GGATATTTAT GATTTTACGC CGATACAATA TCCTGCCGAT GATCAAAATT 180  
 CAGCATGGAT GACGACACAT TTGATTTCCC TTCCTnTCAT GATATGTATT AAAACCTGAT 240  
 AAACnTGGAC ACGTGATCCC ACCATGATCG ATGCCTCCAG ATTATCAGGA ATGATCCAAA 300  
 ACCATACCTG AGATGTAAGA GTATCAGTAT TAGACnC 337

## (2) INFORMATION FOR SEQ ID NO: 3089:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3089:

AAACATTACT TTACGCTATC AATGGTGGTA AAGATGAAAA TCTGGTGCAC AAGTTGGTCC 120  
 AAACCTTCGAA GGTATTAACA GCGAAGTATT AGAATATGCC GAnATTCAAG AATTTGATCA 180  
 5 AATGATGGAT TGGCCTAGCA GGTGTTTACA TTAACCTCATT AAATGTATnA CTACATGCAC 240  
 GATAATACAG CTATGACGAT TGAATGGATT ACATGTACAG AATTGTCCGn CCATGGCACA 300  
 GGA 303

10 (2) INFORMATION FOR SEQ ID NO: 3090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3090:

CTTTCGTAA AGGGGCATAT TCATATAATG GATGGTCATT AATAATAATT CCTGCCGCAT 60  
 GTGTAGATGT ATGTCTTGGT AAACCTTCTA ACTTTTTTACA AATACTGAAC CAGCGTTCAT 120  
 25 GTCGATGGTT TCGATGTACA AACTCTTTAA AATCGTCAAT TTGATATGCT TCATCAAGTG 180  
 TAATTCCTAA TktATGTGGG ATTAAACTTG GAAATTCAT TtAATGTAAC TTCATCAAAC 240  
 CCCATAATTC TTCCAACATC TCTAGCAACT GCTCTTGCAA GCAGATGACC GAAAGTCACA 300  
 30 ATTCCAGATA CATGTAGCTC GCCATATTTT TCTTGACGT ACTGAATGGA CCCTTTCTCG 360  
 GnGTGTATCT GCAAGGTCAA TTTTCATTnT CAGGCATGGT 400

35 (2) INFORMATION FOR SEQ ID NO: 3091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3091:

45 TTGTTTTTTC ACGTTCAATn ATTATCTTCA ACTTGTGACT ACAGATTTTA AAATGGAATT 60  
 TACAAGTATC TTCTTCAATA TTTTGCATCA TGATATCAAA TAATTCATGA CCTTCATTTT 120  
 GATAGTCACG TAATGGATTT TGTGTGTCAT AAGAACGTAA GTGAATACCT TGACGTAATT 180  
 50 GGATCCATGT GTCGATATGG ATCAGTCCAA TGGCTATCAA TAGAACGAGG TAAAATCATA 240  
 CGCTCAAACC CCATCCATTG GnTCCTCTAA GATACCTTTT GACCTTGGAT AGCnGCTCAA 300

## (2) INFORMATION FOR SEQ ID NO: 3092:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3092:

```

CGACACCTCA ATAATCATAT CGTAATGTTT AACTTTTCCT GATTTAAATG TAATTTTCATT      60
TCCATTGATA GCATTAATTT CCTCATTTAA ACGGTATGGA ATCTCCCGCT TATCTAATTC      120
ATCAAGTATA GGTTGATTCA GTCGGCATCC ATAATTTATT TATCTTATCA GATCGATGAA      180
TAAAGTAGGG TGTAACCAC GTTCCATAAA GATTTCAGG AACTCCAATG GAACATAACC      240
TGCACCTACC ACCAATACTT TATCCACTTG GATTGGCTTG GAGGAATGGT CGGATAGGCA      300
TCCAGGGCCT CCAAAATTCC nAGGGGAAAn GGTAAATATCC ACCTTCCAAG GCCAAGGGCC      360
AATTGGCACC TGGCCACCCA GGGnCTTAA AAGGGGTAA      400

```

## (2) INFORMATION FOR SEQ ID NO: 3093:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3093:

```

TTATACCCGn CAAATTCATA AATATAGTnC CTTTCAATA GATTGATATG TATGTCTAAA      60
TGTATCGATT AACTTTGCTA ATGCTGCTTC ATCTAATGGT CGGTCTGCTA ATTTTAAAAA      120
TGTATTCTTC AATAGGTATT CCCATATAAT GCGTTATTTT TTAGATGAT GGTTCCGTTA      180
AGCCACATGC TTAAATGCA CTTTGTGTG CTACTTCACC ACATTTTTTC GTGTCTGCCA      240
ACGTACCATC AA      252

```

## (2) INFORMATION FOR SEQ ID NO: 3094:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



AATCTATTAA TAATGAAGAA AAAATTGTAC TAGCACGTAG ACGGTTAATA AAGTTCGATA 60  
 AAGATATCAG TATTCCATAT ATTCTAAAGC AAGCATATTC TAAAGAAAAA AACAGTTATA 120  
 5 TATTCTTGTT AGAATCACAA GATTCTATAT TCTTTTCACA AACACCTGnn CAATTAATAA 180  
 AGGTCAATAA TAAAATCTAT CGACTAAAGC TGTGCAGGTC AATTAAACGG TCACAAGTGA 240  
 GGCCGAGGTA CAAAAAATGT TGAGCATTTT AAAGTATAAA CTTATCGACA CGnTTGTGTG 300  
 10 CAGTTTTTCAT GTTT 314

(2) INFORMATION FOR SEQ ID NO: 3095:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3095:

GGTGAGGCGG CATTGAGAAA AAATGCTGAA GTAATCGAAG CTGTATCGCA GTCTTGTTTG 60  
 25 ACAACAGGAT TTTGTTTATG GTGCCAATTA GCTTTTTCAA CGTATTTAGA AAATGCCACG 120  
 CAGCCACATT TAAATAATGA CTTACAACAG CAATTGTTAT CTGGAGAAAT ATTAGGTGCT 180  
 ACCGGATTGT CTAATCCCGA TGAAGTCATT TAATGGATTT AGAAnAAGTT GGACCCTTTG 240  
 30 AAACACCACC TTAATGTTGG ATGGGACCAA TTGGGTGGTC CAGTGGGAnC GTAATGCCCA 300  
 GCTGTAAAGT nATAATCCAA GGAAAGACCC AT 332

35 (2) INFORMATION FOR SEQ ID NO: 3096:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3096:

45 TTTATGCATA CGCGCACTCA TCACACTACC GACAACAACA TCATCTTTTC GAGCATATCT 60  
 ACTTAACAAC GTCATGACCA CACTCATAAA GAACATAAAA TCAGTAATTT GATGCTTTTC 120  
 TACATACTTT TGAAGTAGCT GTCTCATTTG TTGATTCATG TAAATGACAT CATGCTCCAT 180  
 50 TTGTCGGTTT AATAATTGGT CTAACATAnT CTGTCGGGTA AGCCTAAAAT AGGGTACTTC 240  
 ATCCTTGAAT TGAGGATACC CATATTGGTC CTAAGGTTTCG GTCCATATCC ACGGATGGCG 300

ATTTAAGGTT GGATAAAGGT GCCGTTAAGG ATCCAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 3097:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3097:

15	ACTCTGGTCC TTCTGCATAA CTGCCGTAAA TAATTCACCT TCATCACACG CTGTACCTAC	60
	CAATAATCCC nCACGATATA CGTGGAATTC GAGGTGTACG GTAGAAATAC TTCACCAATG	120
	ATGCACTTAC AATTTTAAAT AGATTTTTTAA GACCTTGTTG GTTTTGTACA ATTAATGTGA	180
20	CATGACTAGG TCTTGCACGT TTATATGCAT CTTCACTACT GAGTTTTTTG GTTGATTnC	240
	GTTATGATTT AATACGGCTA ATTCT	265

(2) INFORMATION FOR SEQ ID NO: 3098:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3098:

35	CTAATGTATC AGTTTGGCAT GAATTCTTTT GCATCTTTCA ATAATTGTTG TGATCTTTTT	60
	TAGTCACATC ATCAATTTTC TTATCTTCGT ATAATGCTTT TTCAATCTTA TGATATCCTG	120
	ACCATTCTTT TTCCTTTTTT TCTTCTTTCA TATCTGCAAG CGGGCATCCA ATTTTAGGAT	180
40	CCTAAATCTC CCAAATGCTT CTGAACTGGT CAGAGCGTCA TAATACATAC GACTTTTGGG	240
	TATACGCTTT TnCTTGGGCA TACATTATTT CAATCGTTTA CAAATTTTTTC TGACCTTTTA	300
	AAATCATnA CTGTCAnCAG A	321

(2) INFORMATION FOR SEQ ID NO: 3099:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ATCCGCAATC TGAGAAACAT CATCTTCGAG TTGTTGGAGG GTTCCAATTT TCAAGTCATA 60  
 AATCAGATGA TGAATGGCGA GAGTTTGGAC TAAATCATTT TGTATTACCT GAAGTTTAA 120  
 5 TTTCAACTGA TAATAATGGG ACATTTTAA CTTATACAGT TAAAAGGGAA AGTTTACTG 180  
 TTGAGGCATT GAACGATTTA ATGGATTGTT CAACAATATA TCGGACATAG AGTGGACGAC 240  
 CAATGGGGGA ATACCAGAAT GAGATATTAT AAAACA 276

(2) INFORMATION FOR SEQ ID NO: 3100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3100:

GTCATTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAC nTAAACGTT 60  
 GTTAATAACT TGCCGGGCTT CACACTAATC AATGGTGGCA AAGTAGGGGT GTTTAGTCAT 120  
 25 GCAAnGTTAA GAACGAGCAT GTTTGATTCA GGAGATAATA AGAACTATCA AGCACAAGGA 180  
 AATGTAATTG CATTAGGTCG TATACATGGA ACTGATACGA ATGACCATGG CGATTTT 237

(2) INFORMATION FOR SEQ ID NO: 3101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3101:

nCGATATAAC AAGGTTGTTA GACTTAAAGG TGGCGATCCA GCGATATTTG GTCGTGTGCA 60  
 AGAAGAAGTC GACATACTAA ATGAACATCA TATTGCGTTT GAAATTGTAC CAGGGGTGAC 120  
 ATCAGCGAGC GCnAGTTTGG CTACTATGCA GACAGGTTTG ACAATGCGTA CAGTTGCTAA 180  
 45 AAGTGTGGAC ATTTTCTACA GGTCACTTTT AAAGATTCAG AAGAAAATGA AGTGGGATGG 240  
 TCCATTCCTT AAGT 254

(2) INFORMATION FOR SEQ ID NO: 3102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3102:

CAATCACTCA TGTAATAATT GATACCTAAG AAGTCGTTTA AATCTTTGGC TGCATCTAAA 60  
 ATGGCATAAT CTTCAATnTGT AATGTTTAAAT TTACCGCCAn TAACAGATAA GATATGTTGC 120  
 ACACCTTCCA TCGTTTCACG AGTAATACTT ACCTAAATAT GTTGCACTTA AGATGAATTT 180  
 ATTATGGATG GATATCTTCT AAATTCTGCT GCACGGGACA TCTTCAGGAT TTGGATGGTT 240

## (2) INFORMATION FOR SEQ ID NO: 3103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3103:

GTTGTAAACT TCAATTGTTC AAATAAATAA CACATATCAT TGGAGGTGAA TTGATATGCC 60  
 AGATTCAATC ACAATTATAG ATGAAAACAA AGTGGTTGAT GTTGTATTAA TTGCAGGTAG 120  
 AATTTTACTT GAATCAGGTG CTGAnACATA TCGAGTTGAA GATACAATGA ACCGTATCGC 180  
 ACATAGTTAT GGTCTTCATA ATACATATAG TTTTGTCACT TCAACTGCAA TTATTTTTTC 240  
 ATTAAACGAT CGAACAAGTA CAAGATTAAT TCGTTACAAG AGCGTACAAC AGATTTAGGG 300  
 AAnGTGCGAA TAAGCGGGGn AATCTTTC 328

## (2) INFORMATION FOR SEQ ID NO: 3104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3104:

TTTTGCTTTG TCGCTAATA ATCTAATGTT CGTGAACCG nAACCAGAGA TATTACAAAT 60  
 ACATCATCGA CTAATCGCAG GTGTCGTTGA TTCTCCAACA ACATGTGCCT GTTTGCCGAG 120  
 CTGATTTAAG GCGGCATTGC AAACTATTC GCCACGAATC CTGAACGTCC TTTGCCAGCT 180  
 ACAAATATAT GTTCAGCATG TAGTATTTTG GATGCAAAGT TGAAAACTCA TCCGCTTCAA 240  
 CATGTGACAA AGTCACTTTA ATCnA 265

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3105:

ACTAGTAGAG TATCTAATGG TGATTTAATC ATTATTACTG CTGGTGTACC AACTGGTGAA 60  
 ACTGGAACTA CTAATATGAT GAAAATCCAC CTAnTTGGTG ACGAAATTGC TAATGGTCAA 120  
 nGTATTGGAC GTGGATCAGT TGTTGGTACT ACATTATTGC TGAAACTGTT AAAGATTTAG 180  
 AAGGTAAAGA TTTATCTGAC AAATTGATCG TTACTAACTC AATCGATGAA ACGTTTGTGA 240  
 CCT 243

## (2) INFORMATION FOR SEQ ID NO: 3106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3106:

CTATTGCGTT TGGGTAAATC TAAAGCAGGC GTAnATTATC AAAGTTTGGG ATATGCAACC 60  
 AGCACACTTA TTCTTTATGA TTGCAGCGCC AGAAGTGGnG CCCAAACACA TCTAGATGCT 120  
 TTACTAAGTT GTCTGGTATT TTAATGGATG AAAATGTACG TGAGAAATTA TTACATGCTT 180  
 CATCACCTGG AAGAAGTACT AGCGATCATA GATGAGGCTG GATGATGAAG TGGA 234

## (2) INFORMATION FOR SEQ ID NO: 3107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3107:

TTTTGAAGCG GCATAATCAT GAAGAATAGG ACTAGGATTA TAACCTTGTA CAGATGATGT 60  
 CGTTGTAATT GACGCACCCG GTTTTAAATA TTCCAATGAC TTTTGAACGT GTCCAAAATA 120  
 GCGnTAGAn ATTGTTTTCA AATGTTTCTG TAAATGCCTC AGTTGTAAAT CCATGAATAT 180

## (2) INFORMATION FOR SEQ ID NO: 3108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3108:

CTTTAAGTTA CGTTCGGCTT TGATTAAAGT AAAACGTGGT ACTGTTTCCT ATGACAAGAG 60  
 TCTAATTGGA TACAATGTAA ACAAATGGT GnATTTGTAT TATAGATAAT AAACATTCGn 120  
 TATACATTCA ACATATCGAT GACCACTTGG ATTAAGCAAC GTAATATCAT TCGTACTGCT 180  
 CAAGAAATGA CAAACGAAAT ACGAGAAAAT TTTGAGTCAT ACACGTCATT TAGAATGAAT 240  
 AGTATTATGC AAGTACT 257

## (2) INFORMATION FOR SEQ ID NO: 3109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3109:

CTTAAAGCCA AGTCGATCTG CTAATTTTGC AAGTGTCCT GAATCTTGCA ATGCCTTTTG 60  
 TGCATCCTTA CCTTCATCTA TTAAGGCATA GTCTAATACG CTTAATTTAA CCAATCCGTC 120  
 ATCTCCAAAC TTATCCTGTC ATGTCAAACC GACATAACAT TTGTAGCGTT CTTAATACCA 180  
 TTCCCTCTGC ATATACCCAC GTATATGATA ACGTnTTTCA nTTAACT 227

## (2) INFORMATION FOR SEQ ID NO: 3110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3110:

TTTCTTCATC GTTTGTGAGA AAGAGGTATT TTTAATTGGG AAAnCAGGTA AAAAGGATGG 60  
 AAGTACATAA AAAGAGCAAT GCTTGGGCAT TATTCCnCTT GTTATTATTT GTGGCGTTGT 120

GATAACGTAA TTGTGCGTTA TTAATGAATC GAAAAGAATC ATTGCTAAAA AGTGAGTCTC 240  
 CGAAAGGCGG CCTTCAACTG TTAAGAGTGA TTTATTGCAG GCTTCAATCG CGAAATGGTG 300  
 5 CnAAGCGCGT ATTAGCACTA GCCGAA 326

## (2) INFORMATION FOR SEQ ID NO: 3111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3111:

CTACGGCGCC TTGCATCTTT CCCAACAATT AACCCCAACT CTATTAGCAC AGATTATCA 60  
 20 ATTGATTCAT AAGCTTCATC AAAGGGTGAA CTAACATGCA TTAACGCTTC TTTAATATCA 120  
 ATTAAGTCGG CATGTTCAAC ACCAATTTTC CCTTTTTTAT TTTTAGCTTT TTCTCTATCA 180  
 ATATACGCAT GTTTAACACC TTTGACATGT TCAGTAAATT GTGACTTCCT nAATTTTTTA 240  
 25 TCCTCCCTTG GTGnnGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG 300

## (2) INFORMATION FOR SEQ ID NO: 3112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3112:

TTATTGTAA CACAAGnTT CGAACAAGGT TGGTTTAGTA CATTTTCAAT CATTTGTCTG 60  
 40 AGCATTTTTA TCATCACTAC GTTGATATTC ATCATCATCG AACGTCGACA TGAAGTACCT 120  
 TTTATTGATT TCTCAGTATT ACGCAACCGT CCGTTCATTG GTGCATTTTT AAATAACTTT 180  
 GTTTTAAATA GCGGTCTAGC GTAACAGGGT CTTTCATATA TGCTCAACAC ACCTGGTTTA 240  
 45 TCGCGCGCAA TCGGACTGTT ACATGCCAAT GCCATGGGCG TTCGAGATCG TTAGTGAAAG 300  
 CACATAGTTC GGGCAATGAG CCACATGGTC GTGTCCGTCA CGCACACATA TAGCAGCT 358

## (2) INFORMATION FOR SEQ ID NO: 3113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3113:

	TCGGTCTTGA AAACCGACAG GGGACTTAAC GGCTCGCGGG GGTTGGAATC CCTCTTCCTC	60
5	CGCCATCAAT ATTTATATTA AATTCTATAT ATAATGAAGG TAAGTGCTCA AATTTTGAGT	120
	ATTTACCTTT TTTATTGTG TTTGAATGGC TCGTAATTTT TGATAATAGA AATGATAAGG	180
	CATTGAGATT GGAAGGGCAT TTGGCTTGTG CAAATATACAT AGCAAAATGT CGTTGTTGTT	240
10	TTGTGATAGA T	251

## (2) INFORMATION FOR SEQ ID NO: 3114:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                             |
|----|-----------------------------|
| 15 | (A) LENGTH: 6591 base pairs |
|    | (B) TYPE: nucleic acid      |
|    | (C) STRANDEDNESS: double    |
|    | (D) TOPOLOGY: linear        |

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3114:

	TTTAAGTGAA TTnCTTTGGG TTACAGAAWT TTCAACAAC TTAAGCACG TATAATGATG	60
25	ATTTTCAGCT TGTACAAAGG AGAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC	120
	GCCTAATAAT AAAAAGTCTA AAAGTTGTAT TTTAAAAATA GTTCTTTTAA TTATATACCC	180
	ACCACATTG GTGGAGaACC GTTAAACAAT GCATAGTTGC TTAAGTTCCA ATATTGAACT	240
30	CATCATTACA ATTTGACATA GAGTCTATTA AAGCGTGTGC CATTTGAGTC CACTTTTATT	300
	TGTATTGTAT AGAGAGAAAT AAAAAGAAAC CTTGTTTTAC AAGGTTTCTA ATACGTTATG	360
	TTATGTAAAT AACAGTTAAT TATACCGGTG GTCGGGGTCG AACCGACACT CCACAAGTGG	420
35	AACGgGATTT TGAGTCCCGC GCGTCTGCCA ATTCGCCAC ACCGGCTTAA TGGTAAACAA	480
	AAAAGTTCCC TTTGGAAGCA ATTATGGAGC GGAAGATAGG ATTTACACCT ATACCTCGTT	540
40	CCGGAAGGA ACGTGTtCTA AAAGTTGAAC TACTCCCGCA AATATTAAAT TATGGAGCGG	600
	AAGATAGGAT TTACACCTAT ACCTCATTCC AGGAAGGAAT GTATTCTAAG AGTTGAAATA	660
	CTCCCGCATT ATTATTAAAT TATGGAGCGG AAGATAGGAT TTGCACCTAT ACCTCGTTCC	720
45	GGGAAGGAAC GTGTTCTAAA AGTTGAACTA CTCCCGCATA AACCTGGAGG CGGCAACCGG	780
	ATTTGAACCG GTGATAAAGG TTTTGCAGAC CTCTGCCTTA CCACTTGGCT ATGCCGCCAA	840
	TAACTGGGCT AGCTGGATTG GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG	900
50	CTTGGCTATA GCCCATTAAAT AATAAGGGCG GCTGAAGGGG ATCGAACCCCT CGAATGTCGG	960



	CGAACCACACA	CCAAAGGTTT	TGGAGACCTC	TATTCTACCG	TTGAACTATG	CCCCATTATA	1080
	AAATAATAAAA	TGGAGGGGGG	CAGATTCGAA	CTGCCGAACC	CGAAGGAGCG	GATTTCACAGT	1140
5	CCGCCGCGTT	TAGCCACTTC	GCTACCCCTC	CATAAATGGT	GCCGGCCAGA	GGACTTGAAC	1200
	CCCCAACCTA	CTGATTACAA	GTCAGTTGCT	CTACCAATTG	AGCTAGGCCG	GCTAAGAAAT	1260
10	GGTTCAGGAC	AGAGTCGAAC	TGCCGACACA	TGGAGCTTCA	ATCCATTGCT	CTACCAACTG	1320
	AGCTACTGAA	CCATAATAAA	AATGTAATGA	TGGCGGTCTC	GACGGGAATC	GAACCCGCGA	1380
	TCTCCTGCGT	GACAGGCAGG	CGTGTTAACC	GCTACACTAC	GAGACCTATA	AAATATTGCG	1440
15	GGAGGCGGAT	TTGAACCACC	GACCTTCGGG	TTATGAGCCC	GACGAGCTAC	CGAACTGCTC	1500
	CATCCCGCGA	TAATAAAAAA	TAATGGCGGA	GGAAGAGGGA	TTCGAACCCC	CGCGGCCCGT	1560
	TAAGGCCCTG	TCGGTTTTCA	AGACCGATCC	CTTCAGCCGG	ACTTGGGTAT	TCCTCCATTA	1620
20	TTATAGGTAA	ATCGCTATTA	ATTATAAAAT	TAAATGGCGG	TCTCGACGGG	AATCGAACCC	1680
	GCGATCTCCT	GCGTGACAGG	CAGGCGTGTT	AACCGCTACA	CTACGAGACC	ATTAGTAAAA	1740
	CGGAGGAAGA	GGGATTCGAA	CCCCCGCGAG	CCGTTAAGCC	CCTGTCGGTT	TTCAAGACCG	1800
25	ATCCCTTCAG	CCGGAATTGG	GTATTCCTCC	AAAATTATAT	GGaCtTGCAG	GACTCGAACC	1860
	TGCGACCGAA	CGGTTATGAG	CCGTTAGCTC	TAACCAACTG	AGCTAAAGGT	CCTAAATATA	1920
30	ATTTTACAAC	TAATAAATAG	TGGCGGTGGA	GGGGATCGAA	CCCCCGACCT	CACGGGTATG	1980
	AACCGTACGC	TCTAGCCAGC	TGAGCTACAC	CGCCTTATAT	AGTTTGTAAA	TAATATGGTG	2040
	GAGACTAGCG	GGATCGAACC	GCTGACCTCC	TGCGTGCAAA	GCAGGCGCTC	TCCCAGCTGA	2100
35	GCTAAGCCCC	CATAATAATT	ACAGTATATC	GGGAAGACAG	GATTTCGAACC	TGCGACCCCT	2160
	TGGTCCCAAA	CCAAGTGCTC	TACCAAGCTG	AGCTACTTCC	CGTATAATTA	ACGCGCCCGA	2220
	TAGGAGTCGA	ACCCATAACC	TCTTGATCCG	TAGTCAAACG	CTCTATCCAA	TTGAGCTACG	2280
40	GGCGCATATG	TTTTTATTGA	AAATGGTGCC	GAGGACCGGA	ATCGAACCGG	TAcGgTGATC	2340
	ACTCACCGCA	GGATTTTAAG	TCCTGTGCGT	CTGCCAGTTC	CGCCACCCCG	GCACTATAAA	2400
	AATGGAGCAG	AAGACGGGAT	TCGAACCCGC	GACCCCAACC	TTGGCAAGGT	TGTATTCTAC	2460
45	CGCTGAACTA	CTTCTGCATA	TGCGGGTGAA	GGGAGTCGAA	CCCCCACgCC	GTAAGGCGCT	2520
	aGATCCTAAG	TCTAGTGCGT	CTGCCAATTC	CGCCACACCC	GCAAATGGTG	AGCCATAGAG	2580
50	GATTTCGAACC	TCTGACCCTC	TGATTAAAAG	TCAGATGCTC	TACCAACTGA	GCTAATGGCT	2640
	CTTCCATGGT	GCCGGCCAGA	GGACTTGAAC	CCCCAACCTA	CTGATTACAA	GTCAGTTGCT	2700
	CTACCAATTG	AGCTAGGCCG	GCAATATGTA	AGAATAAATG	GTGGAGAATG	ACGGGTTCGA	2760

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	AAACTGCCTG	GCAACGTTCT	ACTCTAGCGG	AACGTAAGTT	CGACTACCAT	CGACGCTAAG	2880
	GAGCTTAACT	TCTGTGTTTCG	GCATGGGAAC	AGGTGTGACC	TCCTTGCTAT	AGTCACCAGA	2940
5	CATATGAATG	TAATTTATAC	ATTCAAAACT	AGATAGTAAG	TAAAAGtGnA	TTTTgctCGC	3000
	AAAACATTTA	TTTTGATTAA	GTCTTCGATC	GATTAGTATT	CGTCAGCTCC	aCATGTCACC	3060
	ATGCTTCCAC	CTCGAACCTA	TTAACCTCAT	CATCTTTGAG	GGATCTTATA	ACCGAAGTTG	3120
10	GGAAATCTCA	TCTTGAGGGG	GGCTTCATGC	TThAgGATtT	TCAGCACTTA	TCCCGTCCAC	3180
	ACATAGCTAC	CCAGCTTATG	CnTTGGCACG	ACAAcTGGTA	CACCAGAGGT	ATGTCCATCC	3240
	CGGTCCTCTC	GTACTAAGGA	CAGCTCCTCT	CAAATTTCTT	ACGCCACGA	CGGATAGGGA	3300
15	cCGAACTTcT	aCGACGTTCT	GAACCCAGnC	sTGTACCGCT	TTaATGGGCG	AACAGCCCAA	3360
	CCCTTGGGAC	CGACTACAGC	CCCAGGATGC	GATGAGCCGA	CATCGAGGTG	CCAAACCTCC	3420
20	CCGTCGATGT	GAACCTTTGG	GGGAGATAAG	CCTGTTATCC	CCGGGGTAGC	TTTTATCCGT	3480
	TGAGCGATGG	CCCTTCCATG	CGGAACCACC	GGATCACTAA	GTCCGTCTTT	CGACCCTGCT	3540
	CGACTTGTAG	GTCTCGCAGT	CAAGCTCCCT	TATGCCTTTA	CACCTCTATGA	ATGATTTCCA	3600
25	ACCATTTCTGA	GGGAACCTTT	GAGCGCCTCC	GTTACCTTTT	AGGAGGCGAC	CGCCCCAGTC	3660
	AAACTGCCCCG	CCTGACACTG	TCTCCCaCCA	CGATAAGTGG	TGCGGGTTAG	AAAGCCAACA	3720
	CAGCTAGGGT	AGTATCCCAC	CAGCGCCTCC	ACGTAAGcTA	GCGCTCACGT	TTCAAAGGCT	3780
30	CCTACCTATC	CTGTACAAGC	TGTGCCGAAT	TTCAATATCA	GGCTACAGTA	AAGCTCCACG	3840
	GGGTCTTTCC	GTCCTGTCGC	GGGTAACCTG	CATCTTCACA	GGTACTATGA	TTTCACCGAG	3900
35	TCTCTCGTTG	AGACAGTGCC	CAAATCGTTA	CGCCTTTTCGT	GCGGGTCGGA	ACTTACCCGA	3960
	CAAGGAATTT	CGCTACCTTA	GGACCGTTAT	AGTTACGGCC	GCCGTTTACT	GGGGCTTCGA	4020
	TTCGTAGCTT	CGCAGAAncT	ArCcACTCCT	CTTAACCTTC	CAGCACCGGG	CAGGCGTCag	4080
40	cCctATACAT	CACCTTACGG	TTTAGCAGAG	ACCTGTGTTT	TTGATAAACA	GTCGCTTGGG	4140
	CCTATTCACT	GCGGCTCTTC	TGGGCGTTAA	CCCTAAAGAG	CACCCCTTCT	CCCGAAGTTA	4200
	CGGGGTCATT	TTGCCGAGTT	CCTTAACGAG	AGTTGCTCG	CTCACCTTAG	AATTCTCATC	4260
45	TTGACTACCT	GTGTGCGTTT	GCGGTACGGG	CACCTATTTT	CTATCTAGAG	GCTTTTCTCG	4320
	GCAGTGTGAA	ATCAACGACT	CGAAGACACA	ATGTCTTCTC	CCCATCACAG	CTCAGCCTTA	4380
	ACGAGTACCG	GATTTGCCTA	ATACTCAGCC	TTACTGCTTA	GACGTGCAAT	CCAATCGCAC	4440
50	GCTTCGCCTA	TCCTACTGCG	TCCCCCATC	GATTAAAACG	ATTATAGGTG	GTACAGGAAT	4500
	ATCAACCTGT	TATCCATCGC	CTACGCCTGT	CGGCCTCAGC	TTAGGACCCG	ACTAACCAG	4560

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	TTCGCTACTC	ACACCGGCAT	TCTCACTTCT	AAGCGCTCCA	CATGTCCTTA	CGATCATGCT	4680
	TCAACGCCCT	TAGAACGCTC	TCCTACCATT	GTCCAAAGGA	cAATcCACAG	CTTCGGTAAT	4740
5	ATGTTTAGCC	CCGGTACATT	TTCGGCGCag	TGTCACTCGA	CTAGTGAGCT	ATTACGCACT	4800
	CTTTAAATGA	TGGCTGCTTC	TAAGCCAACA	TCCTAGTTGT	CTGGGCAACG	CCACATCCTT	4860
	TTCCACTTAA	CATATATTTT	GGGACCTTAG	CTGGTGGTCT	GGGCTGTTTC	CCTTTCGAAC	4920
10	ACGGACCTTA	TCACCCATGT	TCTGACTCCC	AAGTTAAATT	AATTGGCATT	CGGAGTTTGT	4980
	CTGAATTCGG	TAACCCGAGA	GGGGCCCCTC	GTCCAAACAG	TGCTCTACCT	CCAATAATCA	5040
15	TCACTTGAGG	CTAGCCCTAA	AGCTATTTTCG	GAGAGAACCA	GCTATyTCCA	GGTTCGATTG	5100
	GAATTTCTCC	GCTACCCTCA	GTTTCATCCGC	TCACTTTTCA	ACGTAAGTCG	GTTCCGGTCTT	5160
	CCATTCAGTG	TTACCTGAAC	TTCAACCTGA	CCAAGGGTAG	ATCACCTGGT	TTCGGGTCTA	5220
20	CGACCAAATA	CTAAACGCCC	TATTCAGACT	CGCTTTCGCT	ACGGCTCCAC	ATTACTGCT	5280
	TAACCTTGCA	TCAAATCGTA	ACTCGCCGGT	TCATTCTACA	AAAGGCACGC	CATCACCCAT	5340
	TAACGGGCTC	TGACTACTTG	TAAGCACACG	GTTTCAGGTT	CTATTTCACT	CCCCTTCCGG	5400
25	GGTGCTTTTC	ACCTTTCCTT	CACGGTACTG	GTTCACTATC	GGTCACTAGA	GAGTATTTAG	5460
	CCTTAGGAGA	TGGTCTCTCC	AGATTCCGAC	GGAATTTTCA	GTGCTCCGTC	GTACTCAGGA	5520
	TCCACTCAAG	AGAGACAACA	TTTTCGACTA	CAGGATTATT	ACCTTCTTTG	ATTTCATCTTT	5580
30	CCAGATGATT	CGTCTAATGT	CGTCCTTTGT	AACTCCGTAT	AGAGTGTCTT	ACAACCCCAA	5640
	CAAGCAAGCT	TGTTGGTTTG	GGCTCTTCCC	GTTTCGCTCG	CCGCTACTAA	GGGAATCGAA	5700
35	TTTTCTTTCT	CTTCCTCCGG	GTACTAAGAT	GTTTCAGTTC	TCCGGGTGTG	CCTTCTGATA	5760
	TGCTATGTAT	TCACATATCG	ATAACATGAC	ATAACTCATG	CTGGGTTTCC	CCATTCGGAA	5820
	ATCTCTGGAT	CAAAGCTTAC	TTACAGCTCC	CCAAAGCATA	TCGTCGTTAG	TAACGTCCTT	5880
40	CATCGGCTTC	TAGTGCCAAG	GCATCCACCG	TGCGCCCTTA	ATAACTTAAT	CTATGTTTCC	5940
	ATCCTACAGG	AAACGCGTTA	TTAATCTTGT	gaGTGTTCTT	TCGAACACTA	GCGATTATTT	6000
	CTTATGAATT	CAAGCTTATT	TAAAACTCTT	TATTCACCTG	GTTTTGCTTG	GTAAAATCTA	6060
45	TATTTTACTT	ACTTATCTAG	TTTTCAATGT	ACAATTTCTT	TTTAGTCAAG	CGCTCGCATA	6120
	AGCAATATCA	CTTTAACCAA	AAAATATTTG	AATGTTAAAT	AAACATTCAA	AACTGAATAC	6180
	AATATGTCAC	ATTATTCCGC	ATCTTCTGAA	GAAGATGTTT	CGAATATATC	CTTAGAAAGG	6240
50	AGGTGATCCA	GCCGCACCTT	CCGATACGGC	TACCTTGTTA	CGACTTCACC	CCAATCAATT	6300
	GTCCACCTT	CGACGGCTAG	CTCCTAAAAG	GTTACTCCAC	CGGCTTCGGG	TGTTACAAAC	6360

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ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC AATCCGAACT 6480  
 GAGAACAACCT TTATGGGATT TGCTTGaCCT CGCgGGTTTCG cTkGCCTTTG TAATGTCCAA 6540  
 5 TGTAGCACGT GTGTAGCCAA ATCCATAAGG GGCATTATGA TTTGACGCAT C 6591

(2) INFORMATION FOR SEQ ID NO: 3115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3115:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60  
 20 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTCGAATAA AGGTAGCATA 120  
 TGTAAATTGTT TGTGTTTACG TATTTCTGGT GTAAGTTCCG TGAAACCAAT GTCTATATTC 180  
 CCATTAATAC GCTATTATAA TGTGTCAGGT CCAATAAGCC CCGGATGACA TGTGTATCCA 240  
 25 TTTGGAAATG GAACCGTTGG GAAAGTGGGA ATAACATGGG GGAACGTCA<sub>n</sub> TCCCC<sub>n</sub>CCAA 300  
 GCCCAT<sub>n</sub>GAG GTACCTTTAA TTTTA 325

(2) INFORMATION FOR SEQ ID NO: 3116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3116:

CCG<sub>n</sub>TTGAGT TCGGTGGCGA CATGATTGAT TTTGTAAGTA AGTATGATGC AACATGGGCT 60  
 G<sub>n</sub>TTTACCTA CTAAATTTGA GGCGGTACT CCATTAATTG CTCAAGCATT GGGCTTGTC 120  
 GAAGCTATTC GCTATTTAGA ACGCATAGGT TTTGATGCAA TTCATAAATA TGAACAAGAA 180  
 45 TTAACGATAT ATGCTTATGA GCAAATGTCT G 211

(2) INFORMATION FOR SEQ ID NO: 3117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3117:

AACGTnTTTT GAAATGATTG CGGCGATGTT GGCGACAGTT AAAGTAGGTG GCATCTTATA 60  
 5 TACCTATCGA TATTGATTTT CCGAATAAAC GACAAGGTGC AATTTTGGAG GATGCTAAAG 120  
 TAACTGCAGT CATGTCTTAC GGCGTTGnAA TTGAAACGAC ATTACCAGTC ATTCAATTGG 180  
 AAAATGCTAA AGGCTTTGTT GAATCAAAGG 210

## (2) INFORMATION FOR SEQ ID NO: 3118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3118:

TTAATTGATC CTAGCTTGGT TTGCCTCTGT CACTTTATCA TTGATATTTT GGACAGTTGG 60  
 GTTGCCATTC AACACTTGAT TAATTTTCAGT TAACTTTTGA CGCGCTGCTT GTAATTTTGT 120  
 25 GGTGTACGCA TTAAACGAAC GGnCGTCATA CCTGTTGTAT CCGTTGGTTG ATTAATGCTT 180  
 GTTCTAAATT GCGTTTCCAA GTTTnAAGCG GCGCTTATCT GGTGT 225

## (2) INFORMATION FOR SEQ ID NO: 3119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3119:

CCAACATGAT GCTAGTTTGA TTAAGTTTCT TCTAAACAGA CTTCAAACGG CATGGTTTAG 60  
 CATATCCTAT TAAGGTTGAA TCGCGTTAAC AGCACATAGG AAATGCTGTT AGGCGATGCA 120  
 GAGTGCATGATT AGGCAGCTAC TGGAAAATTA TTGTTTGATT TGCCAGTTAT TATAAACTGT 180  
 45 GTGTGTTGAT GnCGAnCACA ACCCCTCCGA ACACGCTTAA TG 222

## (2) INFORMATION FOR SEQ ID NO: 3120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3120:

CGGCGATTAT ATTAAAAAGC CAATTACAGA ATGTAGTGGT AATGAAATAT GCCAAGAATG 60  
 5 GCTGTATCAC TTAGGTGTAT CAACTGACAA AATTGAAGAC TTAGCAAAAC ATGCATCTAA 120  
 TACGATTCCT GTTTATATGC CATATATCAC ATCTTATTTT ATGGACGCGT GCTATCGGCG 180  
 nACAGACCTT TTAGTCGTGC CCGGCATGCA ATCTnCAGGA ACTTAGGCAT TTATTGGTGA 240  
 10 ACTTTG 246

## (2) INFORMATION FOR SEQ ID NO: 3121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3121:

CAAATACCTT CTCAACnTTG TACTTTTTTGC CTAATTGAGC TGCACGAATT GCTGCAACGT 60  
 25 ATCCACCAGG ACCTGCTCCG ATTACTATAG aTCTGTTTCA ATTGGGAAAT CTCCAACCTAC 120  
 CATGTTTTAC CCCTCCATTA ATAATAATTC TGGATTATTT AATAAACGTT TAATGTGATT 180  
 CATTGCATTT TGGCCAGTTG CACCATCAAT TTGTCTGTGG TCAAAGCTTA ATGAkrtGct 240  
 30 AATACTGGTG CTGCAACAAT TTCTCCATCT TTAACGATAG GTTTTTTGAGC AATACGGCCA 300  
 ATTCCTAAGA TTGCTACTTC TGGGGTGATT GATAACTGGA GTGAACCATT GTCCACCAGC 360  
 35 TGAACCGATA TTA CTGATTG TGCATnnGCA CCTTnCATT 399

## (2) INFORMATION FOR SEQ ID NO: 3122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3122:

CAGACAAACC TTGAATTATT CTACCTATAA TTAAAAATGC TGGCAAAGGT GTAATGATGA 60  
 TGAGTAATGA ACCTACAACA TTTAATATCA ATCCTACATA AGTAATTTTG ACGCGACCAA 120  
 50 ATTTATCAGC AACATCACCA GCACCTACGT AAACCAACCA GCCAATAAGG CAGATAAGCT 180  
 AACAGCGTAT TATCGTTCCC ACGTCACTAC TATATGTGGA TGTATGGGAC ACAGTTTACC 240

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## (2) INFORMATION FOR SEQ ID NO: 3123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3123:

```

15  GGAGCAAATT TATCATCTGC AACTAGACAC AACATCACTG TTATTAGTAC CGGGTTATAT      60
    AGTAGCAGTC ATTGTTGGTG CACTAAGTGG TAAATCGGC GAATATCTGA ATTCAAACCC      120
    AGCGATTATC ACAGCAATTA TTAAATAGCA CTGAGCTTGA TTTACCTGCA TTGCAGTAGG      180
20  TAATCACATT CAATCTCGTC ATTCTATGAT ATCTTGCACT AGCTTGCTTA ATGATGCACT      240
    TACTACGAGC ATAAACATGT CTATATGCAG GTGCATGTTA TATTATATAT GGCGACGAGA      300
    TCGTnGGCCn ACGTTAACTA ATTCTnGCATG TCTAGCCTCG AATTATATAG TAGGAGCGTA      360
25  GTACGCCAAC TGCCACGA                                     378

```

## (2) INFORMATION FOR SEQ ID NO: 3124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3124:

```

    TATTGCAAGA AATGAACTGC TGATTTTTTAT AGTTTTTAGTG GTCATAAAAT GCTTGGACCA      60
40  ACAGGTATTG GCGTATTATT TGGTAAACGT GAGTTACTAC AAAAAATGGA ACCGATTGAG      120
    TTCGGTGGCG ACATGATTGA TTTTGTAAGT AAGTATGATG CAACATGGGn CTGATTTACC      180
    TACTAAATTT GCAGGTCGGG TTACTIONCAT TGAATTGGCT CCAAGCCAAT TGGGGCTTGG      240
45  CnAGGAAGCC T                                     251

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## (2) INFORMATION FOR SEQ ID NO: 3125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3125:

	CGGTTAAGTA ATACAGGATG TTCTCTAATT ACTTCTTCCA ATACGTCCCA AACTTCATCA	60
5	TCCATACGTT CGATTTTACT CTTCGCATTT TTAATGTTAG TTGCAATTC ACGTTGAACT	120
	AATTCTTTCA TTACGAATGG TTTAAATAGT TCAAGTGCCA TTTCTTTTGG TAAACCACAT	180
10	TGGTACCATT TCCAnGCTTG GACCCnACGG CAATTACCTG AACGGTCCCG GAA	233

(2) INFORMATION FOR SEQ ID NO: 3126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3126:

	AATAGATTCC CGGGATTCAA AAGCATGGAT GTTGTAACCTT GTTGThCTCC ATTGGCAATG	60
	TACTACCTGA TGTCAAGATG AATTATCCAT CACTTTGTGTG ACGTGCTTTA TTTTACAGCA	120
25	TCAATTTGAT CCAATCGAAA TACCAGATAA CTTAGACTGT GTCCCAGTAA AATAACGATC	180
	AATCACAATCA TGAGACAAGC CAATCGCTTC AAATATTTGT GCCCCTTGAT AACTTTGCAC	240
30	TGTCGAAATT CCCATCTTAG CCATTACTTT AATGACACCT TCTGACAATA CATCCGTATA	300
	TGTCtTAACA TTATCGACAA CGGTGCCTTG TAACCCTTCT GTCAATGTCA GTTGTTC AAC	360
	TGTACGTTGC GCTAGGTATG GCACAATTGa TTCGCGCCAT ATGCGAGTAA ACA	413

(2) INFORMATION FOR SEQ ID NO: 3127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3127:

45	GTCGTAAATA CTGAACAAAA ATCACGGCAT ACTGTGCAAA TTTnTGAAGA AGCTCAAAAA	60
	CTATTACAAG CACATCATGC GATTGTAGAA GGATATATCG AATCAGCTTT AGAGCGTGCG	120
50	TAnATCATCT TCTACATACA TAGGTAATTT TATGGCGATT CCTCATGGAG CATCCTGTAA	180
	AAAGTTTTAC AATCACAATGT GCTTATTTT	209

(2) INFORMATION FOR SEQ ID NO: 3128:



(A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3128:

10 TAAATTAATG GAGTTTGGTA CACGTCGTCG CAAGAAATTG ATGCAGTGGG GCGCTAGAGC 60  
 TGCTTACATC GGGGGCTTTG ATTCTACAAG TAATGTTAGG GCGGGGAAAT TATTTGGTAT 120  
 ACCTGTGTCT GGTACACATG CACATGCATT TGTCCAAACT TATGGAGACC AATATGTTTG 180  
 15 CCTTCnAAAA ATATGCTGAA AGnC 204

(2) INFORMATION FOR SEQ ID NO: 3129:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3129:

GAAATACCAT TAATATAATA GTCGGTAAAT TAAGAAACGT GGTGCGCGAT TCACAACAGA 60  
 30 AATCTTAACT TATCGAAGTA TCCTGTTTTT TCTGCAACAC CAATACCAAT CATCACTGCT 120  
 AGTACTAAGC CTAATGCGGG AACTCTGAGA AATTTTAAAT CGTATTCTTC TTATCATCGT 180  
 AAATCCATCT GGCTATTATA TTTTAATATA AnGGTTTGAG CTACCGGATG CTAACGnAC 239

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(2) INFORMATION FOR SEQ ID NO: 3130:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 259 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3130:

45 ATCACAATAA ACATTTTAAA ATTCTTGTTA TCATAATCAT TAAAAGGTAT TAACCTTAAT 60  
 AATATATTCT CThGTCTCAA CCTTAATCGT ATACTTCAGA CGTCTGTTTG TAGACAATAA 120  
 50 AGTCATTCAC GTCTTCATAT GTCATCAnAT GTTTATCATG ATATGATGAT ATATAATCGG 180  
 TATATACTGT AGATATTACA CATAAGAGAG GATATAATAT GAAAAGGTCA TTAAGATGTG 240  
 CTGAGAGCTG TGTATCAGT 259

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3131:

TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA ATGCACAAAA ATGTTTACCA 60  
 TGTGCATTCA CAACTTCAAA AATATGTTGA CATGTGATGT TACTTGATCA TCACGCGTTG 120  
 CCATGGTATG CAAGTGCTGC GATAAATCTG CGGCACCTTC GACTATCATG CTAACCTTCG 180  
 CTTGTnnATA TCGCAATGGC ATACCCCTTC AACATCTTCT ATCATGG 227

## (2) INFORMATION FOR SEQ ID NO: 3132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3132:

ATCGCAGTGA TGTnATCATC TGCTGCTGTA GcNTAGCAGG TTCAATTTCA TTTATCGGAT 60  
 TAATGGGTCC GCATATTGCC AAACGTATCG TTGGACCACG TCACCAGTTG TATTAACCAA 120  
 TTGCCATTTT AGTAGGGGCA TGTATACTTG TAATAGCTGA TACAATTGGC CAAAATTGTA 180  
 TTACAACCAG GTGGGGTTCC AGC 203

## (2) INFORMATION FOR SEQ ID NO: 3133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3133:

AGCATTTAGT TTAGCGGCAG TAGCTGCAGA TGCACCGTA GCTGGCACAG ATATTACGAA 60  
 TCAnTTGACG AATGTCACAG TTGGTATTGA CTCTGGTACG ACTGTGTATC CGGACCAAGC 120  
 AGGTTATGTC AAACTGAATT ATGGTTTTcN AGTGCTAATT CTGCTGTAA GGTGACACAT 180  
 TCAAAATACT GTACCTAAGG A 201

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3134:

CATTTGTAAC TGTTATTGTT TATAACTTCT GTGTGAAGCG CAATATTACA ATTAAAATGC 60  
 CGAAAGAGGT ACCGnCGAAT ATTTACAAG TATTTAGGAC TTAATTCCAT TTTCAGCGGT 120  
 AATCATCATT CTTTATGCAT TAGGATTTnG TCAATCGCAA CCAGCTTTAA ATCAAAATGT 180  
 AGCGGAGGTA TTTTAAAATT ATTCGGT 207

(2) INFORMATION FOR SEQ ID NO: 3135:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3135:

AACACCTTTA GGTTCGTGCAG GTCAACCTGT TGAGTTATGT GGTACTTATG TGCTATTAGC 60  
 GTCAGAAGGA ATCAAGTTAT ACAACCGGAC AAGTnTTCGG TGTTAGCGGT GGAGTGCAAn 120  
 TAGGTTAGGT TTGTATGAGC TTTTAATTGA GCACCATAAT GTTAATTTAG TTACTTCAAT 180  
 CCATTAAATT AAATGAATTG GTG 203

(2) INFORMATION FOR SEQ ID NO: 3136:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3136:

CACATCCAAT GCAnTCTACT AAATCAGACA CACCACAATC TCCAACCATA AnACAAGCAC 60  
 AAACAGATAT GACTCCTAAA TATGAGGTTT AAGAGCGTAT TATACAAAAC CGAGTTTTGA 120  
 ATTTGAAAGC AGTTTGGATT TATGCTCAAA CCATGGACGA CGGTTAGGTT TATGATGTTA 180  
 TTCCAATAGG TTCACTATAA ATAGCTTAGT T 211

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3137:

ATTGGGAAAT GTTCCCCCAC CACCTACAAT TTGTGAATAC AAACAATACG TATTGCAATG 60  
 GACTTTACCT GGGCTTACCA AGTGAATGTA TACGTCACGT ATGATACGAT TGTAGTTGnA 120  
 AAATAATGCG AACAGAAAAT CGTTATAAGT ACAAATAATA CAGGTGACTC AACTCCTGCT 180  
 TTTAGATTAA CAAATCTCCA ACCGATACAA TGAGTGCTTG CAACATACCA AGCATTATAA 240  
 AGAATCCTGC CTTACCTAAG 260

(2) INFORMATION FOR SEQ ID NO: 3138:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3138:

CATAAGCAAT TAATGACTTC GTTAATTGCG AAAGTGTATC TTTTGTGATTA TCATTCGCTT 60  
 TTGCATCTTC AAGCTTTCTC ACATCTGATT TGACAGCATT ACTTTCCTA TTATCTTCAA 120  
 GCGATAATTT CTAACTGCA CTTACCACIT GCTCAATTGC TTCTGCTAT TGTCATTGCA 180  
 TATCGGAGTA GTAGGAAGTG CnGAATTCGG CA 212

(2) INFORMATION FOR SEQ ID NO: 3139:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3139:

TATTGGTTTT TATGCGAATA TGGATAATAA AAGGTCTCAC GACATCATTG ATAAATCGCT 60  
 TGAATGTTG CGACGCTTAG ATCACAGGGG CGGGGTCGGC GCAGATGGCA TCACTGGTGA 120  
 TGGCGCAGGT ATTATGACTG AAATACCTTT TGCATTTTTC AAACAACATG TAACGGAGGA 180

GCACCTGTTA GAAAAGAAGG GAAATTACCT CGTGAAGTCA TTCGTTATGA GTATGACCTA 300  
 GAATATGGTA CAAATGTTTT AACAAATGGCA CAAAGATGCA ATTGAAACCA GGTnCAACGT 360  
 5 GTGTTAnTAC AGG 373

(2) INFORMATION FOR SEQ ID NO: 3140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3140:

AGCCTTATAA TAAAGTGCCT TTCATAGCAA TAAGTTGTGT CCATTGACCT ATTACATTTT 60  
 20 TCGTTTTGTA CATTAAATAT AAGAAATACG GTGCACCAAT AATTGCTACG ACAATACCTG 120  
 CTGGAACCCC CACCTGGTTG TAATACCATT TTGGCCATTT GTATCAGCTA TAACCAAGTA 180  
 ACCnTGCCCC AACTAAAATG GCATTGGGTA AAACCACnTG 220

(2) INFORMATION FOR SEQ ID NO: 3141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3141:

GAGGAGCAGC ACAACCAAAT ACACAACCAG CTGGACAAGG TGATCAAGCT GATCCGAATA 60  
 ACGCTGCACA ACACAACCTG GAAATCAAGC AACACCGGCA AACCAAGCAG GTCAAGGnAA 120  
 40 TAACCAAGCA ACACCTAATA ATAATGCAAC ACCGGCAAAT CAAACACAGC CAGCGAT 177

(2) INFORMATION FOR SEQ ID NO: 3142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3142:

CTTTTTTAGC ATTTGGTTTA ACAACnGGT GTTGCAGTAT CCCCACTTAA GGTCTGTATA 60

ATTTTCATTTT TATGTTCTC GATAACTTGT ATTGCTGCTT GTTTTCCTCC ATCTGTCAAT 180  
 CCATCATTTG ATTGAGAGAA nCAG 204

(2) INFORMATION FOR SEQ ID NO: 3143:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3143:

GTGATGCCAT ATAAATTGGC AATAATGGCA CAAGTACTGT CAGTCCAGCA ATCGCTATAA 60  
 ACTGACTGAG CCATAAAATG CGAAAGTTAC TGCGCCATAT AGACTGATTA ATCATATGTC 120  
 ACCATTGGAT TTGTACGGT AGTTAAACCT GAAGGCATAC TACCCTCCAC CCACTTATTC 180  
 AACGTTGGAT nATAGGCAAT GGGTAATTAA AAATTTTGTT TTTGAAATGG GCCCACGGGC 240  
 TTGTTTTAAT CAAAATTAAA AAATTGTGGT nCTTGACC 279

(2) INFORMATION FOR SEQ ID NO: 3144:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 514 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3144:

TGACTTAATC AAAGCATTTG ATCAAAACAC CAGAATACCA TTATTCTTTA ATATGTTGTA 60  
 CAGTAACTC TnTATTATTT GTTGCTGTTG GATCCATTGT TCGTCTTTCA ACAAAAACnT 120  
 GACCCAGAAT GAAGTCCGAT AGAGTCAACA AAGCtATAGT ATTTGTAACC ATCTTTTAGT 180  
 TGATaAATGC CACGCGCATC TGtTATTGCG TCATTTTTAG GTAcAAATTG AATTTkGAGA 240  
 TTTCTCaCaT TATCAGGTAC TTTAAATAAA CGCAAAGTTG GACCGnCTTC AACAGTCTTT 300  
 TCAGCAATCG TATCATTAGT ATCAGCATTT TTGATAATAA CATTGTGTTGC GCCTTGACCG 360  
 TTTTTAGTAG TCATTGTATT AAATCAAGGT TAATTCAGAA TTCGGATTTA CTGTTAATGC 420  
 TTTCTCGATA CCATTAAAAT CGCCATGGTC ATTCTGATCA GTTCCAGTAT ACGGCCTAAT 480  
 GCAATACATT TGCCTGTGCh TGATAGTnCT TATT 514

(2) INFORMATION FOR SEQ ID NO: 3145:

(A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3145:

10 ATTCAGACTT TGCATGTGGA ATGGCCACGT TCATGCCAAT AGCTGTCGTA CTCCCATTTTC 60  
 ACGTTCTAGT ATTGCATTTT TTAAATGCGA TGTGTGCTCT ACATAACGGC AAATTTTAAG 120  
 TTTTATGAAT CAACATATCC AATGGCTTCG GTTTCGAGAC ATGTCCGTGG ATTCAGTAAT 180  
 15 TAACCATAGT TTGGTTGGAT CCAAACCAT GAGnAGGGTT TAATGGAGGA TGTnGAATGG 240  
 TTCnCCGGTG GTTAATCCTA CATGGTCCAC CCTCCTGGTA ACCATGGTGG TGGTAATAAC 300  
 CC 302

20

(2) INFORMATION FOR SEQ ID NO: 3146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3146:

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CAGGAATAGG ATCATTGCA TCCATAGCTT CACTTATTTT TTCAGAAGCT AGCGTACAAT 60  
 CATTTAAATC TACGCCACCT TCTTTATCAA TAGAGATTCT AAGAAAATGA TCTCTACCCT 120  
 35 CTTTGACCAT ATTCAACGTC TACAAGTTCC AAAATTCAAG GTCTTCCCAT AATTGGGTTT 180  
 AACCAATCCA CTTTCTACCT GGTTCGGT AAATTTTAC CTCCATACCA GGGnCTCCC 240  
 CCTTTTTTGG GCCAAAATAG GAAAAAnGAG GCGGGGAAAA TCCTCCCCC AATTCnTTC 300  
 40 CTGGCCCTGG AGGTTTCCAC CTAAATTTT TT 332

40

(2) INFORMATION FOR SEQ ID NO: 3147:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3147:

GAGAGTGGTT AACAAGCAAA TAGAAATAAT TAAAAATGCA GATGCAGATG CATCGGCGAA 60

55

ChCCAACAAA TGCAGAAGTT GCTGAATTCC AAATGTAACG ATACCTGCCC ATGAGCGATG 180  
 TGCTCAGAAT GATCAGAGCT AATG 204

(2) INFORMATION FOR SEQ ID NO: 3148:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 217 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3148:

CAACCGGGAC AGGTGGGGTT ATTGGACGTT ATTTTGGCC TTTGGATTTT AAGATATTGG 60  
 TCGAAAAGAG ATTACATAAA ATTGTGGCCA AATGCGGATT GCATATTATT GTAACGCCGn 120  
 CTATTGCATT GTTGATTGTT AGGnCTATTA ACTATCTGGA TCTGTATGCC ATTAGCCAGG 180  
 TTTTGTTCa GACAGTTTAG TTTCAGTAGT TAACGGA 217

(2) INFORMATION FOR SEQ ID NO: 3149:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3149:

CTATTATTAT ATTCCGCGGT GTACGTATAT GTGCTACGTT ATCTTCGTTA ATTGTACCGA 60  
 TTATGGCTAT CATTTACATT GGTATGGTTT TAGTAATATT GCTATTTAAT TTAGATCAAA 120  
 TTGTCCTAT GATAGGTCAC GATTATTAAa AGTGCAATTG GTCATCGAAC AAGT 174

(2) INFORMATION FOR SEQ ID NO: 3150:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 181 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3150:

GGGACCGAAT TGACTTCAGC ATTACCAGCA AATTGATTAA TnTTGTGGGC TGGTATTGGC 60  
 TCTGGCGGTA CCATTTACAG GTACCGCACG TTATTAAAGC AACATCACGG GCAATGTTAT 120



A

181

## (2) INFORMATION FOR SEQ ID NO: 3151:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 172 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3151:

GTTTTAATTG AGCGACATAC TCTTCTGTTA GCTCTGCTAC TTTTAAAAAT AGAGCGATTG 60  
 ACATCAAACA TAACTGCTAA ACGCTCAACG TCTGCCTTCG TAATGGCTTT TGTAGAAATT 120  
 CTAATAAAT AATTTCGAAT GCTATCATTG GTTGThTCAA CAGCTTGATG CT 172

## (2) INFORMATION FOR SEQ ID NO: 3152:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3152:

ATGGACGTTG AGACATTTAT AAGCGATATA GATTTCGCAT GTTGCATTTA TTAAACCTAA 60  
 TAATGGTAAA CGACAAGTGT GACTGTTACT GGACTTTAAT GAAGGTAGTA ATCAGAATGG 120  
 AAATCAACCA AAAGTAGGTA TTTGAAThTT GGAATAATG AGACATAGCG AGAGTGTATA 180  
 TGCAATACGA CAGTACThTA AATTAAGAG 209

## (2) INFORMATION FOR SEQ ID NO: 3153:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3153:

TTCTCACAAA GCGCTCAGTT GAAGTAAATC CACCTGGACA ATCCAAATGT ACCTGCTTCA 60  
 TTGCCTAAAG GTTCAATCGT TAnACCTTCC AATAAATTTG CTGTTGCTGG ATAAGGAGAA 120  
 ATTATTGGTA TATTGTCTTA AATTACTATG ATGCCAATTT AAGGTCTGGA TGAT 174

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3154:

GGATCACATC GTTCATTTAC ACAATCTATT AATATTCAAT GGCACAATAT AGTGTTTATG 60  
 GCATTACGGA TATGATTTAG TAGCnCACCA TTATTAACCG ATCTCTATCT GTTAAAAGGA 120  
 ACTTAAGAGC AATGTTTGCG CATCATCATT TTATGTTGCG TCTTTGCACG AGTTTTGCGA 180  
 AACTTTACAA TATTGTTGCG GGATGATTAT TTAACTTTGG GAGAATGTTG ATGGCACAGT 240  
 CCACTATAnC AATCAGTATC GCAATGG 267

## (2) INFORMATION FOR SEQ ID NO: 3155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3155:

AATTAAAAAT CAAGCAACTG CTGCAAAAAT GCAAGATCAA ACTGTTCCCTC AAGAAGCAAA 60  
 TTCTCAAGTA GATAATAAAA CAACGAATGA TGCTAATAGC ATAGCAACAA ACAGTGAGCT 120  
 TAAAAATTCT CAAACATTAG ATTTACCACA ATCATCACCA CAAACGATTT CCAATGCGCA 180  
 AGGAACTAGT AAACCAAGTG TTAGAACGAG AGCTGTACGT GTTtAGCTGT TGCTGAACCG 240  
 GTAGTAAATG CTGCTGATGC TAAAGGTACA AATGTAAATG ATAAAGTTAC GGCAAGTAAT 300  
 TTCAAGTTAG AAAAGACTAC ATTTGACCCT AATCAAAGTG GTAACACATT TATGGCGGCA 360  
 AATTTTACAG TGACAGATAA gTGAAAyCAG GGgATTATTT TmCacGAgTT ACCAGATatT 420  
 TAcTGgTAAT GGAGACGTGG GATTATTCTA ATTCAnATAA TACGATGCCA ATTGCAGACA 480  
 TTAAAAGTAC 490

## (2) INFORMATION FOR SEQ ID NO: 3156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3156:

CCTTCAGTAC CTTGTAATAG TTAnTTAAAT GTTCCGATCA TCGTGTAGTG TGATTCATCA 60  
 5 TACCGGCCTT TTCAATTGAA TACGATCTAA ACCGTTTCGT CAGGTGCTAG TAAGTTACCT 120  
 TCGCCACCTA AATAAGAAGT TCACTCGTTA CGATTTTTTC AGATAGCATC ATTGGTGGAT 180  
 TCGTAACTTG TGCAACAGCT GTTTAAGTAT TAATAGTGAT TCGGTCGTCT TCACATGCAT 240  
 10 TGGCGCACAA TCCnTGCACC GT 262

## (2) INFORMATION FOR SEQ ID NO: 3157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3157:

ATGGTAAAAA TTGCACTATC TGCTCGGGAA ACGATTTTGC ATAACCTATT GTTAATTTTT 60  
 25 TACCTGTTGA TTTAGCTGTA TCTGnCCATT TTTTGAGCTT CTGCTGTCGT TTTAGCCATT 120  
 GGGTTTTTAC ACATCACATG TTTACCAGCA TGCAACCCTG GCTACAGTAA 170

## (2) INFORMATION FOR SEQ ID NO: 3158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3158:

CCAGGCAGAG GAGCAGCACA CCAATACACA ACCAGCTGGA CAAGTGATCA GCTGATCCGA 60  
 40 ATAACGTGCA CAAGACAACC TGGAATCAAG CAACACCGGC AACCAAGCAG GTCAAGGAAT 120  
 ACCAAGCAAC ACTAATATAA TGCACACCGG CAAATCAACA CAGCAGCGAA TGTCCAGCAG 180  
 45 CAGCGAACCA GCAGCACTGT AGCAGCAACG ACAACTCAGn CCAATGTAGC ATATGGTGAG 240  
 GCAGTTTATA GACATACATT GTGnCCCTGCA TTCACAGTGG ATAGCAGGTC CACTGTACTG 300  
 TACAGTAAGT An 312

## (2) INFORMATION FOR SEQ ID NO: 3159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3159:

AATCACATCA AAAACTTCAA TTGTTTACGT TGGCAACTAA CTTTATGTTA GAACGCACAC 60  
AATATCTAAT GTTTAAAATC TATCGTCGCA AGATGCTTCC TgntAATTAT CAGTGCCATT 120  
TTCGATTGGG TTATACAATC TAGTAATCGC ATGATAATTT AATGCTACAA G 171

(2) INFORMATION FOR SEQ ID NO: 3160:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3160:

CTTGTTTCATT TAATCCATAT AGTATACGAC GATGTACTGG TTTTAAACCG TCACGAACAT 60  
CTGGCAATGC ACGAGCAACG ATAACACTCA TCGCATAATC TAAAAATGAT TCACGCATT 120  
CACTGGTAAT ATTCGTTCA TTAATCnTGA TTGAGGGAAT TCCGCCCATC CAGAnGTCCC 180  
CCCTCCAAAG TTCAGTTCCA CAGGGGCTAG A 211

30

(2) INFORMATION FOR SEQ ID NO: 3161:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3161:

GCACAGGTAG CGGTAGTGGC GGTCTATGA TGACTTTGGT AATCTAAAGC AAAATGTACG 60  
ATAATAATAA ACGTCGTTTC GTTCTCTGA TGTAGCAGGG GCAGTGAAGA AACAAGATTA 120  
TTGAATTGTT GATTTCTTGA AGATATAAAA ATTCAAGAAT GGGTCTAGGA TTCCTAAGGT 180  
GTCTTCTTTT GGGCTCAGTA CGTAAACATA TTGTAGAGCG TGCAGTGAGT GGCGCACCAT 240  
CTCTTTTGGG TCAGnTTTGG AGTTTGTGTT GTCGGCTGTC GGATTnTCGT ATGTAGGAAC 300  
GGCTGTTTAC TTnCGTGGAT G 321

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(2) INFORMATION FOR SEQ ID NO: 3162:

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(A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3162:

10 AACATTTGAG CAATATCAAG AACATTAGA GTATATTTTA TCCCATCATG TAACTCGTAA 60  
 TACAGCAATT ATTGCTTTGG GTGGTGGTGC ACTGGTGATT TTGCTGGGT TATTGCGGCG 120  
 ACACTTTTAC GAGGCGTGCA CTTTATACAA GTGCCAnCG 159

15 (2) INFORMATION FOR SEQ ID NO: 3163:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3163:

25 GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGAC AAGTCTTACG GCATCTTCTA 60  
 TTTTAAAGCT TGAAATTTAA CAAATCATAA GCCGTATGAA TATTAAATA TGCCACCATG 120  
 ATTGAATGGC CCCTTTCTAT TAGTTAnGTT TTGTGCG 157

30

(2) INFORMATION FOR SEQ ID NO: 3164:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3164:

40

TATAAAAATA TAACGCGGAC AAAAAAGTGA GTTATTACTG ACAAAGTATn TGAGATTGTA 60  
 ACAGGATATA TGAAGCAATA TCAGTTGATC CAACTGTCAT AGGTATTTCA TCAGCAGGnG 120  
 45 TTGTTGATGA ACAAAAAGCG AAATTGTATA GCAGGCCAAC ATTCCGATTA TAAAGGTATA 180  
 ATTTTAAGGA TTATTAAAT CATGTCTCTT ATGTCA 216

(2) INFORMATION FOR SEQ ID NO: 3165:

50

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 175 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3165:

5 AGAAACACTT CTATTGAATC GTCTTACTGC TGTTCCTCTAT TTATAACACT TCGTATTGAA 60  
 TGAATTCATT ATGCCTATTT GACACATTAT TGAAGTTTTC CTAATGCCTG GATCCTTTAT 120  
 ACGTTACGGC TTCGTGCTAT GTTTTGGTAC ATAAAGCTTT GACATATCGA nATTC 175

## 10 (2) INFORMATION FOR SEQ ID NO: 3166:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3166:

ACTGTTACAA CAAATTAAAA ATACAACAAG CGAGATATAG TTATTGTTGC TGGAnTGTAC 60  
 CAAGTAGTAT TCCAAGCGAT GCTATGGCAA ATTGCACAAA TTACAGCACA GACAGGTGCT 120  
 25 AAATTAGTAG TCGACGCTGA AAAAGAATTG GGCTGAAAGT 160

## (2) INFORMATION FOR SEQ ID NO: 3167:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3167:

TGTGGGGGAA ACCTGCACAG CAAAACTAA AGCTTATCGA TACATCTAAA CATTGTATTA 60  
 40 TAAAATCAGT GCATCCTAGT CCACTGTCTG CATATAGAGG ATTCTTTGGA TCAAAACCGT 120  
 ATTCCAAAGC GAATGCCTAT TTAGCGTCAG TAGGnA 156

## (2) INFORMATION FOR SEQ ID NO: 3168:

## 45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3168:

55

GTGGCGAGAA ATACCGCAAG CATAAAGATA TCTTTGATCC AACTTACCAA CAGATCAACG 120  
 GAAAAGTACC AGGTAACCAG GAATCAAGAT CCAGACACAG GAAAAGTGAT CGAG 174

(2) INFORMATION FOR SEQ ID NO: 3169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3169:

TCAAACGGGG TCAATTTCAA ATGGA AAAAT TATACCGCAT CTTCTCCTGA TAACTACGTG 60  
 ACCTTATCTT CTTTATATTT GCAGACCACG AACATTCAA CTGCATGCTT GCTCGATTGG 120  
 CAATGTCATA TAACTAGTAA CATGATCATC nCATCAAATT TAGTATGTCA AATGTCCCAA 180  
 TCAnTAATTT GATCGGTGTT GCTCAATTGA TTA 213

(2) INFORMATION FOR SEQ ID NO: 3170:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3170:

AAAGCACCTT TTCCTAATGA AAGTTGTGCT ACTGGTATCT GTGTTTGATT TACAAAATCT 60  
 TCTAATTCTT GATGGAGGTG AAAACTGTTA ATTTTCATGTC CAGTAATGAT GATAGGCTGC 120  
 TTCGCTTGAT GCAGTTTAGT TGCTAATAAC TCTATATATG TTGATGCATC CGTATATTTA 180  
 GTTGCCGTCA CTTCAAATGG TGTCGGTATC TCAATTCAG AGATTGCGAC ATCGATTGGT 240  
 AAATGTAAAt GAACTGGGCG TCTTTCGGCG ATTGCTGTAT TAATTAAACG TGGTATTTTCG 300  
 GTTGTTGCAT TTTCAGGTGT GATATAACCT GTGCACGnTT ATATGTGCAA ACATTTTTTCG 360  
 ATAGTCGTCA AATGTACCnn 380

(2) INFORMATION FOR SEQ ID NO: 3171:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3171:

5 TAGAAgGTAA GAAGGATCCT ATCGGTGCAA TGGGATATGA TGCGCCAATT GCAGTGTGTA 60  
 ACGAGCGACC AGAATCACTA TTAAATTACT TTAAACAGCT GTTTGCACAA GTTACGAATC 120  
 CACCAATTGA TCGGTATCGT GAAAAAATCG TAACGwGTGA ACTTTCTTAT TTAGGTGGCG 180  
 10 AAGGTAACCTT ACTAGCACCT GACGAAACGG TTTTAGATCG TATTCAATTG AAAAGGCCGG 240  
 TATTGAATGA ATCACACTTA GCAGCGATTG ATCAGGAACA TTTTAAATT AACTTATTTA 300  
 TCAACGGTAT ATGAAGGGGG ATTTGGGAAG ATGCGTTAGA AGCATTAGGC CGAGAAGCAG 360  
 15 TGAATGCTG TTAAGCAAGG GCGCTCCAAA TTCCTAGTGG T 401

(2) INFORMATION FOR SEQ ID NO: 3172:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3172:

ACATAATTTA AAATAATATT ACATTTGTAA TGGnCACCAA GTAACGTTTC GGTGCTTGG 60  
 30 TGTTTTTTGG TATGAATTAC TTTCTGTTAC AAAACAATCT AAAGCGTTCT GTTATGTTTT 120  
 ATTAAGATTT AATTACAAAC GGAACTAAA TGTAATAGAA TAAACT 166

(2) INFORMATION FOR SEQ ID NO: 3173:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3173:

45 ATAATGAGAn TGTTGTACGT TATGGTGGTG GAAGTGCTGA TGGTGATTCA GCAGTAAATC 60  
 CGAAAGACCC AACTCCAGGG ACCGCCGGTT GACCCAGAAC CAAGTCCAGA CCCAGAACCA 120  
 GAACCAACGA CCAGATACCA GAACCAAGTA CCAGACCCAG 160

50 (2) INFORMATION FOR SEQ ID NO: 3174:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 158 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3174:

CTTTATATAA AGAAGGAATT ACTAAACATA CAGTTAGATT ACTTCATGCA ATCGAATTAG 60  
 AACGTTTGAA TTTAAGCCGT AGATTAGGTT TTGAATTATC AACAGCnAAA GAATCACGTA 120  
 TTGAACGGGG GTTATTTAGA ACGTGATAAA GAAGGATG 158

## (2) INFORMATION FOR SEQ ID NO: 3175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3175:

TATTTGAAGA TGGCTGTGTA CAAAAATCGG TGTTACGTGA TCATGATACT GTCAGAATTT 60  
 ATAAACCATG GCTAACAGCA CATCAGCTTT CATTGCCnA GTATGTCGTC AGAGAAGATA 120  
 CACCTAATCG CTAATTAATG AGGTTTGGAA ACAT 154

## (2) INFORMATION FOR SEQ ID NO: 3176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3176:

AGAAGGTATT TTAGCTCAAT CTCCAGGTCT AAAGGTTGTT ATTCCTTCAG CCCATACGnT 60  
 GCGAAAGGTT TATTAATTTT TTCTATTAGA AGTAATGACC CAGTCGTATA CTTAGAGCAT 120  
 ATGAAATTGT ATCGTTCATT CCGTGAAGAA GTACCTGAAG AAGAATATAC AATTGACATT 180  
 GGTAAGGCTA ATGTGAAAAA AGAAGGTAAT GACATTTCAA TCATCACATA CCGTGCAATG 240  
 GTTCAAGAAT CAATGAAAGC TGCAGAAGAA CTTGAAAAAG ATGGTTATTC TGTGTAAGTA 300  
 ATTGACTTAC GTACTGTTCA ACCAATCGAT GTTGACACAA TTGTAGCTTC AGTTGAAAAA 360  
 CTGGTCGTGC AGTTGTAGTC AAGAAGCACA CGTCAAGCTG GTGTTGGTGC ACAGTTGTAG 420  
 CTGAATTAGT GACGTGCATC CCTTCATTAG AAnnCCTATG GAAGAGTGCA CA 472

## (2) INFORMATION FOR SEQ ID NO: 3177:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3177:

10 TGAAAGCTGG CGAATACAGT GATTGTCATG ATGCGGATCT AnTTGTCATC TGTGCTGGTG 60  
 CTGCACAAAA ACCTGAGAGA AACACGTTTA GATTTAGTAT CTAAAAACTT GAAAATATTC 120  
 AAATCAATTG TTGGTGAAGT AATGGCATCA 150

15 (2) INFORMATION FOR SEQ ID NO: 3178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3178:

25 TTACTCTATC TTGATTGAC GAAATACTAT TAnGCTAATA TCGATATTTT AAAAACGAGA 60  
 TGATGTTCCA AAGCAAGCCA TTTCGATGGA CTGCTAATAT TCTTCAGCCA AACGTATCAT 120  
 30 TTTACTCGCA TTTGGTGAAA AGAAACGGCT GCTATTACAC ATTTAT 166

(2) INFORMATION FOR SEQ ID NO: 3179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3179:

40 CTTCGACTCT AGAGGATCCC CGCGCTCAAA TTCTAGTGTT AGATGATAGT GGATTAGTTG 60  
 45 ATAGCAATGG CTTTGCAATG CCGATGTTAC TCGCAATAAG TCATGTGCAT CAATTACTTA 120  
 TTAAAGCAGA TTTACGTATG TCTACAAGTT TAnTTGCTA AATCTGGTGA 170

(2) INFORMATION FOR SEQ ID NO: 3180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3180:

AGCTAAGGTT GCCnTGGGCG TTGCCCCAnT TGGTTAGTCC AGGTGGTCGC GGTGGCCATC 60  
 5 GGTGTATTCG CCAGGTCCTT CAGCCAGGGT TTTTACTATT ATATCCAGTT GTAGCAITCA 120  
 TGATTGGGGC GATTGAGAT AGATTCATCA ATGAAATTAA TTTCTGGATT TTATTCGTTG 180  
 GTATTTATTT GGGTATACAT AAGTATGGTA CATGATAGGC AGATATACAA CATTACAACA 240  
 10 TTCATTCTAC TATGCTGGAA ATAACATGAC AGTGATGACA CTACTATCCC CGTCGCA 297

## (2) INFORMATION FOR SEQ ID NO: 3181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3181:

CACTAGGTAC CCCAAAACGC CAGAGGAACT TGGTTAAATC GCACTTACTT GGTGGCTCCA 60  
 25 ATCAACTGGT ACTTCATAAC GTTTGGCATC TTCGCCACTT CACCACTATT ACTCTTTCCA 120  
 CCTAATTGGT TCATGGCTTG TGCTAACGTT TCATGTGCTT CCGCTGAAAT CGATCCATAA 180  
 CTCATCGCCC CTGTATTAAA GCGTTTGACA ATGTCACTTA CCGGTTCAAC TTGGTCGATG 240  
 30 TCAATCGgTG TACATGCTTT AAATTCAAGT AAATGTCTAA TGTGaTCTGT TCTATTTTGT 300  
 TTnCACCGnT TnCAGAGTAT GCTTTAAATT GCGCCATAGT CCATTTTCT 349

## (2) INFORMATION FOR SEQ ID NO: 3182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3182:

TACCAACACG TACACCTTCT AAAATAACTG CATTGACACC GTnTTAATAC ATCATCCTCG 60  
 TTTATAACCG GTGTAAGCAC TAGGGGGTTC AATCACACCT GCTAATACTG CGCCAGCCCT 120  
 ACATGTACAT TTTTACCACT TGTAGCACG 149

## (2) INFORMATION FOR SEQ ID NO: 3183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3183:

GCGGTGCCGG TGTTGCAATT GCGCAGTGG TGTGGTAGC ATGTGGTCTT TCAATCAATG 60  
TTCAATACAC CAGGAGATCC GGAAAAGATG CGTATGAATT TTATGGTAAG TGCACCAGGC 120  
ATTACCACAC CACGCAAnAA CATGCAT 147

(2) INFORMATION FOR SEQ ID NO: 3184:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3184:

CAGCGATATG TTGGCGTTGA AAATCTGCAA TTTGTTTATA ATTCTCTGTT AAAGAACGAC 60  
TTAAATTGAT AAAAATGGAT ACGATCTCTT GGTAAACAGT GACATTTTCT CAATCGGCGT 120  
ATGATGTTTG TGGCACCGAC CATCGAGAAC ATGAAAATCT CATGTCCCAC GCTAGTCGnC 180

(2) INFORMATION FOR SEQ ID NO: 3185:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3185:

GGTAAATACG TATTAATCAG ATTAAGATCT GGTGAAGTTC GTATGATCTT ATCTACTTGG 60  
CCGTGCTACA ATCGGGnCAA GTTGGTAACC TACAACACGG GTTAGTTAAC GTTGGTAAAG 120  
COGGCACGTT CAAGATGGGA AAGGTATCCG 150

45

(2) INFORMATION FOR SEQ ID NO: 3186:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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GAATTTnAGG TGAATCAGAA GATTAACGCT GTTGCGTCCT AAGCTAACAG ATACTGGTTC 60  
 GTCAGTTGTC GTTGAAAAAG CGAATGAACA ATTTAATAAA ACCGTAACTC GAGCATTATT 120  
 5 AGAGGAAGCT AACCAAAGCA GGTTTA 146

## (2) INFORMATION FOR SEQ ID NO: 3187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3187:

AAATTGGCGA GTATGTTGTT ATTGGGTCAG TACTCTGAAA TTAACAATAG nTACGATTGA 60  
 20 AAATGGTGTC ATGTATTCAA CAGTCTGTTG TTAATGTATG CTAGTCGTGG TGCGAATACT 120  
 AAGGTCGGAC CGTTTGCGCA ATTGAGACCA GGCGCGCAAT TAGGG 165

## (2) INFORMATION FOR SEQ ID NO: 3188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3188:

CAGTTTAGTG GAGACGAATC TAAACGAAAC AAAGCGATTG GACGTGCATC AGTTGTACCA 60  
 35 ACATTCTTTG GTGTAAACGn AACCAATTTT ATTTGGTGCC ACCACTAGTT ATTGGAATCC 120  
 TGTGTTCTTT ATTCCATTG TATTAGCACC AATTGTTAAC GTATGG 166

## (2) INFORMATION FOR SEQ ID NO: 3189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3189:

AACCCTTTAT CTAATCCATT TTCAGTTAAG CGATGACCGC CTGCTAAAAT TTGTGCATCT 60  
 GATTCTTTTG CTGCATCAAT ATATGATTGA ATTTATCTA ATTGATCCTT ACCAGTTTGA 120

## (2) INFORMATION FOR SEQ ID NO: 3190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3190:

TCCCCCAAAG GGTTTAAGGG GTTAACCCGG GTTTGGGAAA AATTTTAA CCCCCCTTAA 60  
 AATTCCCGGG AAAAAGGAAA CCCGGGTTT TAAAAAAAC CCGGGTTCC CAAAAATTT 120  
 TTGGGAAAGG GAAAGGAAA AAGGGTTAAA AAATTTTGG GAAAAACCG GGCCCAAAA 180  
 AAAGGGTTT TTTCCCTTA AAAAAATTT AA 212

## (2) INFORMATION FOR SEQ ID NO: 3191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3191:

CTTCACTGAC TTTAGCAATT TCATCACCTT TTGCCCTAC AACGATAGCT AATGATTTAT 60  
 ATTGTAAACT CAAATGACCT TGTGAATAC CTTCTGACAC AAGCGCGCGA CATGCTGCAA 120  
 AGTTTTCGCG TAAACCAACG GCAGCAAC 148

## (2) INFORMATION FOR SEQ ID NO: 3192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3192:

CTGCTAATCC GAAATCTTTT TGGAGTTTTA TTAAACCAGC TGCTTCTAAT AGTTTAAGTG 60  
 CACGTGCTTG GTTTGACACA TCATTTGGAA TGACAACTTT AGCnCCATCT TTAACCTTTT 120  
 TGACATCTTT AATTTTATCT GCAGAAATAA ATCCATCAGG GATGGCTCTT AAATATATGT 180  
 TACGTGATAA TTTCTCGAnA AATGGCTTCC CT 212

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3193:

TCGTGCAGTG GTCTTCTGTT AATTGGTGAA TTTGGATACT GGTTATATTC AGCTGCACCG 60  
 CAAGCAACTT CTATTGATGG CCnAACTGCC TTTTACCTC AAGCAATGGG TATGGTAGTT 120  
 GTTGCAGTCA TTTATGGCTT T 141

## (2) INFORMATION FOR SEQ ID NO: 3194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3194:

AATAACG TTC TGAAAAACGA AGATGTTTTA AATGCCTATA TCCGCGGTCTG TGGCGGAATG 60  
 GCAGACGCGC TAGGTTGAGG GCCTAGTGGG AGAAATCCCG TGGAGGTTCA AGTCCTCTCG 120  
 GCCGCATCAA AATTCTTAAT TTAAATAAGC GGGTGTAGTT TAATGGCAAA ACCTCAGCCT 180  
 TCCAAGCTGA TGTGTGGGT TCGATTCCCA TCACCCGCTC CATAGATAAT TTTAATGAAC 240  
 ATTGAAAAC GAATGACAAT ATGTCAACGT TAATTCCAAA AACGTAAC TAAGTTACAA 300  
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTATGGAGA GTTTGATCCT 360  
 GGCTCAGGAT GAACGCTGGC GCGTGCCTA ATACATGCAA GTCGAGCGAA CGGACGAGAA 420  
 GCTTGCTTCT CTGaTGTTAG CGGCGGACGG GTGAGTAACA CGTGGaTAAC CTACCTATAA 480  
 GACTGGGATA ACTTCGGGAA ACCGGAGCTA ATACCGGATA ATATTTTGAA CCGCATGGTT 540  
 CAAAAGTGAA AGACGGTCTT GCTGTCACTT ATAGATGGAT CCGCGCTGCA TTAGCTAGTT 600  
 GGTAAGGTAA CGGCTTACCA AGGCAACGAT GCATAGCCGA CCTGAGAGGG TGATCGGCCA 660  
 CACTGGAAC T GAGACACGGT CCAGACTCcT ACGGGAGGCA GCAGTAGGGA ATCTTCCGCA 720  
 ATGGGCGAAA GCcTGACGGA GCAACGCCGC GTGAGTGATG AAGGTCTTCG GATCGTAAAA 780  
 CTCTGTTATT AGGGAAGAAC ATATGTGTAA GTAACGTGTC ACATCTTGAC GGTACCTAAT 840  
 CAGAAAGCCA CGGCTAAtAC GTGCCAGCAG CCGCGGTAAT ACGTAGGTGG CAAGCGTTAT 900

CGGCTCAACC GTGGAGGGTC ATTGGAAACT GGAAAACTTG AGTGCAGAAG AGGAAAGTGG 1020  
 AATTCCATGT GTAGCGGTGA AATGCGCAGA GATATGGAGG AACACCAGTG GCGAAGGCGA 1080  
 5 CTTTCTGGTC TGTAAC TGAC GCTGATGTGC GAAAGCGTGG GGATCAAACA GGATTAGATA 1140  
 CCCTGGTAGT CCACGCCGTA AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG 1200  
 TGCTgGCAtA ACGCATTAA G CACTCCGCCT GGGGAGTACG ACCGCAAGGT TGAAACTCAA 1260  
 10 AGGAATTGAC GGGGACCCGC ACAAGCGGTG 1290

## (2) INFORMATION FOR SEQ ID NO: 3195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3195:

TGGTACAGAG TTATCGCTGG TGGTCCTGTT CGTGCCGTAC TTGAATTATC AGGTATCACT 60  
 25 GATATCTTAA GTAAATCATT AGGATCAAAC ACACCAATCA ACATGGTTCG TGCTAACAAT 120  
 CGATGGTTTA CnAAACCTTA 140

## (2) INFORMATION FOR SEQ ID NO: 3196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3196:

CTATTGGATC AGGAGGCAAC TACGCTTAAG CGCAGACTGC CCATTGAAAC GCCATGCATC 60  
 40 GCATTGTGTCG CCTGAAGAAA TGGCATATGA GAGCTTGAAA GTAGCGGCTG ATATTTGTGT 120  
 CTTTACCAAC GnTAATATTG TTGTC 145

## (2) INFORMATION FOR SEQ ID NO: 3197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



TGTCGAGTTG GAATTGGACG ATTGAATATC CCATCTCCAT CACTATCAAA GTATGGGAAT 60  
 TGAATTGTTT CTAATTCGTA TCCACCTTCT GTCATTGATA ATGTAGGGTT AATTTTAGAA 120  
 5 CCATCTkCTG TTTCTAGTTT TAAGTTCCAC TTCTTACCTT CTTCCCAACG TTGACCCATT 180  
 GTGCCATTAG GTACTACTAA ACTATCGCTG ATTGCATCAT GAATAACTGG CTTCCATTcn 240  
 CCTTGCTCTG TTGTTTGACC TAAGTCACTC GCGCTnAAAA ATCGACCCGC TTTATATCCA 300  
 10 TnTTCACTG 310

## (2) INFORMATION FOR SEQ ID NO: 3198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3198:

TGCTTTATTA ATGCATTGGC TAATAATCCA CTTGTACCAC CACCGGCACA AAGTACTAAG 60  
 25 AGGTTTGTTT TGTGATATTT GAAGCTTTAG TGCATCGTCT GATACACCAC TTGCCGCTAA 120  
 AATTGAATCA GCTTTTnTCG 140

## (2) INFORMATION FOR SEQ ID NO: 3199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3199:

TGGTGATTTC AAATCATGAG ACTGGGACAA AATGATGTTT TCATAAAAAT TATTTGTTG 60  
 TTCCACTCTC ATGATTTTTT TGATGAACAT AATTACATGA TTGATTGCAT CATTTGTTAA 120  
 45 AACCAGTGAT TGCAACCTGC CATTACACnG GAAAATTACC TAATAAGTGG CGTATTTACC 180  
 AGTC 184

## (2) INFORMATION FOR SEQ ID NO: 3200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3200:

TTGAGAAGCG TTTAGGAAGT AACGTTTAAC GACGACAGTC GTTCAATGCG ATCAAAATGT 60  
 5 TTTAACACAT GAATCGCTCT CGTACTATTC GTGTGTGACA CATGTTCTTC CAGCATTTC 120  
 TTAATGAATG CTTTTTCTTC TTGGTnTTTA ATCTTTGTAA ACG 163

(2) INFORMATION FOR SEQ ID NO: 3201:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3201:

GTTATGTTTG AGACTATAAT GAATAAATAT TTAGAAATAT GACTCCGATT GTTCGATGCT 60  
 TAATTCAGTT AGAAGCATCA TAAGAATGCA TGATTACTGG TGTAAGATA CGTAATGTnT 120  
 TGTATTGACT GGATGTCTTT GGATAGAGT 149

(2) INFORMATION FOR SEQ ID NO: 3202:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3202:

CAAGTGACTG AGATTACTGA AGTAAACCCG TTACCGCCAC ACTATATTTG TCCGAAGTGT 60  
 AAAACGAGTG AATTTTTCAA TGATGGTTCA GTAGGATCAG ATTGATTTAC CTGATAAACG 120  
 40 TGTGAAnTTG TGGAGGCCAC TATTAAAGAA GACAGAATCC GTTGAACATT TAGATAAGGG 180  
 AAAGTCCGAT TC 192

(2) INFORMATION FOR SEQ ID NO: 3203:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3203:

CGCCATCTAA CGTTTTTTGT ATTGGTTGTT GCTGAGCTAG TTGTAAGTGC CnCATTAAGC 120  
 ATCTTATAGC GTGATAGCCA TGCGCCAACG TACAAATCTG CTCCGTATTG TACGCACCAC 180  
 5 TAAGCAGTAC ACACCAGTAA CATTGATAG CGTTATAGCG CAATATACAG TACA 234

(2) INFORMATION FOR SEQ ID NO: 3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3204:

AACGCCATAA GCTACATGTA TGCTTCTTGC ATGGTTATCA TCCTCTCTTA ATGACTATCT 60  
 20 TTTAATTACG NAATGGCTTA CCAGTTTTTA ACATATGTGC AATTCTTTCA TATGATTTTT 120  
 AGATTTAGTA GCATAAGCAA TTTCTCCACG TTGATGTACG TGATGTAATG ATTCTGGG 178

(2) INFORMATION FOR SEQ ID NO: 3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3205:

TATTAATCAC GTTGTGTGTC GTTCGTGTTT TCGCAGTATT GATTGTGTTGT TCGGCATTAT 60  
 35 GCATTGCATT ATTGTACTGC GTAATTGTAC CTGGCTTTTT ACCTTCAGTG CTTACTGGnT 120  
 CATCTAAATG ATTTTtagCT GTGATTA 147

(2) INFORMATION FOR SEQ ID NO: 3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3206:

CAGCTGTACT AGTTGAGCGT ATTATCCAAA ACATTTTACG TGATGGCATT GATGTCGATC 60  
 50 GACTTTCAGT CGTAACGTTT ACAAACCTTAA GCGCACGTCA nATGAAGCAT CGTGTAGACC 120

## (2) INFORMATION FOR SEQ ID NO: 3207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3207:

TAGGGACTTT GAAGCGGAGA GTCTAATGCA TATGGGCAGC ATTATGATCA GCAACTGCTG 60  
 AGAAAAATCC AGTTCTAGCT TGGGATTTAA ATGTGGAGTG GnTTAATGAA TGCATTAAGA 120  
 AGCTGCAAGA ACTTATAAGT GTGCA 145

## (2) INFORMATION FOR SEQ ID NO: 3208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3208:

AAACGGTTTT AGATCGTATT CAATTGAAAA GGACCGGTAT TGAATGnAAT CACACTTAGC 60  
 AGCGATTGAT CAGaACATTT TAAATTAAC TATTTATCAA CGGTATATGA AGGGGATTG 120  
 GAAGATGCGT T 131

## (2) INFORMATION FOR SEQ ID NO: 3209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3209:

ATAAATTTAT CTATAATCTG TTGCTTGTTT TnCTGTTCTA CAAGTATTTT CACATTAGGT 60  
 CCCGCATCCA TTGTAAAATA ACACGGATAC CCCGCTTCTC GGCATTCGTG AACAGCGCCA 120  
 TGACATCATA ACTTTCTGCA CAGTAGGAAC GGGGGTG 157

## (2) INFORMATION FOR SEQ ID NO: 3210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3210:

AACGTAATAG ATATGGTACT TACTACATGG GAGAGAGTGC TAGATTCACA AACGGCAATC 60  
10 AACCAATCAC AGTAAGAGAA GTGGGGCCAT TCTTATCTnG TCCAGTGGGT TATCAGTTCC 120  
AACCTGGTGG GTATTGTGAT TAT 143

(2) INFORMATION FOR SEQ ID NO: 3211:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3211:

ATGCATACTG TATGTGTTCC AGCATATACA ATTTTnGCCA TCTTTAATGA CAACTGTACC 60  
25 ATTTTTCACA ACATTTAATT CATCTAATTC CTTACCCTTC AAAGTTTATC TGTTGATCTC 120  
GGTAAAATTA ATTCTGC 137

(2) INFORMATION FOR SEQ ID NO: 3212:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3212:

ATTCACGCTT TAAAGGACGT AAATACACGA CTAGGCTGTT TACCTTTAGA TCTAAATCAG 60  
40 AACAAATTTTT TTACCATGGT GTTCCCCTTG AATTAGGAAT TTTATATAAA AATAAGCGGG 120  
AAGCGTTGTG CCCCCTTAC TCATAAGCTT TAATTAATGC TAAATAGTCT GACACTAGCG 180  
45 ATTTGATAAA ACTATACTAA AATTATTTAG AAGTCACTAA GATGCTAATG ACGACnAnT 239

(2) INFORMATION FOR SEQ ID NO: 3213:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3213:

CATCCTCAGA GTAGGAATAG CCATACCATC GAATAATTCA CGTACTGTTT CGAATTGAGG 60  
 5 TTCAAATTCT TGAGTTGTAT AGAGCTCGAA AATnTTTGCC CATTAGCATA ATCAGACTTT 120  
 TCAAAAGTCT TGATATTTGA TACCCACGCT 150

## (2) INFORMATION FOR SEQ ID NO: 3214:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3214:

CTAAGCATTG GTTTAAACTA ATGTTTCAGAG CTTTnTGTGG TTTGTAAAnA CAAGTATATT 60  
 nCGAGAACAC GTTTTTGTAT AGAGTCTCAA TTATAAAAGT TAGAATAGTT GACAACAGTG 120  
 TTACGATATT ATTAAACAAC TGTcTATCAT TAACGAAAGC AATTAACAAG AGTACTtGTT 180  
 25 GTGAAATCAT CGTTTAATAG TCAAAGATGA TCATCGTAGG gTAGACAACA TATCaTTGAC 240  
 TtAAGGAAGG GGAATGACCG ATGGGATTAA AAGATCAAGC TGTTACCTGG AGAAGGTATT 300  
 TTCATCAATT TCCAGAACTA TCCGATAAAG AATTTAAGAC TACACAAAAA ATTAAAGATA 360  
 30 TTTTAACAGA ACATCATATT AGAATATTAG ACTTACCAC 399

## (2) INFORMATION FOR SEQ ID NO: 3215:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3215:

CAGGTGAAAG CACAAGAGGA TTTGCTGTTT ATTTCTCTCC TGAAATTAAG AAATTCATTG 60  
 45 CAGATAATTT AGATAAATAA TTAAAACTTA GACATTCACC CAATCCTGAC AAAATATACT 120  
 ATAACTAACA TTTATTAATA TATATTGCAT TATTTAATAT GCATCAAAGC CAATCAACGr 180  
 TTGATTTTCA CCAACTCAAT TGTTGATTGG TTTTATTTAT GTATGAATGA ACAACTTTTT 240  
 50 GACATCATTA AGAATATAAA TCGGTTTGAA AGCATTTGAA AGCnACAACA TTTCTATAAA 300  
 ATTTTTCAAT AACAATTGCG CCACTAAAAC TCAAAATTTT CACCACCAAC ATCCAAATTA 360

## (2) INFORMATION FOR SEQ ID NO: 3216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3216:

AGTTGCATCA ACTGAATCCA ACGCTACGCA ATACGAATTA TTCCAATCTG GCATGCGTGT 60  
 TGGTAGAGAA ATTTTAGCGA CATCTCGAGC ACGGTTTACC TTGCCTTTnT TGGTGGCCAA 120  
 CTTGCTTTAT GCTATGGGTT TTTCAAACCTT AAA 153

## (2) INFORMATION FOR SEQ ID NO: 3217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3217:

CTTTGCATAT TCTGGTTTGT AGTATTCATG GTCCGTCAAT TGTAGACCCA TCAATTGCAG 60  
 CCATTACATA TGCGGAATAT CGAAGCGAAC TTCAAGTTGC TTCAAGCTGG TAGAACACGC 120  
 AnATAAAATT ATTACATC 138

## (2) INFORMATION FOR SEQ ID NO: 3218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3218:

CACTCCAAAC CAAGGATTTA CGTGCTTTAT ATnGAGGTAA AGCACATCAT GTkGTTaATT 60  
 TTATGCMTTT TaTTGCMcMa GraTTAaGAG AAATTTTAGC nTCTTTAGGT TTGAAACGTG 120  
 TAGAAGACTT AGTTGGAAGA ACTGATTTAT TACAACGATC aTCAACATTA AAAGCGAATA 180  
 GCAAAGCGGC TAGTATTGAT GTTGAAAAAC TGTTATGTCC TTTGATGGG CCAAACACAA 240  
 AAGAAATTCA ACAAATCAT AATCTTGAGC ATGGATTGTA TTAAACAAAT TTATATGAAG 300

AACAACGTGA TGTAGGGGTT ATTACAGGTA GTGAGATTTC GAAACAATAT GGAGAAGCAG 420  
 GACTTCCTGA AAATACAATT AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTTGCAGC 480  
 5 ATATGCA 487

(2) INFORMATION FOR SEQ ID NO: 3219:

- (i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 176 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3219:

ACCAACTCGG AATCATGCAA TGAACACCAT GGTGAAATA AGTGAATTGC ATAAGTATCC 60  
 20 TGGCCTGGCA ATGCTGGTAT AACCTAAAC CTTGTTGCAC GAAATGTATT CGCTACAATT 120  
 AATGTACCTG CAAAACCGTT TAATAAGAAG TTCGAAATCG TTGCACCTGT ATATGG 176

(2) INFORMATION FOR SEQ ID NO: 3220:

- (i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3220:

CTGATTTAGG TAATCTTTCG GCAATTGTTT TTTTACAGTT TCGGCAAATG GGTGCCCG 60  
 35 CAAATAAATA TTGGCTATGC TCAAACCTGA ATTAATGGTG GGTGTGTCCG CCATCGTAAT 120  
 TGGGnCCGCC TGAAGGGCCG CATATAAATG ATAGTGCTCT TCCGAATAAA AGGTAGGCCA 180  
 40 TATGTAATTG TTTTGTGGTT ACG 203

(2) INFORMATION FOR SEQ ID NO: 3221:

- (i) SEQUENCE CHARACTERISTICS:  
 45 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3221:

AGCTAAATCT TGCCAATATG GTATCAACTT TTCATTCCAC TGATAATCAT AAATTCAGA 60



GCAATGCCAG AAATGTATTA ACAACTGGCA CGTCTAATAG ATTGCTAACG GATTGTTTAC 180  
 GTACGTTTCAT CGGCTTCTTT CGCTTCTATC GGATCTGGAG AATTGGGATG TTATGACCAC 240  
 5 TGAACCACTT ATTTGTAAGC TCTGTCGTGA TTGACTTCAT AATGCTTGCG CTTGnCCCTCA 300  
 TTTCTAACAA CTCATCCTAC TTACnAAATT ACCCCnGGGG TACACCTGGT CCACTTCATC 360  
 A 361

(2) INFORMATION FOR SEQ ID NO: 3222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3222:

GGGGCTCCGn GGAGGCAAGG GTAGAAAATG ATGTAAACGC TGCATTACTA GGCGAATTGA 60  
 AATTACATCA ATATCAAGCA GAACGGATCT TTTGTATGAC GCTTGGTACA GGCATTGGGG 120  
 25 GTGCGTACAA GAATTAATCA AGGTTCATGT TG 152

(2) INFORMATION FOR SEQ ID NO: 3223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3223:

TTTGTTAAAT ATAGGCCCTG CAATGAGTGT ACTGGAATGG CAATAATCAT ACCATACAGT 60  
 40 AATACATCTC CAACATTTGC CTThAATTCT TTTCCCATGA CTACCGGTCC TGGGATGTGG 120  
 TGG 123

(2) INFORMATION FOR SEQ ID NO: 3224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3224:

TGGTTGGTAA CCGTAAATTA ATGCCTGACA ATGATATTAG CTnCTAAGC ATATTTCTGA 120  
 TGATTTAACA CATTATGAAA CGAGA 145

(2) INFORMATION FOR SEQ ID NO: 3225:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3225:

GGTATTGTCT AGTCAATTAC TAACACCATT TAATTGTGGn AAGCAAAAGC TAAAGGTTAT 60  
 CGTGCCTAT TGCAGGCATT GATGCTTCCA ACAAAGTCGA GTATTCAGTT GCATCAAAAG 120  
 TTTGCTTTT 129

(2) INFORMATION FOR SEQ ID NO: 3226:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3226:

GAACTACCG TTCCACGTA GCATCAATCG TCTCAGTCGC ATCGTAGTCA TCTGTATGTG 60  
 TTCCAGCATA TACAATTTTG CCATCTTTAA TGACAACGTA CCATTTTCAC AACATTTATT 120  
 CATCTAnTCC TACCCTCAAA GTTATCGTTG ATCTCGTAAA TAGTCGGCAA 170

(2) INFORMATION FOR SEQ ID NO: 3227:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3227:

TTACTGCTTT ACGTTTATCA TTTTCTAATT CAnAAATTCG TCATTCAGTT TCAACTTTAT 60  
 CGACAGCTGG ACTTTGCGCA GATAAATGTG CTGCTGTAAT ATCTAACACA TCGATTGCTC 120  
 TTATCTGGCA ATAATCGTTG 140

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3228:

GCGCCTATAA TTGCGCTACT TGATTTAATT GAGTAGATAA ATCTAATCCG AATAAATCCG 60  
 TGACTTGCTT GATAAATAGC AACAAATGCTn CAACTAAACC AGTTAGTACT GCTTTGTTTT 120

(2) INFORMATION FOR SEQ ID NO: 3229:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3229:

GGCTATACAC CGACTACAGT AACATCTGGT AGCGACATTG AAAAAGACTC TAATGGTTTA 60  
 ACAACAACAG GTGTTATTAA TGGTGCTGAT AACATGTACA TTAGATAGTG GnTTCTACA 119

(2) INFORMATION FOR SEQ ID NO: 3230:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3230:

TGGAATAGC AACCAACAAT GCGACAACAA AGCCCGCTAC AAATCTCCAT nAACTAATTG 60  
 CTAAATGTTG GAAAAATTTC TCCAGTCAAC AATGAAAGGC CATATGACTT TTTCCTACAA 120  
 GAGCAGGG 128

(2) INFORMATION FOR SEQ ID NO: 3231:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATGCAGCTA TTACTTTTCA CAGATTCCAT ATCGTTCAAC ATTTAAATAG AGAACTTAAT 60  
 AAGTATCGTG TACAAGTTAT GAATGAnTAC CGTAATAAAA AAGGACCTGA TTATACAATT 120  
 5 TTC 123

## (2) INFORMATION FOR SEQ ID NO: 3232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3232:

GCCTCAAAGA ACATGCTGAA CAGTCATCGC aTTCATATAG TTTGAAGTCT CGTTTAAAC 60  
 20 CATATCTATC ATTACGGTAT GCATATCTTT TAAACCTAT TCTTTTGTTA TTAGGACATA 120  
 TAAATTCATC ATTAAGTTCG TCATATTTCC AATTTTGAGT GTCGAAAATG TCACTTTTAA 180  
 25 ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT TTATTAAAT 240  
 CATCTATAAT GGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT ACAATAACC 300  
 GAAGtATTTT GAATCATTGT TAAAAATGGA ATTAAAGTTC TAGTATCTGT CGGGTTTGA 360  
 30 AATAGGTCAT AGGATAAAAC AAATTGAGAA TTTGTCGCTA TTTGTAAATT GTATCCTGGC 420  
 TTAAGTTGGC CATTTTTCAT ATGGTCTTCC TTCATTCTCA TAAAAGTTGC ATCATGATCA 480  
 GTTTTAGAAA ArCTATTTCT ATCTTTAAGA ATCGATTTTT GTTCTTCATA TTTATTTTTT 540  
 35 CTTTCGGAAT AATCATCAAA TTTmTTTTTG AACTTCTTAA TCTTAGTTCT TTTTaCGGG 600  
 TCTGTTTTCT AATTGAGTA CTATCTTCGT TCTCAATAGA ATGATTTAAA yCTTCGATTT 660  
 CTTTATCTAA ATGACTACCA ATTAAATCTA TTTCTTCTAT TGTAAATCG CTATCTCCAT 720  
 40 CTTCTTTTAT CTCTGGTATT ATTTTTTCTT CAACTAAGTC ACGATATAAT GTTTTGAAT 780  
 TTTTCGTTCAA TTTTCGATTCG TGATTTTGAA TACTTTTCTT CCACACAAAT GTATACCTAT 840  
 45 TGGCATTAGC TTCTACTTTT GTACCATCAA TAAGATTTTG CTTTAAACAT TGACTATGAA 900  
 ACTGGATAAA TAAAGATTCA ATTAACGCAT CAGTATTAGG ATTCACTCTA ATACGATTAA 960  
 TAGTTTTATA AGAAGGTGTT TGATTTTGAG CTAACCACAT CATTCGAATA CTGTCATGAA 1020  
 50 GTAATTTCTC TATTCTACGA CCAGAAAATA CAGATTGAGT ATATGCATAT AAGGTGATTT 1080  
 TTAACATCAT TTTTGGATGA TAGGATGTTG CGCCACGATG ATGTCTGAAT TTATCGAATT 1140  
 CGCTATCAGG TATCGTTTCA ACAATTTTCA TAACATATCG CGAAATATCA ATTTGAGGAA 1200

GGCACTTCAT TAATTTAGTT TAGTGGTATT TATTAAATTA TACGAAGGGA CCCAACACAG 1320  
 AAAATTCAAA TTATTGAATT AAACATTTAT GTGCAAGTTT GGCAAAGTGT CTTATTTTTT 1380  
 5 AAAAGTATGT AAAAGTAAAA TTACATGTTA ATACGTAGTA TTAATGGCGA GACTCCTGAG 1440  
 GGAGCAGTGC CAGTCGAAGc CGAGGCTGAG ACGGCACCCT AGGAAAGCGA rCCATTCAAT 1500  
 ACGAaGTATT GTATAAATAG AGAACAGCAG TAAGATATTT tCTAATTGAA AATTATCTTA 1560  
 10 CTGCTGTTTT TTTAGGGATT TATGTCCCAG CCTGTTTTTT GTGATTTTTA ATAATTTGAA 1620  
 TATGGrAAAT GTATTaWTct CTCATTTGTA TAGATT 1656

(2) INFORMATION FOR SEQ ID NO: 3233:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3233:

25 TTGCTCATAA ATCTTTTCTT GCGCTCTGA AACTATCTT CTATTCTGTC GGAATTTTTC 60  
 AAACATAGTC TTATCATTTn CTTCTAATCG CGTTAAACGC CAATCTTGTT CATGTCGTTT 120  
 GGTAATCCA 130

(2) INFORMATION FOR SEQ ID NO: 3234:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 122 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3234:

40 GCCACGATAA AGAAGTAAGA ACAACACATG GTGTTACTGG TACAGGCTCA TGTTCTTGGG 60  
 AAAGTTATTT GTGnAAAATG GTGTGAATTA CCTGGGGAAA AATCAACAAA CTGACTATCC 120  
 45 AA 122

(2) INFORMATION FOR SEQ ID NO: 3235:

- (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

5 AACCAGGATA TGAAATCTGT GACTTATTGC GTTAGATCGT TTTGTAAGT CTACTATTGA 60  
 AGAAGCAGAC CAATATAAAG GTACCATTCA TTGCAAAGC ATTACATGCA TGAACCCAGT 120  
 TGACATTTAG TTAGAGATGG AAGATAGTAT TGTGCATTTG CAGnTTCCAC ATG 173

## (2) INFORMATION FOR SEQ ID NO: 3236:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3236:

20 GCGGTGTGCA TTTGAAATG TTATCAAGAA TATTGAGTTA ATTCGCAACG ACATTATACC 60  
 AGCGATTAnA AAGCATTTAT CAAATACGA GGGCGTCAT CATGAATATT GTATTATTGT 120  
 CA 122

## (2) INFORMATION FOR SEQ ID NO: 3237:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3237:

35 TTTTTTGCCC AAAATTTTTG GGTTTTTTT GGGTTAAAGG AAAAAAAATT TTAAAGGGG 60  
 GGGGGGGGTC CCCCAAAAT TTTTTCCCT TCCCTTTGGT TTGGTTTTTT GGGGGGGGGG 120  
 40 CCCCCCCCCT TTGGAAGACC CCTTAAAAA ATTTAAAGGT TAAATTGGAA AAAAAATTT 180  
 AA 182

## (2) INFORMATION FOR SEQ ID NO: 3238:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3238:

GATGAnGTTc GACAACGTAT TGTGGCAGAT GTTGcAGTTG ACTTTGAAGA A

111

(2) INFORMATION FOR SEQ ID NO: 3239:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3239:

AGTTGATCGT ATTTTCCAGA AGAGACAGAA TTAATTGATT ATCGTGTTAG TTCTGTCACT 60

GAAGGTACTG ATGCCCAAGC AGnAGTACAT GTAAGTTTAT TGATTGAGGT AAGACTGTCA 120

(2) INFORMATION FOR SEQ ID NO: 3240:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3240:

TACACATCTn TCTACGATTG TAGTTTATCG ATAGGTTTCG CATCATGAAA CGTGATAAAC 60

AACCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCAGTGTTT 120

AGCATAT 127

(2) INFORMATION FOR SEQ ID NO: 3241:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3241:

GACTAAAATA CATGTTGGAA TACTTGGTCC CATGGGAAAA TATTGGACTG GGTAACCCAA 60

TCACGGCTTC TGAAGTAGTT CTTTnTCTTC TATTAAAATA GCGACGGAAT CACACCTTCT 120

GCGG 124

(2) INFORMATION FOR SEQ ID NO: 3242:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 122 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3242:

TACGTGTATA CACCGTTATC TTTATGGCTT TGAATTTCCA TAATAAATAC ATACGGnTTT 60  
10 TGTGCAGAGC TCAGCACATA ATCATCTTTA ACTATAGTTT CTGGGAATCA CTTCATAGTT 120  
TT 122

(2) INFORMATION FOR SEQ ID NO: 3243:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3243:

25 AACCTTTTCT GCAACCATAC GCCATAGgTA TGtTTTCTTT TTACAATTAA AGaGCCAACC 60  
GTTGTTATAG TCTAACAATG GTTGGCTCCT CTTAtTTTAT GTGCTAAAAA TTTATAGGCA 120  
ATTTTATTAC AACAATGTAC ATTTAAGGTG ACCTTCATGC CAAAATCGCA TCACTCATTT 180  
30 AATGGAAGCA GCACGTCTTC ATACAAAGTC ACGATCCTAA T 221

(2) INFORMATION FOR SEQ ID NO: 3244:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3244:

TTGCATTTTG ATTGTCTGGT GACCTTGGCA ATGACAATTC CCGCTTGCAA TCGGTATCTT 60  
45 CAATATTATA ATCAGGTCTT GCCTTAGATT TTCGCTAAGT ACCGGTGATT CTCTACCATC 120  
ATACTCACCT CATGnGCTAT TTTTCTAGAG TGCTTCTTTT CACACTTTAT CTTATAAAAG 180  
GCTAGCTACT ATTACCGATT TATCATTATT AGTGGTTTTT ACCn 224

50 (2) INFORMATION FOR SEQ ID NO: 3245:

55

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3245:

GAAAGAGATT AGTGACAAGT TGGTTGTACT ATTACGTAA AATTGGAGA TTATGTGTGG 60  
 TGTTCAGTA TCGTTCAAT AATTGATATT GGCGCACCGT ATAACCATGT CAAAGTA 117

(2) INFORMATION FOR SEQ ID NO: 3246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3246:

CTACAGGCTT TCGTACCACA GGATCAAAAC TACGCACTGT GCCTTGTTACA TACGCATGAT 60  
 CAGCAATGAC ATTCCAAGTA TTACCACATG ATATTTGnCC AATTGTTACT ACCGTTTC 117

(2) INFORMATION FOR SEQ ID NO: 3247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3247:

TACACAnCTT TCTACGTGTG TAGTTTATCG ATAGGTTTCG CATCATGAAA AGTGATAAAC 60  
 AGCCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCATGT 117

(2) INFORMATION FOR SEQ ID NO: 3248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3248:

CCCGTCCTTT GGTGGAACCG TTTTGTAGAA TTAAATAATA TTACAGAGCC GCTAGCAGTA 60  
 ACGATCCAAA CGAATTTACC ACCATCACGT GGATTAGGAT CGAGTGCACT GTCGCGGTTG 120  
 CnTTTGGTCC TGCCA 135

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3249:

AAAAGCCAAC CCATGnAATG TTGGATTGGC TTTTACATG CCATCTGAAT CTCTAATTTT 60  
 AAAAAAATAT GGAATATAAA TAAGACAGTA AAAATTAAAT TTCAGT 106

(2) INFORMATION FOR SEQ ID NO: 3250:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3250:

AACGCTGAAG CAGATAAAAA ACGTCGTGAT AGAAGTAGAC TTAAGAAACG AGTCTGACAn 60  
 TCTAGTATTC CAAGTTGAAA AAACTTTAA CTGTATTTAG GCGAAAATAT CGGTGAAGAA 120  
 GA 122

(2) INFORMATION FOR SEQ ID NO: 3251:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3251:

GAACGTTGAG ATGTCACAAA CTGGTGAAAG TGCACGTTCA ATGCCAATGA CTGATAAAAC 60  
 CAAATTCATC AATCACAATT ACTCCGAAAG CnGGTACAGG TCACTCAGTA AGTAGTAATC 120  
 CCAGTACATT AA 132

(2) INFORMATION FOR SEQ ID NO: 3252:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3252:

GGAAAATCTT CAAATTCTGC AAATTGCCAA TTTACCTAAT AACCAAACAT CTAAGGCATG 60

5 TGTAATGCTG CTACnTCCGC TTCGTCATCA GCTACAATGA CAAATACAGG TGCCA 115

## (2) INFORMATION FOR SEQ ID NO: 3253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3253:

TTTCGTCAAA TTATGGGAAT AAAATAATCA TATTTAAGAT AGTAAATATT GAATAAGTTG 60

20 CTTTGAAATT TATAAAATGA AAGTATAGTG TCATGGGnAG TATAATAGTC AGATATATAT 120

GTAACGGCAC TATATTGAAA 140

## (2) INFORMATION FOR SEQ ID NO: 3254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3254:

AAATCTCCTA CTTTTTCTAC CCATAAATAA TTGGCTAACT TTTTCATCTT ATCTTCATCC 60

35 TTTCTCTTCT ATTTAAATG CTACAAATAA ATTTCCGCGA GTAATTTTAA TGTTTTACAA 120

CGCTGTTCAA TACCTGGAAT AAGCGGTGCT ACTAACACCT CATCAACTTC AaACGTAGCA 180

40 ATGAAATCAT CTAATTGTGC TTAAACCTWT TCTTGTGTAC CTGcAATGAT GCGTGCTTGg 240

ATGTGCTTGA ATCATCTCTT TGTCTCGATC ATTAAGCTTA TACTTTTGTG CTGTGTCTAC 300

TGAAGGAAAA TCTTCAAATT CTGCAAATGT AATTTACCnA ATAACCAAAC ATCTAAGGCA 360

45 GTTGTAAGCG GChACTTCCG CTTCGTTATC AGChACAAG 399

## (2) INFORMATION FOR SEQ ID NO: 3255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3255:

ACCATTCGTC AAAATATTCC AACACGCATT TAGGTGTGCA AGGTATCGGT ACCTAACAAC 60  
 5 GAAGCTATCG TCTCACTAnC CTAAAAGAT TTTAGAACAA CAGCTGCACT CATCAT 116

(2) INFORMATION FOR SEQ ID NO: 3256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3256:

AAAGACCTAA GGTTATGTAA TTGGCCTAAA TTTATTAATC GTTTAAAnTC AGTTAGTAAA 60  
 20 AAGTCTGTGA GTAAGGGTGT ATGGAAACTG GTTAAATATT ATAGAG 106

(2) INFORMATION FOR SEQ ID NO: 3257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3257:

AACGTCCATC GTAATACCTT TTGTGTCTAA TGTAACCTGT ACATCGTCTA ATAATAAGTT 60  
 35 GACGATATCT TGACAATGCA TCTTTATCTA GATGTAAGAn TTCAACGGAT GCCG 114

(2) INFORMATION FOR SEQ ID NO: 3258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3258:

TTAAAGCAGT TAATCCACAG GGAAAGTGGT TAATACAGTT GGGCTCTGGT GGATAGTACA 60  
 50 GTTGCAGGCA TGGTGGGCTG GGAATTGCTT CAGGGTTTAA CGAnTGGGAA AAGCCTT 117

(2) INFORMATION FOR SEQ ID NO: 3259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3259:

	GGACCGCCAT ATCGTTGGCA ATCATCGCAC CTATAATCAT CGCAAGTATA ATAATATTAG	60
10	CACCTTGCACT ACTTTTAAAC CAGGTTGTTA ATGCCTCAAA AATATTAGAA ATTGGTGCCC	120
	GnTT	124

(2) INFORMATION FOR SEQ ID NO: 3260:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

25	TACCAATGTA TATCCATATA CTTTATCAT AATCATTTCA GCCGACTTTA GTTTGATGTT	60
	TTTGCTTGAT TAAAATCTTT CGGCGATCTT CAGCTTGATG TTTTCGTTTG ATTAAATTGG	120
	TACAATAnAT	130

30

(2) INFORMATION FOR SEQ ID NO: 3261:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3261:

40	GGCCTTTTTG GGCCGGGGTT GGAAATTGGG GTTGCCTTAA TTTTTTAATT AAATTTTGGA	60
	ATTAAAAAAG GAAAAAnTCC AAAGGTTAAT TTTAAAAAAA GCCCAAGGTT TTAAAAATTC	120
	CCCCAACCAA AAAGGGGGGG AAAAAAGGTT GGGGGTTTTA AAAATTAnCC AAGGTTTTTG	180
45	GGGCCCTCCC TTGGGGGTTG GGAATTAAAG GTTAACCAAG GTTTTTGGCC AAGGGGCCCA	240
	ATTGGGGGTT GGGGCCCTGG GGGAAAATTT TTGCCCTTTC CCAAGGGGTT TTTTAAACC	300
	CGGATTTTTG GAAAAAAnAA AGCCCATTTT CCCCCAACCC CnAAAGCCCA GTTCCCGCCC	360
50	ATTTTCCCGG GGTAACCCTG CCCCCACCGG GGCCATTTTT	400

(2) INFORMATION FOR SEQ ID NO: 3262:

55

- (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3262:

10 TGGTTCAATG GAAACGTGTA CCGCAAATnC CGTTAAATGT TGTTGGATGT TGAGAGACGT 60  
GGCTGAACTG GCACATTTGG GCAATGACCA ATGGAACAAG CTAATGGGCA AGCGATTATT 120  
GCGACGGCTG ATGG 134

15

(2) INFORMATION FOR SEQ ID NO: 3263:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3263:

25

TTTTTTTCTG TTGGTACTTG TTTTGTGGTT GGCGATTGTG GTGTGTCTGA nTTAGTAGAT 60  
TGCATTGGTT GTGGCGTGTT TGCTTGATGG AGGTGTTGTC ACTTT 105

30

(2) INFORMATION FOR SEQ ID NO: 3264:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3264:

40

GTTCCATCAT TCCCACnAT ATCCAACATG TGGGCTACTG CAATGCTTTA GGCGTCAATG 60  
CCTCATCATC ATCACAGCGC CAGTAAATGC GTATAATTAA ATTAATT 107

45

(2) INFORMATION FOR SEQ ID NO: 3265:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3265:

55

GTCGTAACAA TGGTTCGTTA CCAAAGCATA nTTCGCCTTC TTGGCATCG

109

(2) INFORMATION FOR SEQ ID NO: 3266:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3266:

TTACCTTTAA AATAAnGTTC TCCACTAGTT GGGCTAAACA AATTACATAT TTTGCTTTTG

60

GAAATGTACT TTTTACCACT ACCTGATGGA CCTATAATGG GCAA

104

(2) INFORMATION FOR SEQ ID NO: 3267:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3267:

TAAGCCATCA GAAACAAATG CATATAACGn AACAAACACAT GCAAATGGTT CAAGTATCAT

60

ACGGTGCTCG TCCGACATAC AAGAAGCCAA GCGAGAACGA ATGCATACAA TGTAACA

117

(2) INFORMATION FOR SEQ ID NO: 3268:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3268:

GCTGCACAAG CACAACCTGG AATCAGCAAC ACCGGCAAAC CAnCAGGTCA AGGAATAACC

60

AAGCAGCACC TCATAATAAT GCAACACCGG CAATCAAACA C

101

(2) INFORMATION FOR SEQ ID NO: 3269:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3269:

CATACCCTAT TTTAGATATT ACCTTATTAC AAAATATTTT TACATTAATG TCAGCTGCAG 60  
 5 GTTAGTATTG TTTTCCAAAA TTTACCGGTC ATCTTTGCCA ATTGGGTGTC GCCAATCGGG 120  
 ATTTATCCTA GGAAGCCGAT TAAAAGGGTA CTGCCAGGGT TTTAGCCTGC nGCTGCCTCG 180  
 GGGTTTTCTT TAAATTAATG nAACCGC 207

(2) INFORMATION FOR SEQ ID NO: 3270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3270:

ATATTCGCAC CACCATAAAC ATAGATGGTG TTTTGTCTT CTGCATTCAC AGTGATAAAA 60  
 GGGCTTGnC CCGTTTTTGC TTCAGCTGTT TTGAATAATA TATGATG 107

(2) INFORMATION FOR SEQ ID NO: 3271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3271:

TTGGTTACAC TTCTGCTAGT TTTAGTAACG ATGGTCCAAG ATTGTATGAG CCTATTTCATG 60  
 GATCAGCACC AGATATTGCA GGTAAAAACG TTGCCAATCC ATTTGGGATG GTTCTnATGC 120  
 TT 122

(2) INFORMATION FOR SEQ ID NO: 3272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3272:

GAAGGATGAT GATTCGGAGC AnCTTCTTGC AGAAGAnGCG GnAATAACGT GACATATTGT 60



TGCGAGCGCT TGACAATCTA TTCTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA 180  
 GAAATTAAAG CGGmGTTTAC TTTTGTAAT GAGCATTGA TTTTtTGAAA ATAAAGCAGT 240  
 5 ATGCAGGCGC TTGACTAAAA AGAAATTGTA CATTGACAAC TAGATAAGTA AAGTGAAAAT 300  
 ATAGATTTTA CCCAAGCAAA ACCGAGTGAA TAAAGAGTTT TAAATAAGCT TGGATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 3273:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

20 TCAATTTTAA CTGCAAATAA TAAAGCTGCA TGATTTACTT TGTACATTAT TGTAATTTCA 60  
 GTAATACGAG GCAATGTCAG TnGCAGTGTT TAATAAATTT TGTTCGCTAT TT 112

(2) INFORMATION FOR SEQ ID NO: 3274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3274:

35 TACATTTATG CAATCAACGT TACATTCAAT CGTTGGAGAA AATTGGCTTT ATTGACTTAC 60  
 TAAAATCTAA AAAATCATAT GAAAGAATTG CACATATGTT AAAAActGGT AAGCCATTAC 120  
 GTAATTAAAA GATAGTCATT AAGAGAGGAT GATAACCATG CAAGAAAGCA TACATTGTAG 180  
 40 CTTATGGGCG TTCAGCGCAG CGAAAGCAAA GCAAGGCGCA TTATTCCACG AAAAGACCTG 240  
 nTGATGTCGC AGCCAAAGTA ATTACAAGGC GTATTTGAAA ACGTATTGAC GGGAnAAATT 300  
 CCAATAAGGA TTATGGATTG nAAGATGGTC CATTG 336

45 (2) INFORMATION FOR SEQ ID NO: 3275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 50 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC TGTTTTCGAA ACTAATTTTA 60  
 CCGGCGATAT CTGGCATCTT TTATTTTCGGC ATTTTTCCTAA ATCATGGTTA TTCCAGTTTG 120  
 5 GCGGCTTAAA AATTCTTT 138

(2) INFORMATION FOR SEQ ID NO: 3276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3276:

CATTATACGA GATAAGTAA AATTGATGAT GTGACTAAAA AAGATGCACA ACAATTATTG 60  
 20 AAGATGCAAA AGAATTGCAT GCCAAGCTGA TACATTAGAT A 101

(2) INFORMATION FOR SEQ ID NO: 3277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3277:

TGGTTATTCG TTCCTGATCG TTGTTGGTAT CTCACTATTC AATATTTATC GTGTGGCATT 60  
 35 ACTTTAGTTA CACCAGGTAC ATTTGAACCT GGCACTTGTT GCGAGTATTT CCGGTCTCGT 120  
 CATT 124

(2) INFORMATION FOR SEQ ID NO: 3278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3278:

GACTTTTTGA CCAGTTGTAG CACGACCACC GAGAGTAGCA TTGCATATGC AATCATTGTA 60  
 50 CCTTCGCCAA CGACTGCGCC AATATTAATT GTTGCGCCCA TCATAACGAC 110

(2) INFORMATION FOR SEQ ID NO: 3279:

(A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3279:

10 TTGGTATATA GAGGGCAACC GCACCTGATA AAATGTGnCA CAGTTTTTAC AAGAGGTTAA 60  
 GGAATGAGTT TGGAGGCATA CGAGCATCAA GATACCATTC GATGTTAGTA ATT 113

(2) INFORMATION FOR SEQ ID NO: 3280:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3280:

25 TTACCGTCAC CGTAATCAGT CCATACTTTA TCAGCTATAC CGGCTTTAAC AGCATAAATG 60  
 TTCGTTCCCTG TAGGCATACC AAAGnCGATA CCATAGTGAC G 101

(2) INFORMATION FOR SEQ ID NO: 3281:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3281:

40 ACTATGTTTG AnAAATTCGA CAGAATCAGA AGCACAGTCT GAGAACGCAA GAAAAAATTT 60  
 ATGACAAGTT AGATAGAAAT TTCGACGAAC TAAGGGCGTG ACCAAGAAGA AGATGA 116

(2) INFORMATION FOR SEQ ID NO: 3282:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3282:

ACTTGGTTAG ATAATATAGC GTCGATTGTA TCACGAGTGT CTGTTCCAGT CATTATAAAA 60

55

CGTCGTTCTG ATGCTTTTCC TGAATCAT

148

## (2) INFORMATION FOR SEQ ID NO: 3283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3283:

AAATGACGAT AGAGTCAGGT ATTAATCAT TTTnCAATAG TATCAGGAAG ACTACCAAGC 60

TTATGTTGAA GGGCATCTTT TGGCGTTACC GGGTTGGGCA 100

## (2) INFORMATION FOR SEQ ID NO: 3284:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3284:

TTAAGAAACC GAGCAGCGCA TAAncCTGCA GTACCTTATC GCTTCTAGAT AATCCGATTG 60

CGACACCATT GCAAGATGAC CGGTAATTTT GGAACATATA C 101

## (2) INFORMATION FOR SEQ ID NO: 3285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3285:

TAAATATTT CGCATCCCTA CACGCTAAAA TAATACATTA CACTTAAAC GGCTGTTTTA 60

AAGCATCCTC CCATAACAT CATCTAGTTG ATAATAGGGG GGGGGn 106

## (2) INFORMATION FOR SEQ ID NO: 3286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3286:

TTTAACAATA CCTCAGAACA TACTATGGAA ATTGCTGCAA AGTTAATTGG GCATGCATAT 60  
 5 TGATCATAAT GCGCTTTTAA ATAAATGGT GGAGA 95

(2) INFORMATION FOR SEQ ID NO: 3287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3287:

TCGAAATAAT ATCTACGCAC ACTGATAACA TAAAAATGCC TGGTAGAATA CTAATGAAAT 60  
 20 AAGTGCATAC ATGACCACAT GAATGCTAAT AACATGCnAG AACCCATTTT TTGAATATTT 120  
 CACCACTCGA ATCATCAATA C 141

(2) INFORMATION FOR SEQ ID NO: 3288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3288:

TAGCTGGACC AGAACACGGT TCGACGTTGC AGGAAGTCTT GAACAGTCGC TGAACGCCAA 60  
 35 GGCGATACTT GGGTTATCCA TGGTGAAAGn AATGGATTGG TGGTGCA 107

(2) INFORMATION FOR SEQ ID NO: 3289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3289:

GCTTTGCAAT GCCGATGTTA CTCGCAATAA TCATGTCGCA TCAATTACTT ATGGAAAGCA 60  
 50 GATTTACGTA TGTCTACAAG TTTAGGCGC 89

(2) INFORMATION FOR SEQ ID NO: 3290:

(A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3290:

10 TGTTACGCCA ACAACAAATC CTACGTCGAC AACTATTTTT AAGCGATGAT TGCAATTAGA 60  
 CAGAAATCCA ATCATTTTTG CATTCCATCC AGTGCACAGA ATnTCGAG 108

(2) INFORMATION FOR SEQ ID NO: 3291:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3291:

25 GATCAAGnCC TGAGAATTTA ATTTAATTTA TTTTATATT GGAGATGGTT AAAATGCTAA 60  
 AACTCAACAT GAGTAACCAA AATATTGCCC TAAAAAATGC TGATCATTG 109

(2) INFORMATION FOR SEQ ID NO: 3292:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3292:

40 TTGATAATTT TGATATAGAA AGTTATTTAA AATTCGAATA AAAATAATAA CTCATCGACG 60  
 TTTAATGGCT AGGTTCCAAT CAACTATGnG ACATAAATTC AAATTCGATC ACGTAACGAA 120  
 A 121

(2) INFORMATION FOR SEQ ID NO: 3293:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3293:

55

GCGCGTAATA CCTGCAGTAC CTCTATCGCT TCTAGATAAT GCGGTTG

107

(2) INFORMATION FOR SEQ ID NO: 3294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3294:

AAAATGTTAA ACCAAAAAGT TTGGTGAGTT ATAATATGGA ATATTAAATC TGTAGAAGAT 60

AAAGCGAATA TAAAGTGATT AACTTTGGTA ATAAAGAATT AACAGCGAAA n 111

(2) INFORMATION FOR SEQ ID NO: 3295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3295:

CCCCGACTAA ATCGAACGCT TTAATGTAAT GATTTGTCCG AATCCCCATC CTGCACCTGA 60

TAATAAGGCG AATAGCAAGT TGGTTCCCGT nGGGAAGCCA CTGA 105

(2) INFORMATION FOR SEQ ID NO: 3296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3296:

ATTTATTCAA AACCCGCCAC ATGGGGCAAC GGTGCCATG GCATGATAGT CCAGATACAT 60

GGAAAGGAAT ACAGTCCGGT TAACACTCCA TTAAAAACCT GCGGGTTGGT TAAACCATT 120

AACCTAAATG GGTCCAAGG GTTAACGCGG TTAAATGTT TGGAAAGGTT TnCCCAGTTT 180

CCAAAAAGTT TTnATTCCC C 201

(2) INFORMATION FOR SEQ ID NO: 3297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3297:

	TTTAGACTTT CATCAGTGTT GAATATTICT CCTTTAACGG TTATAGGTAA TATTCCTGA	60
10	GAAATATTTC CATTCTTTAC ATTTCCGCT GTCAATTGAT GACTTCGATA AGCAAATTCA	120
	TCTTGTAATT CTCTGAAAC ATCATACATC TkGGCCACAT TTTCAGCACC TkGAATCATT	180
	GATGGGTCGC TCATTTTCAGG TGCAAATGAT GCACGCTCAT AAAACTCAGG TAATGCTGTT	240
15	TCGTACACAG AATGCGGTCG TTTGATTTTC CAAGGTGCTC GACTTGTAATC TTCAACACCA	300
	CCTGCAATAT ATACCTTGCC AGCTCCGGCT TGGATCATGC GACATGCATA TTGaACACTT	360
	TCAAGTCCAG ACCCACATTG cCGATCGrTT GTGaGCCAG TATTGAAGCT TAAGC	415

20

(2) INFORMATION FOR SEQ ID NO: 3298:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3298:

30

	TTAATTGCAG CAGAGCGACT AGCTGATTCA GAGGTGTTAG TTTGTACGGT AATAGGATTC	60
	CCATTTAGGT GCATCGACCA ACTGCCCCGAC GAAAAGCCAT TTTGAAAACC AGAaGATGC	120
35	CGATTCAAAA ATGGGTGCCA AGATTGAAAA TTTGGACCAA TGGG	164

(2) INFORMATION FOR SEQ ID NO: 3299:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3299:

45

	GTAGATGCCA TTTTCACGTT TCTTAGTTAT TGGCATTTTT TAAATGCGAT GTGTGGCTTC	60
50	TACATAACGG GAAATTTTAA GTTTTATGAA TcACATATC AATTGC	106

(2) INFORMATION FOR SEQ ID NO: 3300:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs

55



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3300:

AAAAGGTGTT ATGAGATTAG TAAATCAnTA GACAAGCAGG TAAATTAAGT GATGTCGCGT 60

10

CATTTAAGGA AGCGATTAC AATCGAGAAC ACAAAGTACA AC 102

(2) INFORMATION FOR SEQ ID NO: 3301:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3301:

TTAAAAGTTT GGAGATTATC GTGTCGTCTT CAAGTATGCG TTCATTAATT GATATTGGCG 60

25

CACCGTATAA CCATGTCAAA GTACCATTG nAATCAGTCA TTGGCGCATT GGCTGCCCTA 120

GCGTTCA 127

(2) INFORMATION FOR SEQ ID NO: 3302:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3302:

CCAGCTAGAC GATTGCTAAG GTATTGGATG TTTGAAACGT CCATGGACCC AATTGATTAA 60

40

TTGGnTGTAa CTCGGTCAAT GGGTATATCC TAAATGCACT GGCCTGCTGG TGTTCTTCTG 120

GGCGTTGCTT CGGAAAT 137

(2) INFORMATION FOR SEQ ID NO: 3303:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3303:

55

ATATAAATTA ACGACGCGTT AATGCAGGCT GATGTGATTT TTATTGGTTT CCCAATTTTC 120  
 AAGCTTCCAT CCCTGGTGCT TTGAAAAATG TGTTTGATCT ACTTCCAGTC AATGCGTTTC 180  
 5 GTGACAAGGT AATAGGACTT GTAGCGACAG CAGGTTCTAG TAAACATTAT TTAATTCCTG 240  
 AAATGCATTT AAAACCAATA TTGAGTTACA TGAAAGCACA TACGATGCAA ACGTATTATT 300  
 TATTGAAGAG AAAGATTTTT CAAATCAACA AATTGTCAAT GATGATGTTG TATTTGCGTT 360  
 10 AAAAGCGTTG GCACAATCCA CAATGCGAAC TGCCAAAGT 399

## (2) INFORMATION FOR SEQ ID NO: 3304:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3304:

CACCATTATT TACAGGACCT nCGATGACGT GTGGTCCTGT GTTAAGACAT AACATAATAT 60  
 25 TCTACCTTTG TAATCAGTAC GGGTTTATCT ATCACAGTAC GG 102

## (2) INFORMATION FOR SEQ ID NO: 3305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3305:

TCAGCGTTAT CAATGAnTGA CTCTAATGCC TTTTACCCA TTTTGTAAA TGGAACATGG 60  
 40 AAGCATAGAG ATGCGrAGTC AGCTAGCGAC TTACCTTGAC GTTTGCGTA TTCATTCCAG 120  
 CTTTGTGGr ATGAGCGGAT ATAAGCATCT TTAGATAATG CACCATCAAC TAATGGATAT 180  
 TTATGTCCAG TTGGACGCCA GA 202

## (2) INFORMATION FOR SEQ ID NO: 3306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AAGATAGGGA TTTACACCTA TACCTCGTTC CGGGGAAGGG TCGGTGTTCT GAAAAGTTGG 60  
 AACTACTCCC GnCAAATATT AAATTATGGG AGCGGGAAGG ATCAGGGATT TGACACCTAT 120  
 5 GACCTCCATT CCCAGGGAAG GGAATGTGAT T 151

(2) INFORMATION FOR SEQ ID NO: 3307:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3307:

AATTTCTGTTA CTGCGCCTT CTTTTGCGG TTTTAAATA AGCGAAAATT TCAGGCGGTA 60  
 20 AGACATAACG TCCCAGAATA GCTAGGG 87

(2) INFORMATION FOR SEQ ID NO: 3308:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

ATGATGGCAA AGTCACCAAA CTGATTGTGC ACACCAATCC ATCCATCTGC GCTGTAAATA 60  
 35 ATGGTTTCGCA ATAATTTTAA AATACCTTCC GCTACATTG ATTTAAAGCT GGTTCGCGCA 120  
 TGGACTAGA 129

(2) INFORMATION FOR SEQ ID NO: 3309:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3309:

GTTCTTTTTA TCGTAGTTGG TGGGACTCCT TATCGGCATC GCGGCTGGAC TCTAGGCGGT 60  
 50 GGAAACGGAC ATTCAAAGG GATTTAGTTC ATCCAGATG GATTTCAATT TGGGGAATTC 120  
 CATTGGA 128

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3310:

GTACGATTCA GCATAAAGTA CACCACATTT GTCACCTACGA CATCTGTAGC TGGTATTGAT 60  
 CATGCAATCA TGAATAACGC TAA 83

(2) INFORMATION FOR SEQ ID NO: 3311:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 85 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3311:

CTGAGGATAA AGCGTCTCCA AGATAAGTCT AAAGATCATC ATAATGGGCA AAAAAGGTGG 60  
 CAGCGATTTCG GTGGCTGGGA ACAAG 85

(2) INFORMATION FOR SEQ ID NO: 3312:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3312:

ATTTTATGTC TAAATGCTGG ACCAACAGTA TTGGCTATTA TTTGGTAACG TGATTACTAC 60  
 AAAAAATGGA CCGTTGAGTT CGTGGCACAT GATTGATTTT GTAAGTAAGT ATGATGCACA 120  
 TGGGCTnTT 129

(2) INFORMATION FOR SEQ ID NO: 3313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TCACCTAAAA TTAATCAAGG GACTTAACAT TGGCGAGTCA AGGTATTGAT CAAGCTAATG 60  
GCACAGTTAA ATGATGCCAA AG 82

(2) INFORMATION FOR SEQ ID NO: 3314:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3314:

ATGTTATGGA AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCCT 60  
TTATCAAAAT AGTGAGGGGC GTCATCA 87

(2) INFORMATION FOR SEQ ID NO: 3315:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3315:

TGAACCCGTC GTTGCCCAT T GCCCGTTCC CGAAAGCCGG CGCCnACGGT TCTCCCTGCC 60  
TAAATAGGGG ATGGAATATT AAACCATCTG CACCTGGTTT AACACGCTTT GCAATTTGAG 120  
TTAAGACATC ATAAGG 136

(2) INFORMATION FOR SEQ ID NO: 3316:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3316:

CATTGGCTGT GTCCATTTTT AATCGTTGCG AGTACGThTA TTAGCAACTT GGAAGTGCCA 60  
TTGTTAATTT CAGCTGTCTG TTACATTTC ACCATAGTCT TTCACAAT 108

(2) INFORMATION FOR SEQ ID NO: 3317:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3317:

ATCTGAAGCT GGGTTTACTA GAGAAGGTAT GTACGTGACA TGAATTACTA ATGGATTAT 60  
TCATCGAGTT ACATCTATAG TTTATTAAAT CAGATACGCC AAAATGCnAA TTAGCTTACA 120  
AAGATGATGC ATTAAATGCA CG 142

(2) INFORMATION FOR SEQ ID NO: 3318:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3318:

AACATTATGT TAATCAACCT AATGAACGtC TTTATAAATT ACGCTAAACA ATATACAGAT 60  
ATGCCGTTTC TTATCATGCT GGATGAAGAT GAAAATGGAT ATAAAGCGGG TCGATTTTTA 120  
AGAGCGAGTG ACTTAGGTCA AACACAGAG CAAGGCGAAT GGAAGCCAGT TATTCATGAT 180  
GCAATCAGCG ATAGTTTAGT AGTACCTAAT GGCACAATGG GTCAACGTTG GGAAGAAGGT 240  
AAGAAGTGGA ACTTAAAACT AGAAACAGAA GATGGTTnTA AAATTAnCCC TACATTATCA 300  
ATGACAGAAG GTGGATACGA ATTAGAAACA ATTCAATTCC CATACTTTGA TAGTGATGGA 360  
GATGGGATAT CATCGTCCAA TCCnAC 386

(2) INFORMATION FOR SEQ ID NO: 3319:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

ACAATGAATG ACATGATTG AGGTGGACGA CCCCTCCTAT TTTGCATAAA TGCTTTTTGA 60  
ATCGCCGGTC ATAATGTTG TTGnCCAATT AACTCAATAT TCTTCATGAC ATTTTCAAAT 120  
GGC 123

(2) INFORMATION FOR SEQ ID NO: 3320:

55

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3320:

10 GGC GAACTGT CAATTGCCGG TATACAACGT ATTTTAAGAG CTGCAGAACA TnCGGGTGTT 60

AAACGTGTGG TCAATGACTG CCAACTTTGG TGCAGTTGGT TTTA 104

(2) INFORMATION FOR SEQ ID NO: 3321:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3321:

25 GCGCCGGTTT TAACAGGTAA TTAAAAACCA AATACTGATA GTAATGCATT AATAGTCAGC 60

AAAATACAAG TATT 74

(2) INFORMATION FOR SEQ ID NO: 3322:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3322:

TCACTCAGGG GGAGATGTCA ATGGGTCAAC ATTATTTGAC AAGGTGTGGA CAGACATGTG 60

40 TTATACGGGA AATTGGGCGA CCGCACT 87

(2) INFORMATION FOR SEQ ID NO: 3323:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3323:

TGCCAAATGT TCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA TTACGATGCG 60

55

AATGCGGTCG GAAAGATAAA TAGCTTCATC AATGTCATGC GTCACTAAAA TAATAGTTGA 180  
 TTGCGTTTTA TGTTTTAGTT GCACTAGTTG ATCCTGAAGT TTATAACGTG TAAATGCATC 240  
 5 TAATGCACCT AATGGCTCAT CCATCAATAT AACGTTAGGC TTATGCACAT GCGCTCGACA 300  
 TAGTGCCAAA CGTTGTTTCA TACCCCGGA CAGTTGCTCG GGAAAATGCT TTCCCCTGTC 360  
 TTCTAAATCA ACTAATTTAA GCTGTGCGTT AATCTCTTCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3324:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3324:

GAAACCATCG ATTGTAGCAC GAACCATGTT GGATTGGTGT GTTTGnATCC TAATGTATTT 60  
 ACTTAAGATA TCAGTGATAC CTGTCTAATT GCAAGTACGG TCAGGA 106

25 (2) INFORMATION FOR SEQ ID NO: 3325:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3325:

35 TCTGAAnTCG CTGTCTGAAT CTGGAATCAC TGTCTGAAAT CCGAAATCGC TAATCTGAAA 60  
 TCCTGAAATC CGCTAATCTG AAACCTGGAA GTCGCTGGTC TGGAAGCCCT GAA 113

40 (2) INFORMATION FOR SEQ ID NO: 3326:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3326:

50 TGTCACGTAC TTGCTGTTCA ACAAATACGT CTTACTGGAC GTGCACCTCA TTCTTCATCA 60  
 TAGCCTTCTT CATTAAAC 78



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3327:

AATTGAAAAT TATCTTACTG CGGTTTTTAG GGGTTTATGT CCCAGCCTCT TACTCnAATT 60  
 ATATTCACTA TCCATTAGAC CAAATGGGCC ATTTCCAATA ATCCCGCGGT GGTTCCTGA 119

(2) INFORMATION FOR SEQ ID NO: 3328:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3328:

GTGTTAAAAC GTCACGACGT TTGTTTAAAA TGATGCGTCA TAATGTCTAC ACTTTGCTTG 60  
 CGATCATTCA T 71

(2) INFORMATION FOR SEQ ID NO: 3329:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3329:

CTGACGAACC TTGCATCATT TAACTGTCCA TTAGCTTGAT CAATACCTTG ACTCGCAATG 60  
 TTAAGTCCTT 70

(2) INFORMATION FOR SEQ ID NO: 3330:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3330:

CCAATCTCG

69

## (2) INFORMATION FOR SEQ ID NO: 3331:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3331:

GGACACTAAC ATTAATATGG ACTGGTAATG TTGCTGTTAA TAAACTCATA CCAAATCCTG 60  
GGCATCTCTT 70

## (2) INFORMATION FOR SEQ ID NO: 3332:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3332:

CCTTGGGCAC CTTCAATTTG CATATTACGA CGTTTTGCAG CTTGGTTCAA TTGGCAATAA 60  
CTACACCTAG TGCAGTTGGA TC 82

## (2) INFORMATION FOR SEQ ID NO: 3333:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3333:

ATAAAATAAT TAGAACTCTA ACATTGGTTT AACTAATGTT TAGACTTTTT GTGGTTTGTA 60  
AAAACAAGTA TATTGA 76

## (2) INFORMATION FOR SEQ ID NO: 3334:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3334:

TGGTAAGTTG AATAAAGTAT TGAAATCGTT GCCAATATCT TTATACCGTT GGTCCTGGC 60

ATTTATTGGG AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3335:

AGATAGTTAT GCGCAGTTAA AAACGGTGAA ATGTATTTGC AATAATATGC ATATAGGCAC 60

CATACGAGTA AGGG 74

(2) INFORMATION FOR SEQ ID NO: 3336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3336:

TTGAATCATT GTTAAAAATG GAATTAAAGT TGCTAGTATC TGTCGGGTTT TGAAATAGGT 60

CATAGGAGAA AACAGG 76

(2) INFORMATION FOR SEQ ID NO: 3337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3337:

CCAAAGAGGC GTTATTAAGC TATTGATAAA AGTTATGTTA CTAATAAATG TATTTAAATA 60

AGTAGTACCT AA 72

(2) INFORMATION FOR SEQ ID NO: 3338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3338:

ATAAGTCGTT CTACCGTATA GCCGTCATTA TTAATCACAA ATAATACCGG TTTAATATGC 60

10

TGTCTGGTCA TAGTT 75

(2) INFORMATION FOR SEQ ID NO: 3339:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3339:

TTCATCAAAG TATTCCAATG GGAGAAAAAG CACAATAACA TTATCACTGG ATGCTAAATC 60

25

TAAAGGAACC TC 72

(2) INFORMATION FOR SEQ ID NO: 3340:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3340:

GTAAAAATAT TTTAATGAAT GTCTTCACTG GAGAACCATT GACAACCTGG TACAAGTGGG 60

40

ATTATTGGCG TTATTTT 77

(2) INFORMATION FOR SEQ ID NO: 3341:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3341:

AACCAAGGAT GGATTGCTAT TTTAATCCTT GGTGCTCTT TATTTTATTT AAATTGTAGA 60

55

ACCTAGA 67

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3342:

CTGGCAAAAG CACGTTTTAC AAGCATCAAT CCATTAATTA ATAATTCCAT TAAATGTAGA 60  
 TTCACAGGGA TATG 74

(2) INFORMATION FOR SEQ ID NO: 3343:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 415 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3343:

GTTTGATCAT TAGAGAGATA TAGATATGCC GTAGAAAATA ATATGTCATT TGCGGATATC 60  
 ATGGTTAAAG AAGAAATGGA ATTAAGCGGT AAATCACGTG ATGAAGTGCG AGCGaAATGA 120  
 AACAAAATTT AGATGTCATG CGAGACGCAT AATCAAAGGG ACGACAGGTG ATGGGGTTGA 180  
 AAGTGTAcGG TCTACACTGG TCATGATGCT GCTAAACTAC GTGATTATAA TGAAACACAT 240  
 CATGCTTTGT CTGGGATATG AAATGATTGA CGCACAAGGG TGCCATTGCA ACAAATGAAG 300  
 TCAATGCTGC CGATGGGTAT TATTTGTGCA CGCCAACAGC TGGTTCCTCG GGTACCATTC 360  
 CCGGTGGCAC TTTTAAATTA GAAAAACAC TGGATnGAAC CAGAAGAGCC AATGn 415

(2) INFORMATION FOR SEQ ID NO: 3344:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3344:

TCCTATACCA CCACCGTCAA CAGCTCCTGC CATCGATCGT ACTTTCAATA AGTCCAATAA 60  
 TCGCAGTGGT AATTTCTAAT ACTA 84

(2) INFORMATION FOR SEQ ID NO: 3345:

- (A) LENGTH: 474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3345:

10 CGGGAGGTGT TAAntCTTCA CAAAATGCCG TACTATTCTT TGATGnAATC CATCAAATTA 60  
 TCGGTTTCAGG TGCCACAGGA AGTGATTcAG GTAGCnAAGG GTTATCTGAT ATTTTGAAAC 120  
 CTGCATTAAg TCGTGGTGAG ATTTCTATTA TTGGTGCaAC AACACAAGAT GAATATCGAA 180  
 15 ACAATATTCT TAAAGATGCT GCATTAACGC GCAGATTTAA TGAAGTGCTT GTTAATGAAC 240  
 CAAGCGCTAA AGATACTGTT GAAATTTTAA AAGGTATTcG CGAAAAATTC GAAGAACACC 300  
 ATCAAGTAAA ATTACCAGAT GACGTATTAA AAGCATGTGT TGACTTATCA ATTCAATATA 360  
 20 TTCCACAACG ATTATTACCA GATAAAGCAA TCGATGTGTT AGATATTACA GCAGCACATT 420  
 TATCnGCGCA AAGnCCAGCT.GTCGATAAAG TTGAAACTGG AGAACGAATT TCTG 474

25 (2) INFORMATION FOR SEQ ID NO: 3346:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3346:

35 AAAATTAATA ACTCCTTGGT TATTGATATG CCTAAAGAAG AAGGTACAAT ACAACTAACA 60  
 TTAG 64

40 (2) INFORMATION FOR SEQ ID NO: 3347:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3347:

50 AGGAATAACT TGATATTGAT GATAAAATCG TCAAACGGCA CTAATATTTA AAAAACAAAT 60  
 GTTTTAAGTT GTTGATTTAA AATATTAAT 89

55 (2) INFORMATION FOR SEQ ID NO: 3348:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3348:

10   ATAACTTGTA CTGCTTCCCA TTAATCACTG TGTCTCTTCA CCAGGAGCTG GCATTTCITT   60  
 AAAGAACAAT TCTGATAAAG GTACAATTTC ACCGGGCATA ACTTCAT   107

(2) INFORMATION FOR SEQ ID NO: 3349:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3349:

25   CAACGCATCC TGCACCTTTTA CCTATTCCTG AATCACCGGT AATTAGTACA CCAACACCGT   60  
 AAACATCTAC TAAA   74

(2) INFORMATION FOR SEQ ID NO: 3350:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3350:

40   AGATGCACCT ACTTCTAACT GTCGCCAACA TCGCCGCAAT CATTTCAAAA CTACGTTCTG   60  
 TA   62

(2) INFORMATION FOR SEQ ID NO: 3351:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3351:

55   GCTGCAAACA ACAAACTATT TTTGATTAAA TTGTGGATAT GATGGTAACC AACCAAGTCT   60

## (2) INFORMATION FOR SEQ ID NO: 3352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3352:

ATTGAACGCA AGATTTGAT ATAGAACATC TAGCGACGTC GATTCGCAAG GTTGAACCAT 60  
CTACATTAGG TGAGGAA 77

## (2) INFORMATION FOR SEQ ID NO: 3353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3353:

TAATCAACAC GAGGAGATGC TATTTAATGT CATCTGACAC AAACAGTTTA GCACATACA 59

## (2) INFORMATION FOR SEQ ID NO: 3354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3354:

TTATGTAACC GACGAATGCT GCGATAGTGC TACGCCATCA CCGCCAGCTA ATCCGATTG 59

## (2) INFORMATION FOR SEQ ID NO: 3355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3355:

TAACTATAACC TTTAGGGTTA CTACCACGCT TAGGTAGGTC ATAACCTTTA ACCACATCT 59



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3356:

AATAACGCTA AACCTAAAAT GCTAAATAAT CCGCCGAACA ACATGCCGTT GTTTGTTGA 59

(2) INFORMATION FOR SEQ ID NO: 3357:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 77 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3357:

CCAGAACCAC CCACGCCCTT TGAATATGGG AACTCAAAAC GATCTACTGG CTGATGTAAT 60

TACCCCTGTT TTGATTG 77

(2) INFORMATION FOR SEQ ID NO: 3358:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3358:

AAGTTAGGTC TAGGGAACAT CGATAAATTA CCAGTAGTAA ATGCAGTTGA ACAACCAGA 59

(2) INFORMATION FOR SEQ ID NO: 3359:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3359:

CATGACCTTT AAATTGCATA TCTTCTGCAT CAGGTGCATC GCTTTTAACA ATAACGTCA 59

(2) INFORMATION FOR SEQ ID NO: 3360:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3360:

10 ACGCGACAAC ACCGCCCTCA ACTAAAGTAG AAGCACCGCA ACAAACAGCA AATGCGACA 59

(2) INFORMATION FOR SEQ ID NO: 3361:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3361:

GATTTGATCG AATTGAACGA ACATTTGCTT CTCAAACGAT TGCATCTATT AAAGAAGTAT 60

25 GTCTAG 66

(2) INFORMATION FOR SEQ ID NO: 3362:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3362:

GGTTGCACAT CTTTACTAC AAATTTGCTT GGTAAAGATG TTGCAAAAGT ATGTCCGT 58

(2) INFORMATION FOR SEQ ID NO: 3363:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3363:

50 CCTTGAAACG GCAACATTTT TGGGTCCTTC TCCATCATTT TATTTAAAAG CGCATTAT 58

(2) INFORMATION FOR SEQ ID NO: 3364:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 58 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3364:

TTGAGAATTT AGGAGGTAA TGC GTT GATT AAAAGTGGCA AAGCACGTGC ACATACGA 58

10 (2) INFORMATION FOR SEQ ID NO: 3365:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3365:

GTTTTTTTAT TTTGATAAA AGGAGCAAAC AAATGGATAT TAACTGGAAA TTGAGATT 58

(2) INFORMATION FOR SEQ ID NO: 3366:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3366:

ATTCATCGGT AATGACATTA TTTTACTTT GTAATTCAG TAACAGTTGA TCATCATG 58

35

(2) INFORMATION FOR SEQ ID NO: 3367:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3367:

TAAATTAACA GCCGGATGAA ATGAAAGGTG CTACATGCAC AATCAGTAAT ATCGGTTC 58

(2) INFORMATION FOR SEQ ID NO: 3368:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3368:

TACCTACTGG TGAGATTGGC GAACTTGCAA TTAAGGCTAA AAATGTCACG CCAGGATA 58

(2) INFORMATION FOR SEQ ID NO: 3369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3369:

TTAAACGGAG AAGGCTTTAC TTTACATGTT GAGGAAGGTC AAGAAGTTAA ACAAGGTG 58

(2) INFORMATION FOR SEQ ID NO: 3370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3370:

CTGCTAAACT ACGTGATTAT AATGAAACAC ATCATGTCTT TGTCTGGTAT ATGTAAATGA 60

TTGACGGC 68

(2) INFORMATION FOR SEQ ID NO: 3371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3371:

ATTACCAACA GCGAAAATAT TGAAAAGCTG TAAAAAGCT GGTGCAsmCm TACTTGGATT 60

GAGAATTTAG GAGGTTAATG CGTTGATTAA AAGTGGCAAA GCACGTGCAC ATACGAATAT 120

TGCACTTATA AAATATTGGG GTAAAAAGA TGAAGCACTA ATCATTCCAA TGAATAATAG 180

CATATCTGTT ACATTAGAAA AATTTTACAC TGAAACGAAA kCACTTTTAA CGACCAGTTA 240

ACACAGGATC AATTTTGGTT GAATGGTGAA AAGGTTAGTG GCAAAGAATT AGAGAAAATT 300

TCAAAATATA TGGATATTGT CAGAAaTAGA GCTGGCATCG ATTGGTATGC AGAAATTGAA 360

## (2) INFORMATION FOR SEQ ID NO: 3372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3372:

ATTTCACAA CTTTAAAGCA CGTATAATGA TGATTTTCAG ACTTGTACAA AGGAGAAA 58

## (2) INFORMATION FOR SEQ ID NO: 3373:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3373:

AAACCGAGCA GCGCAGTAAA CCTGCAGTAC CTTTATCGCT TCTAGATAAT CCGATTG 57

## (2) INFORMATION FOR SEQ ID NO: 3374:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3374:

AGTACGAATA TTACCTTTAT TTAATGGGTG AGCTAAGTTA CTTTTCATT CTTCGTG 57

## (2) INFORMATION FOR SEQ ID NO: 3375:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3375:

GGTGAAGTAT AACTTTGTA TGGCAGCGCA CTTAATGACT GCCAATAATT GTGACCAACA 60

ACTAACAGAC 70

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3376:

TTCCAAACTT CATTAGGTGA TAGCTTTAAT TTCAAGGCTG GCAATCGCCA TAACAAG 57

(2) INFORMATION FOR SEQ ID NO: 3377:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3377:

TCCTTCAAAG TCAATGGATT TGATCCTCAG AGGACTCAGT GTATCCTCCA AGTGACCTGG 60  
CTCGCATCCA 70

(2) INFORMATION FOR SEQ ID NO: 3378:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3378:

ATGAATCATT AAGCCTTTTCG GTGCATATGC TGCAAGACTT TGACCAGCAT GACCAT 56

(2) INFORMATION FOR SEQ ID NO: 3379:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3379:

CCAACGACTG CGCCAATATT AATTGTTGCG CCCATCATAA CGACAGCACC ATCTTC 56

(2) INFORMATION FOR SEQ ID NO: 3380:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3380:

10 ACAAAAGCAT CAAGCTGTTG AAACAATCAA TGATAGCATT CGAGATTATT TAGTTAG 57

(2) INFORMATION FOR SEQ ID NO: 3381:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3381:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA AATAACCGAA GTATTT 56

(2) INFORMATION FOR SEQ ID NO: 3382:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3382:

35 GAACACACAG GCAACCCAAA GCAGTGACGG CGAAAnTTGG ATTGATCTTG CAGCATTGAA 60

GAAGATCGCG ATGACTATAC AATCAATATC GAGTAGAAGA CCGAT 105

(2) INFORMATION FOR SEQ ID NO: 3383:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3383:

50 nGTATGTGAA AACTATTTTG CGATATTTTA GTGATGAGCC TCAGTGATCC TGGTTCCTGG 60

TTATCACCTC TGCTAGTTTA GTACCGATGG TCCAAGATTG ATGAGC 106

(2) INFORMATION FOR SEQ ID NO: 3384:

55

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3384:

10 TTCTTCGTCA AGATCAATCT CTTCAAGTAC AATCTTTAAT ACCTTCTGCA CCCATTT 57

(2) INFORMATION FOR SEQ ID NO: 3385:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3385:

CGGGCATCTT AAAGCCGATG TTTATCCTGT AATCCTCCAA AAGGAAACAT GTACCTCAAT 60

25 TAGAG 65

(2) INFORMATION FOR SEQ ID NO: 3386:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3386:

CATTTTTAAT TATTTCTATT TGCTTTTTAA CCACTTCTCT GACTGCTTCC GAATCATTTT 60

40 TCTTAACTGC A 71

(2) INFORMATION FOR SEQ ID NO: 3387:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3387:

TTAGAAAATG ATAAACGTAA AGCAGTAAGT GCTGAAGAAT ATAAAAAAGC TGACG 55

(2) INFORMATION FOR SEQ ID NO: 3388:

55



- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3388:

10 TCTTCGACAA CTTTAATAAT ATTAGCCAAC GCAGTGTCCC CGCCAACTTT TGTTCG 56

(2) INFORMATION FOR SEQ ID NO: 3389:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3389:

ATTATTAAC GATTAATGAC GCTGGCATGC CAATTCCAGA TGATCATCGT CGTATC 56

(2) INFORMATION FOR SEQ ID NO: 3390:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3390:

35 AAATGCTATG TACCCACTTT AGATGAAATT TTAGTAACGT TATGGCCCGA AATGCCAACT 60

ATTATATTGA 70

(2) INFORMATION FOR SEQ ID NO: 3391:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3391:

50 CAAACGCAAT AGCTGGTGAC TTAAGTGGG GCACTTGGCA TGTGGATGGC AATACTTCG 59

(2) INFORMATION FOR SEQ ID NO: 3392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3392:

GCATCTACTG GGAAACGATT ACAAATTGGT GATTTATTAC AAAAGCCAAC TGTAT 55

10

(2) INFORMATION FOR SEQ ID NO: 3393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3393:

20

TTTATAAATA TCCAGTCTG AACGCGATTCC CCATAACGGA TCAATGGCAG GATTG 55

(2) INFORMATION FOR SEQ ID NO: 3394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

TGCTTACGCT CAGTGACATA ATCTAATGTG GCACGTAAAG CGCCACCATA CCACC 55

35

(2) INFORMATION FOR SEQ ID NO: 3395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3395:

45

AGTCACCATT TGTGTTGACG GGTATGGAA CACGTTGCAG CACGTGATTC TGGTGCGG 58

(2) INFORMATION FOR SEQ ID NO: 3396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3396:

CAAATGCATT TAAAACCAAT ATTGAGTTAC ATGAAAGCAC ATACGATGCA AACGT

55

(2) INFORMATION FOR SEQ ID NO: 3397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3397:

TGTTGATGAG TCGTGTTTTA TCTCAAGATG TGTTACTCAA AAAGTTATAG AAGA

54

(2) INFORMATION FOR SEQ ID NO: 3398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3398:

CTTCGTCAAG ATCAATCTCT TCAAGTAAAT CTTTAATACC TTCTGCACCC ATTT

54

(2) INFORMATION FOR SEQ ID NO: 3399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3399:

AATGAAAAGC TAGCTGTAGT TGCAAGAAAA ACTGGCTTAG CGATGGCAGT TGGAT

55

(2) INFORMATION FOR SEQ ID NO: 3400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3400:

## (2) INFORMATION FOR SEQ ID NO: 3401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3401:

TAAAAATCGC GCACTTAAAC CGCTTATGAC AATCATTATT ACCGCAATAT GCTTG 55

## (2) INFORMATION FOR SEQ ID NO: 3402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3402:

GGCACCTCCT TGGATTATTT TTCTTCTACT GTTACTAAGT GCTTAACTTT GTTG 54

## (2) INFORMATION FOR SEQ ID NO: 3403:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3403:

GATAAGTCTA ACAAGTGGCA CCCATAATCG ATTAACTAC CGCCACCTTG CAACGTTT 58

## (2) INFORMATION FOR SEQ ID NO: 3404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3404:

TCGTTTTTCGT CCCCAAATTC TGCCAACTTA TTCATGAACT TATCTAGCGC TATTGTTCTT 60

TGTCT 65

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3405:

AAATTTTCAGC ACCAATTGTT ATTGGACGAC ACCATTTAGA TGCTGGTTCA GTTGC

55

(2) INFORMATION FOR SEQ ID NO: 3406:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3406:

TCGATTTTCAG CGGAACACAT GTAACGTTAG CACAAGCCAT GAACCAATTA GGTGGC

56

(2) INFORMATION FOR SEQ ID NO: 3407:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 74 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3407:

AATTGCTAAT GGTCAAGTAT GGACGTGATC ATTGTTGGTA CTACTTATTG CTGAAACTGT

60

TAAAGATTAG AAGG

74

(2) INFORMATION FOR SEQ ID NO: 3408:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3408:

TGATTTTACA CTTGATAACG GATACTTCGA AGAGATACAT CAGCAGCGTT CAGCTCAGAT

60

AGTGCTCA

68

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3409:

TATGATTAGA AAAAGGGGAA TTTTATGGA GTATAAGAGT TACTATGATT CGCC

(2) INFORMATION FOR SEQ ID NO: 3410:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3410:

TATCTTTCAT CATTGAAGAA GATCGCGATG ACTATACAAT CAATATCGAG TATA

(2) INFORMATION FOR SEQ ID NO: 3411:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3411:

TTGAAGTGCA CGAATCGAAT TATTGTAAGC AGTAATACTT GCCGGCTTCT TAC

(2) INFORMATION FOR SEQ ID NO: 3412:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 63 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3412:

TAGCCGATGG AACCCCATAA CGGTTGCCCT ATAAAAGTAT TGTTTTTGTA TAGTGCTAAA

TCA

(2) INFORMATION FOR SEQ ID NO: 3413:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3413:

10 ACTACCATTG CTTGTTCCGG TTTCACAACT GGTTCAGTAT CATTTACAAC TGC 53

(2) INFORMATION FOR SEQ ID NO: 3414:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3414:

ATGCTGTTGT AAACGGTAAT ACAACATACC TGCCCAACCC GGTAACGCCA AAAAATGTCC 60

TT 62

25

(2) INFORMATION FOR SEQ ID NO: 3415:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3415:

ACTTAGATCA ATCACATGAT GCCTCACGGA ATCCATTATT TGAAGGTCAT GTTAG 55

(2) INFORMATION FOR SEQ ID NO: 3416:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3416:

TTAGTTCCAG CAATACCTGC TACAGTTGCT GCAGATGCTT CTTTCACCCA TGG 53

50

(2) INFORMATION FOR SEQ ID NO: 3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3417:

TGATTTAGGT GCAAAAATTG TAGGTATCGC TGAGGCTTAC GGTGCATTAC ACGATCCAA 59

10 (2) INFORMATION FOR SEQ ID NO: 3418:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3418:

20 CGTGGTCACC ATCACCAATT GCTCGATCTA ATTCAGTAAT TCAGATTCAT GTT 53

(2) INFORMATION FOR SEQ ID NO: 3419:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3419:

TGGACCTACT GCAATAACTG AACGTCCTGA ATAGTCAACA CGTTTACCAG TAAGT 55

35 (2) INFORMATION FOR SEQ ID NO: 3420:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3420:

45 TGTCTCCGGT ACCGTTTGCA CCAGGAATAA AGATGAGCAC GGGTCCTTGT CCG 53

(2) INFORMATION FOR SEQ ID NO: 3421:

(i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3421:

AAATTAAGAA AATTCATTGC CAGATAATTT AGATAAATAA TTAAAACTTA GACCATTAC 60  
5 CCCAATCCCT GA 72

(2) INFORMATION FOR SEQ ID NO: 3422:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3422:

CATATGTTAA ATGGACTCGC TAGATTTAAG TCGCAATAGT AGCGGCCGTT TCTT 54

20 (2) INFORMATION FOR SEQ ID NO: 3423:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3423:

30 CACGTTTCAA ACCTAAAAGA TGCTAAAAAT TTCTCTTAAT TCTTGTGCAA TA 52

(2) INFORMATION FOR SEQ ID NO: 3424:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3424:

ATCGCCTAAC CAAGATGCAC CATCGGTGAT TTTATCGCCT GCCGCTTCAA CCAT 54

45 (2) INFORMATION FOR SEQ ID NO: 3425:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

AATAGAAAAT GTACGTAGCG GTATGATGAG GATTTCGCAG ACTAGTTTAG GGTCAAGTG

59

(2) INFORMATION FOR SEQ ID NO: 3426:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3426:

CCAACGCCAG ATCCAGAACC AAGTCCAGAC CCAGAACCGG AACCAAGCCC AG

52

(2) INFORMATION FOR SEQ ID NO: 3427:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3427:

CCATATTAAT GGTTATGTTT ATGTGAATGC TTGCTTGCTG GACTTGTCTT TT

52

(2) INFORMATION FOR SEQ ID NO: 3428:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3428:

TAAACAGAG AITGATACTG CAGAAGATAA CTGTATCTCT CCATCTACTG TA

52

(2) INFORMATION FOR SEQ ID NO: 3429:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3429:

TGAAAATCCA CAAGTCGCAC GTACAGTGTT TGAAAAAGGT ATTATGGCGG CA

52

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3430:

ATAATTCTTC CAAATATATG AAAATGGATT TGTTCTTTTT TTATAAAAAT CTTATGCTTT 60  
TTAACTAATT GTAAGA 76

## (2) INFORMATION FOR SEQ ID NO: 3431:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3431:

CTGCGGGGGA TAACTGTATC TCTCCATCTA CTGGTAAGTC GTATTAGAAC TAAAGCGGCT 60

## (2) INFORMATION FOR SEQ ID NO: 3432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3432:

GGCTTCAGGC TCATTGATAG GTAAAAGTTG CAAAGCCTGC AAAGCGATTG GG 52

## (2) INFORMATION FOR SEQ ID NO: 3433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3433:

TCGCACGATA CGCCTCCGAA TGAAGAAGGT TTATTGTGCG ATTCTTTTAT TGTTAAATTT 60  
TAAATTTTT 69

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3434:

GATCGCTATC CATTAGCTAA ATTTAAACGT TCAAACCTCAG GTACATGTTA C

51

(2) INFORMATION FOR SEQ ID NO: 3435:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3435:

TATAGCTACT GCTGCAGCTG CGGCCATTGC AGATGCTGAA CCAACTTCAG C

51

(2) INFORMATION FOR SEQ ID NO: 3436:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 70 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3436:

ATTAAAGCCA ACATTAATTT ATCCACTATT AACATAACG GCTACAGGCT TATTAATGAT

60

TTATACCTTT

70

(2) INFORMATION FOR SEQ ID NO: 3437:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3437:

TTTGTGTTGTT GATTCTTCTC CACCTGTTTC AGGTAGTTCA GATTCTTAG A

51

(2) INFORMATION FOR SEQ ID NO: 3438:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3438:

10 GTGAATTCCG TAATTACATT TTAGGCTTGA TTTTCTATCG CTTCTTATCT G 51

(2) INFORMATION FOR SEQ ID NO: 3439:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3439:

TTAAGACAGG TTCCTTATGG GACTCTAACA ACGTATGGTG CTATTGCCAA A 51

(2) INFORMATION FOR SEQ ID NO: 3440:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3440:

35 CACTAGAAGA AACGGATTCA TCAGCTATTG GTATCGATTA CCATACTGCT GTGGA 55

(2) INFORMATION FOR SEQ ID NO: 3441:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3441:

CTTCTGGCAA TAGACCGCGA GTTACTGGGG GCAAAACCAG TGTGTAAAAC CGGAACTACT 60

50 ATGAGGGGCA TGAAAGT 77

(2) INFORMATION FOR SEQ ID NO: 3442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3442:

GTTCGGTTGT GACAGTCAGT GGACGCGTTA CCAAATGGGC GGGAATTAAA GCAAA

55

10

(2) INFORMATION FOR SEQ ID NO: 3443:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3443:

20

ATGAACCTTTG GGATAAAGGT GATGCCCAAA CTTCCGTAA CTCATGATGA T

51

(2) INFORMATION FOR SEQ ID NO: 3444:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3444:

CAACGCAGCA AAGCGGAGTG GCCCTTTACC TTCACAGAAT AATGGTCTAA T

51

35

(2) INFORMATION FOR SEQ ID NO: 3445:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3445:

45

ACCGAGCAGC GCACTAAACC TGCAGTACCT TTATCGCTTC TAGATAATCC

50

(2) INFORMATION FOR SEQ ID NO: 3446:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3446:

CCAATGCAAC GATCCAGTTA TTGTGTTGGC GCAATTGATT AATAGTATTC

50

(2) INFORMATION FOR SEQ ID NO: 3447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3447:

GCGCATCATA TCCCATTGCA CCGATAAGAT CCTTCTTACC TTCTACAAGT

50

(2) INFORMATION FOR SEQ ID NO: 3448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3448:

GTTCTTACTT CTTTATCGTG GCTCCAACGT GCTCTGTACA TTTTTCCTCA TCTCTCTACT

60

(2) INFORMATION FOR SEQ ID NO: 3449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3449:

CAACACCACC GACACCAGAA GTACCAAGCG AGCCGGAAAC ACCAACACCG

50

(2) INFORMATION FOR SEQ ID NO: 3450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3450:

TTATCACGGT ATATGAGGGG ATTTGAGG

88

## (2) INFORMATION FOR SEQ ID NO: 3451:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3451:

TGCAAAACGT TATGAAGTAC AAGTTGATGG AAGCAACAAA GTAAGTGCGn

50

## (2) INFORMATION FOR SEQ ID NO: 3452:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3452:

CAGTTAAGTC ACCAGCTATT GCGTTTGGTG ATCTTAAGCA GCGGTGGATT ATCAAGTTTG

60

GGTA

64

## (2) INFORMATION FOR SEQ ID NO: 3453:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3453:

TCGTAAACAA TATACTATCT CAACATTTAT TCATCCAATG GAGATAACGT ATTGCGCGGT

60

TTAACAGGTA ATTTAAACCA AATACGGTAG TAATnATTAA TAGATAGCAA ATCAAGTATA

120

AAGAATAAGT A

131

## (2) INFORMATION FOR SEQ ID NO: 3454:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3454:

TTAAAAATGC AGTTATGGCC TCTAAAATCG TATTAAGCAT ATTAGCGCCC

50

(2) INFORMATION FOR SEQ ID NO: 3455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3455:

TGCTACATGG CGTTACGGTC AAGATCGTCA ACGATTGATG GGTACAATTG A

51

(2) INFORMATION FOR SEQ ID NO: 3456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3456:

ACAAACTGCC AACGATTGGT CGTGTGAATC ATCCAGTGGA AGAAGCGCAn

50

(2) INFORMATION FOR SEQ ID NO: 3457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3457:

AATCACGTGA GAAGGATACA GCTATTAGTA TCGGTATCAT CGCATTGATT

50

(2) INFORMATION FOR SEQ ID NO: 3458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3458:

## (2) INFORMATION FOR SEQ ID NO: 3459:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3459:

GGGCCAACAA ATCGGAAACT GCCAATTGGA CGGTTGCCGT CATCAAACCC

50

## (2) INFORMATION FOR SEQ ID NO: 3460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3460:

TGCTTCCGCT AGAGGATCCG GTATTGCTAG TCAATTACTA CACCATTAA ATTGTGGAAG  
CAAAAGCT

60

68

## (2) INFORMATION FOR SEQ ID NO: 3461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3461:

TGGTCTTCGC AATCCACGGA TATACCTTAG TACCAGGTAA TTGACCACCT T

51

## (2) INFORMATION FOR SEQ ID NO: 3462:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3462:

AAGCTATTAA TGTAATTTAT CAATTGATTG TGCAACGGAC ATCATCTACA AGACCG

56

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3463:

ATACCAAATG TGAGAAACTG GAGCAGCAAn TTCAATGTGA CCCATTCTTT

(2) INFORMATION FOR SEQ ID NO: 3464:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3464:

TCTTTACGGC GTGGTTCTAA TCGCATCTTT TTCAATCTAA GTGCGTTTnT

(2) INFORMATION FOR SEQ ID NO: 3465:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3465:

AAAGAAGATT GGAACGTGTA TTGACGACTG CACCCAGGTA TGGGTGTTTCG CCCGACA

(2) INFORMATION FOR SEQ ID NO: 3466:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3466:

ACATCCGAAA GATGACTTGT TTAAAAAAGC AGAGCATGAT TTGCTTACTA TGATTACACG

CGG

(2) INFORMATION FOR SEQ ID NO: 3467:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3467:

10 TACCGATGAT TTCCGAGACA TAGACCGGCC TGTCTGGGGG TCAACTGGAA CTTGGTC 57

(2) INFORMATION FOR SEQ ID NO: 3468:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3468:

TGTTCTAAT ATTTATGTTG TAAAAATGTA CAATCTAATT AAAGCAATAG TCTTGGGCA 59

25

(2) INFORMATION FOR SEQ ID NO: 3469:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3469:

35

TCCATGATCG TTCAACATTT AAATACACAA CTTAATAAGT ATCGTGTACA AGTTATG 57

(2) INFORMATION FOR SEQ ID NO: 3470:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3470:

50

CCCTGTTTCAG GCTATCCTCT AAAGTGACGA TATAGAATAG CGATTAAATAT CGCGATAGT 59

(2) INFORMATION FOR SEQ ID NO: 3471:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3471:

TACGCCATCA nCGCCAGCTA ATCCGATTGC GACACCTAAT GCGAAATCAT

50

(2) INFORMATION FOR SEQ ID NO: 3472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3472:

AACGTCATCA AATGGAAGTA CGTGACGTTT ACTACTCTCA CTATGGCCGT ATGT

54

(2) INFORMATION FOR SEQ ID NO: 3473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3473:

TAATAGGCAT TCCCATTAGG TCGCTCGACA ACTGCAACGC AAGCATTGGA AACAGA

56

(2) INFORMATION FOR SEQ ID NO: 3474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3474:

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGGATTGACA TACTTCATAC GTATA

55

(2) INFORMATION FOR SEQ ID NO: 3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GCCTTTAGGT AAAATGGGCA GAAATGCTAA TCATTTTGGC GGCGAAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 3476:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3476:

AAAnCATTCTG CAATCGACCA TAATTTTTTTA TGTAATTCAG CTTGTTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 3477:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3477:

GGAnGACCAT TAATCGATAT CGGTACACAC GCTTTAGATT TAACGTTATG

50

(2) INFORMATION FOR SEQ ID NO: 3478:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3478:

TGCCTCCTTA CGCCATGATG CTTATTCAAA GTAAATTGCT TTGCCGGACT TTGCAGACTG

60

(2) INFORMATION FOR SEQ ID NO: 3479:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3479:

GGTCTTTTCAG CTGCTAACGA GTTCCTGTTA CTGTTTCATGT CTATCACTTT GCGTTCCTC

60

## (2) INFORMATION FOR SEQ ID NO: 3480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3480:

CAAGTATCAT ATGGACGGCT CGCCCAACAC AAAACAAGnC CAAGCAAAAC 50

## (2) INFORMATION FOR SEQ ID NO: 3481:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3481:

ATTAAACAAC ATAGCTCGGC TAATCCTTTA AAGCTTTTGA GTTTTTCTGT TGTAGAACAA 60  
GA 62

## (2) INFORMATION FOR SEQ ID NO: 3482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3482:

TGTGGCTAGC TGTTTCTTTT TTAGGTGCTG TGTAGGAGAT GAACTGATCG T 51

## (2) INFORMATION FOR SEQ ID NO: 3483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3483:

GCAGTTTATA AGTAGAGAGA CAGCTGATCA TGAGATAAAA ATGGGTAAAT ATTT 54

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3484:

TTATCTATCA CAGTACGAAT CCCCCAGAGT ACCGATTGTG ACAGCAACTT CTGCG

(2) INFORMATION FOR SEQ ID NO: 3485:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 52 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3485:

ATCTCTGGTT CGATTCCCGT CGAGACCGGC ATCATTACAT GTTTATTATG GG

(2) INFORMATION FOR SEQ ID NO: 3486:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3486:

TGTGTCACGA TAATAGGCGT AATATCACTC TTTGGCATGA TTGCCGGATG

(2) INFORMATION FOR SEQ ID NO: 3487:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 67 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3487:

TATTTTGTGAT CACTCAAC GCACAAACGA ATGGCCTTTA CCTTCACAGA ATAATGGTCT

AATGTAA

(2) INFORMATION FOR SEQ ID NO: 3488:



- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3488:

10 TAGGTGGTCA ATTACCTGGT ACTAGGTATA TCCGTGGATT GCGAGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 3489:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3489:

CAATTGTACT TCATAACGTT TTGCATTTTCG CCACCTTCAC CACTATATTT TCCCATGGTC

60

25 (2) INFORMATION FOR SEQ ID NO: 3490:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3490:

CTAAACTGAT TGTTTTACGT AACGTTTCAT CGGCTTCTTT CGCTTCTATC

50

(2) INFORMATION FOR SEQ ID NO: 3491:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3491:

TCGATTTACC TTTCATCATT GAAGAAGATC GCCATGACTA TACAATCAAT AT

52

50

(2) INFORMATION FOR SEQ ID NO: 3492:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3492:

AACCTTTTCA CAAATATCAT ATAACCTCTC TAATGGGATA ATCTCTTCAT GT

52

(2) INFORMATION FOR SEQ ID NO: 3493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3493:

GGTTTTAAAC CGTCACGAAC ATCTGGCAAT GCACGAGCAA CGTACATACG TATCTAAAGT

60

TACGCTT

67

(2) INFORMATION FOR SEQ ID NO: 3494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3494:

TACGTTATGT TATGTAAATA ACAGTTAATT ATACCGGTGG TCTGGGTCGA

50

(2) INFORMATION FOR SEQ ID NO: 3495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3495:

CGCTTGTTGT TGTACTTTGG CAGTTCGCGT TGTGGATTGT GCCAGCGCTT TTAAACCGTA

60

(2) INFORMATION FOR SEQ ID NO: 3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3496:

GGCACCGGCT TCTCTATTGC TTCTTTAGCA TATCTGCAGC TCTCTCAAGG GACATG

56

(2) INFORMATION FOR SEQ ID NO: 3497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3497:

CACCTTTAGG ATACGCGTCT AACCACTGTG TCGCGTCTCT ATATATCGCT AAACACGTA

59

(2) INFORMATION FOR SEQ ID NO: 3498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3498:

AAGTAATATC TGAATGCGTA TATTGTCTAA TTTCAAATTC TACAGACATC GACGT

55

(2) INFORMATION FOR SEQ ID NO: 3499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3499:

AntGTACACG TCCATCTTCA CATGACAACA ACGATATTTT GACCATCACA

50

(2) INFORMATION FOR SEQ ID NO: 3500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3500:

## (2) INFORMATION FOR SEQ ID NO: 3501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3501:

TGTGTGCCTT TAAGTTGTTG ATGACACGCA TTCACGACAA CAGACATGAC AC 52

## (2) INFORMATION FOR SEQ ID NO: 3502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3502:

CTGGCTTCAA TGGCAACTTC TGTACCTGGT ACCAATGGGC GATGACCGAT 50

## (2) INFORMATION FOR SEQ ID NO: 3503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3503:

TGTCCGACTT GCGGnATCG TAATTTAGCG CnTGTAATTC TAAAGGGACC 50

## (2) INFORMATION FOR SEQ ID NO: 3504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3504:

AACCTTCATA TTGCTTCTAA TAAGAAACCG AGCAGCGCAC CAAACCTGGC AGTACCTTTA 60

TCGC 64

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3505:

TATTGATGTT GAAAACTGTT ATGTCCTTTC GATGGGCCAA CACnAAnATA

(2) INFORMATION FOR SEQ ID NO: 3506:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3506:

GAATATGGTA TCAATGGTAT GCACTAAGGC TTTATGAAAT TCATTTAAAA T

(2) INFORMATION FOR SEQ ID NO: 3507:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3507:

CGGTTTTAAT CGGTAAATTA AATATGGATG AGTTTGCAAT GGTGTTTACA GAACATCTAT

TTAA

(2) INFORMATION FOR SEQ ID NO: 3508:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3508:

CAAGGCCTTG TTTTAAAGC AGCTACAGTT GGCAATATGT CCACTCATGT

(2) INFORMATION FOR SEQ ID NO: 3509:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3509:

10 CAGATGCAAA TTGACATGGT CATCAACATC nGTnCATTA AAGATGGACG 50

(2) INFORMATION FOR SEQ ID NO: 3510:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3510:

ACAAGAGGGT CACCCAGCTC GGTGATTCC CACCGCCACA TCATGATATT TATTCATAGA 60

GTTTACGCAC TGTACATGAT TGAATGCGAT AAAG 94

25

(2) INFORMATION FOR SEQ ID NO: 3511:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3511:

ACTCAACAAT GGATATTCTT ACACTGAAAA ATGGGTAATG GTGCAAACAT AGTA 54

(2) INFORMATION FOR SEQ ID NO: 3512:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3512:

50 CCGGATGCAC ATTTGATGAC TGAAGTCCGC GATAAAGGGA CAAnAGTCAn 50

(2) INFORMATION FOR SEQ ID NO: 3513:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3513:

GCATTAAATT GAAACAATCG GATTTACAAT TTTCTCTTAA TGCTGTCGTC TACACAGC 58

10 (2) INFORMATION FOR SEQ ID NO: 3514:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3514:

20 GTGTTTCGTGT TCATGCAAGG TGAATGCGAG TGATCTGTTG GTATGGGCTT TATGCATGGC 60

AATCTG 66

25 (2) INFORMATION FOR SEQ ID NO: 3515:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3515:

35 ATGCCACTGA TAATGCnnCT GAACTTATTG ATGACTTCTC ATTAGACTAT 50

(2) INFORMATION FOR SEQ ID NO: 3516:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3516:

CGGCGACAAA GAGTAAACAC AGCGGAGGGA CAAAGCCCGC GACTAGCAAC 50

50 (2) INFORMATION FOR SEQ ID NO: 3517:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3517:

5 ATGCCTATGT AGCACCGAGT ACCGATACCG AACACTTAGC TACGCCAGTT C 51

(2) INFORMATION FOR SEQ ID NO: 3518:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

GAGCATnAAG GTGATTnGA TCGCTATCCG TTAGCTAAAT TTAAACGTTC 50

20 (2) INFORMATION FOR SEQ ID NO: 3519:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3519:

30 GATTGGTATT TAGCTTTAAA TTTATGGTTG GAATAGTAGG TGGCATATAT CGCTGTTAGT 60

ATCG 64

(2) INFORMATION FOR SEQ ID NO: 3520:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3520:

45 TCTTCAATCT CAGGGGCATC TACTAACATA TCATCCAGTC AATATTGCGT CACATTGTTA 60

ATCGGTTCCG ATC 73

(2) INFORMATION FOR SEQ ID NO: 3521:

50

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3521:

5 TCAAATTGGC AATTGGTACG AATGTCGACT GTACTAACAT CATTAGCTCA TGATTGCCAG 60  
 GTGATTTTCAT GGATG 75

(2) INFORMATION FOR SEQ ID NO: 3522:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3522:

TTCCAATGGG CTTCTGACTT TGGCGGTTTT AGTGCTTGGG TGCCGGCGG TTTTGA 57

20 (2) INFORMATION FOR SEQ ID NO: 3523:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3523:

TGGTGGAGGT TTTGTTTTT CCGTGTCGGT TTTTGTTTTC GTCTTGGTTT CTTTTGTTTT 60  
 TGTGTTCTCT TT 72

35 (2) INFORMATION FOR SEQ ID NO: 3524:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3524:

ATATCACAAT ATACCGGTTT ATATGCTGTC TAATCATAGT TGAATAGTGA C 51

(2) INFORMATION FOR SEQ ID NO: 3525:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3525:

5 TAGACCGTCG TGGATAGTTT TGGGTACGGT AACCAATTTA TTTTGAAGAG ACCATCCTC 59

(2) INFORMATION FOR SEQ ID NO: 3526:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3526:

TAATAACGTT GCCCTCCCAT GTATATCCTA CCAACATGAC ATCTTGATACA 50

(2) INFORMATION FOR SEQ ID NO: 3527:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3527:

30 TTCCCAACGA GCAGTCGCAT GCGGTACTGC CACGGCATT TGTATGCAGGC CT 52

(2) INFORMATION FOR SEQ ID NO: 3528:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3528:

AAAGAAAnGA TnGnnnGnnn GnAnAAAnnn nnCCATnnnn nTAAAAAAA 50

45 (2) INFORMATION FOR SEQ ID NO: 3529:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

CATTAGCCTC ATCCCTTCG TTTAGACTCG CTATAGATGC ACTAAATGGC GATATATTTT 60

TC 62

(2) INFORMATION FOR SEQ ID NO: 3530:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3530:

CACTACCACA AAAATTATAG GTGTTGACCT TCAGGnGCAA GTAGTATGAT 50

(2) INFORMATION FOR SEQ ID NO: 3531:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3531:

GAATGCAAAA TCCATTTGTA AGGAnATCGA ATGGTTTAgT AnCTCGTGCA 50

(2) INFORMATION FOR SEQ ID NO: 3532:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3532:

GGTAGAnCnC TGTTTAGTAC TAGGGGCCCC TCTCGGGTTA CCAATTCAGA 50

(2) INFORMATION FOR SEQ ID NO: 3533:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3533:

## (2) INFORMATION FOR SEQ ID NO: 3534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3534:

CGTCAACGAT GTAAAGTAAA GCCTTGTTCCA GTTTAATTGA CGAGTGGCGT AA 52

## (2) INFORMATION FOR SEQ ID NO: 3535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3535:

TTAATCCAGA AGTACCGGTG GATTTAGTTA TTGACCACTC AGTTCAGTG GATAGCTATG 60  
 CAAATCCAGA AGCTCTTGAA CGTAATATGA AATTAGAATT TGAACGTAAC TATGAACGTT 120  
 ATCAGTTTTT AAATTGGGCA ACGAAAGCAT TTGATAATTA CAATGCAGTT CCTCCTGCAA 180  
 CTGGAATAGT TCACCAAGTT AACTTAGAAT ATTTAGCAAG TGTGTACAT GTTCGTGATG 240  
 TAGATGGTGA AAAAAGTGCA TTTCCAGATA CATTAGTTGG TACTGATTCA CATAACAAC 300  
 TGATAAATGG TATTGGCGTA CTAGGATGGG GTGTTGGTGG TATTGAAGCT GAAGCTGGAA 360  
 TGCTTGGACA ACCTTCTTAT TTCCCAATTC CAGAGGTTAT 400

## (2) INFORMATION FOR SEQ ID NO: 3536:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3536:

CGTATAGAGT GTCCTACAAC CCCAACAAGC AAGCTTGTG GTTTGGGCTC TTCCCGTTTC 60  
 GCTCGCCGCT ACTAAGGGAA TCGAATTTTC TTTCTCTTCC TCCGGGTACT AAGATGTTTC 120  
 AGTTCTCCGG GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC 180

GCATATCGTC GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC 300  
 CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGCTCA CATACGGCTT 360  
 5 CGTTTTTCATT ATTTTAAATG CTCATTTACA TAAGTAAACT CTGCTTTAAA ATAATTTAAC 420  
 TCATTGTCTG CTAAACGTTT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTGA 480  
 GTGTTCTTTC GAACACTAGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACCTCTTA 540  
 10 TTCACTCGGT TTTGCTTGGT AAAATCTATA TTTTACTTAC TTATCTAGTT TTCAATGTAC 600  
 AATTTCTTTT TAGTCAAGCG CTCGCATACT GCTTTATTTT CAAAAAATCA AATGCTCATT 660  
 15 TACAAAAGTA AACTCCGCTT TAATTTTCT TAATGCATTG TCTAACAACC GCTTTCTTTA 720  
 AAAAGAATAG ATTGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 780  
 ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG 840  
 20 AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT 900  
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 960  
 TTACTIONCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGcGGT GTGTACAAGA 1020  
 25 CCCGGGaaACG TATTCACCGT AGCATGCTGA TCTACGaTTA CTAGCGtTCC AGCTTCATGT 1080  
 AGTCGAGTGC AGACTACCAT CCGGACTGnG GACCAACT 1118

(2) INFORMATION FOR SEQ ID NO: 3537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3537:

GGGGATCCCC AGCCAGAAGA TTTATTCAGT GCGATGATTC GTGAAATTGA AACGCAAGAT 60  
 TTCGATATCG AACACCTGGC GACGGCAATT CGTAaGTTG AAACATCAAC ATTAGGTGAA 120  
 GAAAGTGAAA ATGACTTTAT CGGTCTGTTC AGCGATATGG ATTTGAGTTC AACGCGACTA 180  
 45 GGTAACAATG TCAAAGAACG TACTGCTTTA ATCTCTAAAG TCATGGTTAA TCTTGACGAC 240  
 TTACCATTCTG TTCACAGTGA CATGGAAATT GATATGTTAG GTGATGCATA TGAATTCCTA 300  
 50 ATTGGGCGCT TTGnGCGACA CGGGTAAAAA AAGCAGGCGA GTTCTATACA CCACAACAAG 360  
 TATCTAAGAT ACTGGCGAnG ATTGTACAG ACGGTAAAGA TAAATTACGT CACGTGTATG 420  
 ACCC 424

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3538:

ATCTCATATG	TTAAAAGGTA	AACAAGGTCG	TTTCCGTCAA	AACTTACTTG	GTAAACGTGT	60
TGACTATTCA	GGACGTTTCA	TTATTGCAGT	AGGTCCAAGC	TTGAAAATGT	ACCAATGTGG	120
TTTACCAAAA	GAAATGGCAC	TTGAACTATT	TAAACCATT	GTAATGAAAG	AATTAGTTCA	180
ACGTGAAATT	GCAACTAACA	TTAAAAATGC	GAAGAGTAAA	ATCGAACGTA	TGGATGATGA	240
AGTTTGGGAC	GTATTGGAAG	AAGTAATTAG	AGAACATCCT	GTATTACTTA	ACCGTGCACC	300
AACACTTCAT	AGACTTGGTA	TTCAAGCATT	TGAACCAACT	TTAGTTGAAA	GGTCGTGCGA	360
TTCGTCTACA	TCCACTTGTA	ACAACAGCTT	ATAACGCTGA			400

(2) INFORMATION FOR SEQ ID NO: 3539:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1171 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3539:

AATAAGTAAG	TTATTTTGTC	TGGTGACTAT	AGCAAGGAGG	TCACACCTGT	TCCCATGCCG	60
AACACAGAAG	TTAAGCTCCT	TAGCGTCGAT	GGTAGTCGAA	CTTACGTTCC	GCTAGAGTAG	120
AACGTTGCCA	GGCAAATGAC	AAATCGGAGA	ATTAGCTCAG	CTGGGAGAGC	ATCTGCCTTA	180
CAAGCAGAGG	GTCGGCGGTT	CGAACCCGTC	ATTCTCCACC	ATTTATTCTT	AGATATAGCC	240
GGCCTAGCTC	AATTGGTAGA	GCAACTGACT	TGTAATCAGT	AGGTTGGGGG	TTCAAGTCCT	300
CTGGCCGGCA	CCATCTTTTG	AGCCATTAGC	TCAGCTGGTA	GAGCATCTGA	CTTTTAATCA	360
GAGGGTCAGA	GGTTCGAATC	CTCTATGGCT	CATTACGATT	TAATTTTTAT	ATTTAGCAAA	420
ATAATGCAGA	AGTAGTTCAG	CGGTAGAATA	CAACCTTGCC	AAGGTTGGGG	TCGCGGGTTC	480
GAATCCCGTC	TTCTGCTCCA	TTATTTTGCC	GGGGTGGCGG	AACTGGCAGA	CGCACAGGAC	540
TTAAAATCCT	GCGGTGAGAG	ATCACCGTAC	CGGTTGATT	CCGGTCCTCG	GCACCATTTT	600
AGCGCCCGTA	GCTCAATTGG	ATAGAGCGTT	TGACTACGGA	TCAAGAGGTT	ATGGGTTCGA	660

GAGCACTTGG TTTGGGACCA AGGGGTCGCA GGTTCGAATC CTGTCTTCCC GATTACTTCT 780  
 TAAATTCCAT TTTATGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 840  
 5 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTTATTTTT TACACGATGA ACATTGAAAA 900  
 CTGAATGACA ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT 960  
 TTAGTATTTA TGAGCTAATC AAACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAG 1020  
 10 GATGAACGCT GCGGCGCTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT 1080  
 TCTCTGaTGT TAGCGGCGGA CGGGTGAGTA ACACGTGGgA TAACCTACCT ATAAGACTGG 1140  
 15 GaTAACTTCG GGaAACCGGA GCTAATACCG G 1171

## (2) INFORMATION FOR SEQ ID NO: 3540:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3540:

CTCGGCAGTG TGAAATCAAC GACTCGAAGA CACAATGTCT TCTCCCCATC ACAGCTCAGC 60  
 CTTAACGAGT ACCGGATTG CCTAATACTC AGCCTTACTG CTTAGACGTG CAATCCAATC 120  
 30 GCACGCTTCG CCTATCCTAC TGCGTCCCCC CATCGATTAA AACGATTATA GGTGGTACAG 180  
 GAATATCAAC CTGTTATCCA TCGCCTACGC CTGTCGGCCT CAGCTTAGGA CCCGACTAAC 240  
 CCAGAGCGGA CGAGCCTTCC TCTGGAAACC TTAGTCAATC GGTGGACGGG ATTCTCACCC 300  
 GTCTTTCGCT ACTCACACCG GCATTCTCAC tTCTAAGCGC TCCACATGTC CTTACGATCA 360  
 TGCTTCAACG CCCTTAGAAC GCTCTCCTAC CATTGTCCAA AGGCATwCrC ACAGCTTCGG 420  
 40 TaATATGTTT AGCCCCGGTA CATTTTCGGC GCAGtGTCAC TCGACTAGTG AGCTATTACG 480  
 CACTCTTTAA ATGATGGCTG CTTCtnAGCC AACATCCTAG GTTGGTCTGG GGCACGCnAC 540  
 ATCCTTTTCC ACTTAACATA TATTTTGGGG ACCTTGGCTG GTGGGTCTGG GGCTGnTTCC 600  
 45 C 601

## (2) INFORMATION FOR SEQ ID NO: 3541:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1311 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3541:

5 GCnAGGACCT ThCCAAATTT GAAATCCTTT GACCACnTTT GGGGTAGAGC CCTTTCCnC 60  
 GGGGACAAAG TGACCAGGTG GTGCATGGTT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT 120  
 TAAGTCCCCG CAACGAGCGC AACCCCTAAG CTTAGTTGCC ATCATTAAGT TGGGCACTCT 180  
 10 AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG ACGTCAAATC ATCATGCCCC 240  
 TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA AAGGGCAGCG AAACCGTGAG 300  
 nTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC TCGACTACAT 360  
 15 GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG GTGAATACGT TCCCGGGTCT 420  
 TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC CGAAGCCGGT GGAGTAACCT 480  
 TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG TGAAGTCGTA ACAAGGTAGC 540  
 20 CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA ACATCTTCTT 600  
 CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTT GAATGTTTGT TCATTCAAAT 660  
 25 TAATGGGCCT ATAGCTCAGC TGGTTAGAGC GCACGCCTGA TAAGCGTGAG GTCGGTGGTT 720  
 CGAGTCCACT TAGGCCACC ATTAATTTAA TACCTATTG GGGGCTTAGC TCAGCTGGGA 780  
 GAGCGCCTGC TTTGCACGCA GGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTATT 840  
 30 TGTACATTGA AAAC TAGATA AGTAAGTAA ATATAGATT TACCAAGCAA AACCGAGTGA 900  
 ATAAAGAGTT TTAAATAAGC TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAAGAACA 960  
 CTCACAAGAT TAATAACGCG TTTAAATCTT TTTATAAAAG AACGTAACCT CATGTTAACG 1020  
 35 TTTGACTTAT AAAAATGGTG GAAACATAGA TTAAGTTATT AAGGGCGCAC GGTGGATGCC 1080  
 TTGGCACTAG AAGCCGATGA AGGACGTTAC TAACGACGAT ATGCTTTGGG GAGCTGTAAG 1140  
 40 TAAGCTTTGA TCCAGAGATT TCCGAATGGG GAAACCCAGC ATGAGTTATG TCATGTTATC 1200  
 GATATGTGAA TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC 1260  
 CGGAGGAAGA GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCGAAATG G 1311

## (2) INFORMATION FOR SEQ ID NO: 3542:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3542:



CGCTAGAGTA GAACGTTGCC AGGCAAATGA CAAATCGGAG AATTAGCTCA GCTGGGAGAG 120  
 CATCTGCCTT ACAAGCAGAG GGTCGGCGGT TCGAACCCGT CATTCTCCAC CATTATTCT 180  
 5 TAGATATAGC CGGCCTAGCT CAATTGGTAG AGCAACTGAC TTGTAATCAG TAGGTTGGGG 240  
 GTTCAAGTCC TCTGGCCGGC ACCATCTTTT GAGCCATTAG CTCAGCTGGT AGAGCATCTG 300  
 ACTTTTAATC AGAGGGTCAG AGGTTCGAAT CCTCTATGGC TCATTACGAT TTAATTTT 360  
 10 TATTTAGCAA AATAATGCAG AAGTAGTTCA GCGGTAGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3543:

GTGAGAGTGA CGTTATGTTA TGTAATAAC AGTTAATTAT ACCGGTGGTC GGGGTCGAAC 60  
 25 CGCACTCCAC AAGTGAAGA GaTTTTGAGT CCCGCGCGTC TGCCAATTCC GCCACACCGG 120  
 CTTAATGGTA AACAAAAAAC TTCCCTTTGG AAGCAATTAT GGAGCGGAAG ATAGGATTTA 180  
 CACCTATACC TCGTTCCGGG aAGGAACTGg TTcTAAAGT TGAACTACTC CCGCAAATAT 240  
 30 TAAATTATGG AGCGGAAGAT AGGATTTACA CCTATACCTC ATTCCAGGAA GGAATGTATT 300  
 CTAAGAGTTG AAATACTCCC GCATTATTAT TAAATTATGG AGCGGAAGAT AGGATTTGCA 360  
 35 CCTATACCTC GTTCCGGGAA GGAcKTGTTt CTAAAGTTG AACTACTCCC GCATAAACCT 420  
 GGAGGCGGCA ACCGGATTTG AACCGGTGAT AAAGGTTTTG CAGACCTCTG CCTTACCACT 480  
 TGGCTATGCg CcAATAACTG GGCTAGCTGG ATTCGAACCA ACGAGTGACG GATmAAAGTC 540  
 40 CGTTGCCTTA CCGCTTGGCT ATAGCCCATT AATAATAAGG GCGGCTGAAG GGGATCGAAC 600  
 CCTCGAATGT CGGAACCACA ATCCGATGTG TTAACCACTT cACCACAGCC GCCATGGCAG 660  
 GGGCAGTAGG AATCGAACCC ACACCAAAGT TTTGGaGACC TCTATTCTAC CGTTGAACTA 720  
 45 TGCCCCTATT aAAAAATaaTA ATkGGAGGGG GGCAGATTCG AAnTGCCGAA CCCGAAGGAG 780  
 CGGGATTTAC ATTCCGCCGG GTTT 804

(2) INFORMATION FOR SEQ ID NO: 3544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3544:

5 ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60  
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120  
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180  
 10 GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240  
 CATCGCATAA GTTTGATKAC AAACAAGCTT CCATGACAAA AGTACTGACG AATATCGCAT 300  
 TTGCGAAAGT CTCTACAAAT GCCTTTGAGG CACGTCGTTA TGGTTATTTA CGTGGATACA 360  
 15 GATACGATTA TTTTCAATAC AGCACAACGT GTCCGAAGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3545:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3545:

CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA TCATGCTTCA ACGCCCTTAG 60  
 30 AACGCTCTCC TACCATTGTC CAAAGGnATC nCACAGCTTC GGTAATATGT TTAGCCCCGG 120  
 TACATTTTCG GCGCAGTGTC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGATGGC 180  
 TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCaCA TCCTTTTCCA CTTAACATAT 240  
 35 ATTTTGGGAC CTTAGCTGGT GGTCTGGGCT GTTTCCTTT CGAACACGGA CCTTATCACC 300  
 CATGTTCTGA CTCCCAAGTT AAATTAATTG GcATTCTGGAG TTTGTCTGAA TTCGGTAACC 360  
 CGAGAGGGGC cCCTCGTCCA AAcAGTGGCT CTACCTCCAA TAATCATCAn TTGAGGCTAG 420  
 40 CCCTAAAGCT AATTCGGAGA GAACCAGTAT CTCCAGTTCG ATTGGAATTC TnCG 474

## (2) INFORMATION FOR SEQ ID NO: 3546:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3546:

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GCAATTCGTA AAGTTGAAAC ATCAACATTA GGTGAAGAAA GTGAAAATGA CTTTATCGGT 120  
 CTGTTTCAGCG ATATGGATTT GAGTTCAACG CGACTAGGTA ACAATGTCAA AGAACGTACT 180  
 5 GCTTTAATCT CTAAAGTCAT GGTTAATCTT GACGACTTAC CATTTCGTTCA CAGTGACATG 240  
 GAAATTGATA TGTTAGGTGA TGCATATGAA TTCCTAATTG GGCGCTTTGn GCGACACGGG 300  
 TAAAAAAGC AGGCGAGTTC TATACACCAC AACAAGTATC TAAGATACTG GCGAGATTGT 360  
 10 CACAGACGGT AAAGATAANT ACGTCACGTG TATGACCCAA 400

## (2) INFORMATION FOR SEQ ID NO: 3547:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3547:

AACGTTTTCA CTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GACGTTTTAG 60  
 25 ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT CGCATCCATT TTTGCCTGG 120  
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG ACGCTAAGAA CCTTTCTTGA 180  
 CTTGTGACAA TCGCTTGCTT CTTTCCTCTT CTTGCGCTCT CGCTTACTCA TTTAGCTCTA 240  
 30 CTAAACTCGT TCGCTCTTT TCTCGTTTCG TCAGATTCAA ACGTTTTTCAC TTCGCCAAGC 300  
 CATTTTTCTT TGTGTTTGCT TTTTATTTTG ACGTTTTAGA CATAAAAAA AGAGACCTTG 360  
 35 CGGTCTCAAT GCGGCTCATC GCATCCANTT TTTGCCTGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3548:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60  
 50 GTTTGAAACC AGTAGTACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120  
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180  
 GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

TTGCAAAGTC TCTACAAATG CCTTTGAGGC ACGTCGTTAT GGTTATTTAC GTGATACAGA 360  
TACGATTATT TTCAATACAG CACAACGTGT CCGAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 3549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3549:

AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC GGTGTGTACA 60  
AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA TTCCAGCTTC 120  
ATGTAGTCGA GTTGCAGACT ACAATCCGAA CTGAGAACAA CTTTATGGGA TTTGCTTGAC 180  
CTCGCGGTTT CGCTGCCCTT TGTATTGTCC ATTGTAGCAC GTGTGTAGCC CAAATCATAA 240  
GGGGCATGAT GATTTGACGT CATCCCCACC TTCCTCCGGT TTGTCACCGG CAGTCAACTT 300  
AGAGTGCCCA ACTTAATGAT GGCAACTAAG CTTAAGGGTT GCGCTCGTTG CGGGACTTAA 360  
CCCAACATCT CACGACACGA GCTGACGACA ACCATGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3550:

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 60  
TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATAATATTT 120  
TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 180  
TGCAATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG CCGACCTGAG 240  
AGGGTGATCG GCCACACTGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTA 300  
GGGAATCTTC CGCAATGGGC GAAACCTGAC GGAGCAACGC CGCGTGAGTG ATGAAGGTCT 360  
TCGGATCGTA AAACCTCTGTT ATTAGGGAAG AACATATGTG 400

(2) INFORMATION FOR SEQ ID NO: 3551:

(A) LENGTH: 506 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3551:

10 ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA 60  
 ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAAGTTT GAATGTTTAT 120  
 TTAACATTCA AATATTTTTT GGTAAAGTG ATATTGCTTA TCGAGCGCT TGACAATCTA 180  
 15 TTCTTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA AAAATTAAAG CGGAGTTTAC 240  
 TTTTGTAAT GAGCATTGA TTTTTTGAAA ATAAAGCAGT ATGCGAGCGC TTGACTAAAA 300  
 AGAAATTGTA CATTGAAAAC TAGATAAGTA AGTAAAATAT AGATTTTACC AAGCAAAACC 360  
 20 GAGTGAATAA AGAGTTTAA ATAAGCTTGA ATTCATAAGA aTAATCGCTA GTGTTGAAA 420  
 GAACACTCAC AAGATTAATA ACGCGTTTAA ATCTTTTAT AAAAGAnAAC GTTTAGCAGA 480  
 CAATGAGTTA AATTATTTTA AAGCAG 506

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## (2) INFORMATION FOR SEQ ID NO: 3552:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3552:

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AAGCTGAGGC CGACAGTGGn GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT 60  
 CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGACGTG TCGATTGGAT TGCACGTCTA 120  
 AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTGATGGGGA 180  
 GAAGACATTG TGTCTTCgAG GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA 240  
 AAATAGGTGC CCGTACCGCA AACCGACACA GGTAGTCAAG ATGAGAATTC TAAGGTGAGC 300  
 GAGCGAACTC TCGTTAAGGA ACTCGGCAA ATGACCCCGT AACTTCGGGA GAAGGGGTGC 360  
 TCTTTAGGGT TAACGCCAG AAGAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA 420  
 AACACAGGTC TCTGCTAAAC CGTAAGtGAn TGTATAGGGG CTGACGCCTG CCCGGTGCTG 480  
 GAAGGTTAAG AGGAGTGTT AGCTTCTGCG AAcTAcGaAT CGAAGCCCCA GTAAACGGCG 540  
 GCCGTAACTA TAACGGTCCT AAGGTAGCGA AATTCCTTGT CGGGTAAGTT CCGACCCGCA 600

GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 720  
 5 GATATTGAAA TTCGGCACAG CTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGAGCGCT 780  
 AcTTaCgTGG aGGCGCTGGT GGGATACTAC CCTAGCTGTG TTGGCTTTCT AACCCGCACC 840  
 ACTTATCGTG GTGGGAGACA GTGTCAGGCG GGCAGTTTGA CTGGGGCGGT CGCCTCCTAA 900  
 10 AAGGTAACGG AGGCGCTCAA AGGTTCCCTC AGAATGGTTG GAAATCATT C ATAGAGTGTA 960  
 AAGGCATAAG GGAGCTTGAC TGCAGACCT ACAAGTCGAG CAGGGTCGAA AGACGGACTT 1020  
 AGTGATCCGG TGGTTCCGCA TGGAAAGGCC ATCGCTCAAC GGATAAAAGC TACCCCGGGG 1080  
 15 ATAACAGGCT TATCTCCCCC AAGAGTTCAC ATCGACGGGG AGGTTTGGA CCTCGATGTC 1140  
 GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCAAGGGTT GGGCTGTTG CCCATTAAAG 1200  
 CCGTACrmGg CTGGGTTCAG AACGTCGTGA GaCAGTTCGG TCCCTATCCG TCGTGGGCGT 1260  
 20 AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 1320  
 TACCAGTTGT CGTGCCAACG cATnAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA 1380  
 AAcATnCTnA AGCATGAAGC CCCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC 1440  
 25 CCTCAAAGAT GATGAGGTTA ATAGGTTCTGA GGTGGAAGCA TGGTGACATG TgGGAGCTGA 1500  
 CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACAAA tnCaCTTTTA 1560  
 CTTACTATCT AGTTTTGAAT GTATAAATTA CATTCAATG TCTGGTGA CT ATAGCAAGGA 1620  
 30 GGTCACACCT GTTCCCATGC CGAACACAGA AGTTAAGCTC CTTAGCGTCG ATGGTAGTCG 1680  
 AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAGTTT TTTAATCAAA TTTGGTTAA 1740  
 35 AAAATAAAAT GGACAAGATA AAAAAAGTTA TTGACTTAAA TGTTAATAAA ATGTATAATT 1800  
 AATTCTTGTC GGTAAGAAAA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 1860  
 TCCAAAAAAC GTAACATAA GTTACAAACA TTATTAGTA TTTATGAGCT AATCAAACAT 1920  
 40 CATAATTTTT ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA 1980  
 CATGCAAGTC GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG 2040  
 AGTAACACGT GGATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GGAGCTAATA 2100  
 45 CCGGATAATA TTTTGAACCG CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA 2160  
 GATGGATCCg CGCTGCATTA GCTAGTTGGt AAGGtAACGG CTTTACCCA 2209

(2) INFORMATION FOR SEQ ID NO: 3553:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 518 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3553:

5 CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC CGAGTGAATA AAGAGTTTTA 60  
 AATAAGCTTG AATTCATAAG AAATAATCGC TAGTGTTCGA AAGAACACTC ACAAGATTAA 120  
 TAACGCGTTT CCTGTAGGAT GGAAACATAG ATTAAGTTAT TAAGGGCGCA CCGTGGATGC 180  
 10 CTTGGCACTA GAAGCCGATG AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA 240  
 GTAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT 300  
 CGATATGTGA ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC 360  
 15 CCGGAGGAAG AGAAAGAAAA TTCGATTCCC TTAGTAGCGG CGAGCGAAAC GGAAGAGCC 420  
 CAAACCAACA AGCTTGCTTG TTGGGGTTGT AGGgACTCT ATACGGAGTT ACaAAGGmCG 480  
 20 ACATTgGACG AatCATCTGG gAAAGwTGaT CCAAGGAA 518

## (2) INFORMATION FOR SEQ ID NO: 3554:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 587 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3554:

30 AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60  
 CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTsGAC 120  
 35 TACCATCGAC GCTAAGGAGC TTAACTTCTG TGTTCCGCAT GGAACAGGT GTGACCTCCT 180  
 TGCTATAGTC ACCAGACATA TGAATGTAAT TTATACATTC AAAACTAGAT AGTAAGTAAA 240  
 40 AGTGATTTTG CTTGCAAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 300  
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGAT 360  
 CTTATAACCG AAGTTGGGAA ATCTCATCTT GAGGGGGGCT TCATGCTTAG ATGCTTTCAG 420  
 45 CACTTAtCCC GTCCACACAT AGCTACCCAG CTATGCCGTT GGCACGACAA CTGGTACACC 480  
 AGAGGTATGT CCATCCCGGT CCTCTCGTAC TAAGGACAGC TCCTCTCAA TTTCTACGC 540  
 CCACGACGGa TAGGGaCCGA ACTGtCTCAC GACGTTCTGA ACCCAGA 587

## (2) INFORMATION FOR SEQ ID NO: 3555:

## (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 399 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3555:

	GAATCTGAAT CGCTATCTGA ATCCGAGTCA CTGTCGGAAT CTGAGTCACT GTCGGAATCT	60
10	GAATCGCTAT CTGAATCTGA ATCGCTGTCT GAATCTGAAT CGCTGTCTGA ATCTGAGTCG	120
	CTATCTGAGT CGGAATCGCT ATCTGAGTCG GAATCACTGT CGGAATCTGA ATCGCTGTCT	180
	GAGTCGGAAT CACTGTCGGA GTCAGAATCG CTGTCTGAGT CGGAATCACT GTCGGAATCT	240
15	GAATCGCTAT CTGAATCTGA ATCGCTATCT GAATCCGAGT CACTGTCTGa GTCAGAATCG	300
	CTATCTGGAA TCTGGAGTCA CTGTCGGAAT CTGAGTCACT GGTCTGGAGT CAGAATCGCT	360
20	ATCTGGAATC CGAnGTCATG GTCTGAGTCG GGaATCGCT	399

(2) INFORMATION FOR SEQ ID NO: 3556:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3556:

	ATTCATCTTT CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT	60
	ACAACCCCAA CAAGCAAGCT TGTGTTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA	120
35	GGGAATCGAA TTTTCTTTCT CTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG	180
	CCTTCTGATA TGCTATGTAT TCACATATCG ATAACATGAC ATAACATG CTGGGTTTCC	240
40	CCATTTCGAA ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG	300
	TAACGTCTTT CATCGGCTTC TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT	360
	CTATGTTTCC ATCCTACAGG AAACGCGTTA TTAATCTTGT	400

45

(2) INFORMATION FOR SEQ ID NO: 3557:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 657 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3557:



ACAACTGGTA CACCAGAGGT ATGTCCATCC CGGTCCTCTC GTACTAAGGA CAGCTCCTCT 120  
 CAAATTTCTT ACGCCACGA CGGATAGGGA CCGAACTGTC TCACGACGTT CTGAACCCAG 180  
 CTCGCGTACC GCTTTAATGG GCGAACAGCA AnCCCTTGCG ACCGACTACA GCCCCAGGAT 240  
 GCGATGAGCc GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGAGATA 300  
 AGCCTGTTAT CCCCAGGGTA GCTTTTATCC GTTGAGCGAT GGCCCTTCCA TGCGGAACCA 360  
 CCGGATCACT AAGTCCGTCT TTCGAcCCTG CTCGACTTGT AGGTCTCGCA GTCAAGCTCC 420  
 CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT GAGGGAACTT TGAGCGCCTC 480  
 CGTTACCTTT TAGGAGGCGA CCGCCCCAGT CAAACTGCCc GCcTGACACT GTCTACcmCC 540  
 ACGATAAGTG GTGCGGGTTm GmAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGCCTn 600  
 CCCACTAATA GCGCTCACGT TTCAAAGGCT CCTACCTATC CTGTACAAGC TGTGCCG 657

(2) INFORMATION FOR SEQ ID NO: 3558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3558:

GAGTCCATGG GTGAAAGAAG CATCTGCAGC AACTGTAGCA GGTATTGCTG GAACTAATAA 60  
 TGGTATTACT GTTGCGAGCAG GTACTTTCAA CCCTGCTGAT ACAATTCAAG TTGTTGCAAC 120  
 GCAAGGACAG CGGAGAGACA GTGAGTGATG AGCAACGTAT nnTnGATTTC ACAGTTGTCG 180  
 CACCACAACC GAACCAAGCG ACTACTAAGA TTTGGCAAAA TGGTCATATT GATATCACGC 240  
 CTAATAATCC ATCAGGACAT TTAATTAATC CAACTCAAGC AATGGATATT GCTTACACTG 300  
 AAAAAGTGGG TAATGGTGCA GAACATAGTA AGACAATTAA TGTGTTTCGT GGTCAAATA 360  
 ATCAATGGAC AATTGCGAAT AAGCCTGACT ATGTAACGTT 400

(2) INFORMATION FOR SEQ ID NO: 3559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3559:

CGACACAAAA CAAGCCAAGC AAAACAAACG CATATAACGT AACAACACAT GGAAACGGCC 120  
 AAGTATCATA TGGCGCTCGC CAACACAAAA CAAGCCAAGC AAAACAAATG CATAACACGT 180  
 5 AACAACACAT GCAAACGGTC AAGTGTCTATA CGGAGCTCGC CCGACATACA AGAAGCCAAG 240  
 TAAAACAAAT GCATACAATG TAACAACACA TGCAGATGGT ACTGCGACAT ATGGGCCTAG 300  
 10 AGTAACAAAA TAAGTTTGTA ACTCTATCCA AAGACATACA GTCAATACAA AACATTACGT 360  
 ATCTTTACAA CAGTAATCAT GCATTCTATG ATGCTTCTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3560:

TTTAGGTTAT ACAGCATTGC AGGCAGGATA CTTATCAATT ACTTATTTAA TCATGGTGT 60  
 25 ATTGATGATT CGAGTTGGTG AAAAATTATT ACAAAAAATG GGTCTAAGC GACCAATGTT 120  
 ATTAGGTACA TTCATTGTGG TCATTGGTAT TGCATTATT TCATTAGTAT TCTTACCAGG 180  
 30 CATATTTTAT GTTATCAGTT GTGTCGTAGG ATATTTATGT TTCGGACTAG GCTTAGGTAT 240  
 TTATGCAACA CCTTCTACAG ATACAGCTAT TTCGAATGCA CCGTTAGATA AAGTTGGCGT 300  
 TGCTTCAGGT ATTTATAAAA TGGCTTCATC ACTTGGTGGG CGCATTTCGGT GTCGCAATTA 360  
 35 GTGGTGCTGT ATATGCTGGT GCAGTTGCTG CAACGAGCAT TCCATACAGG TGCGATGATT 420  
 GCACTTTGGG TTAACGTATT GAATGGGGAA TCCATGGCCA TTTATCGCAA TTTTAATnCG 480  
 CGATT 485

## (2) INFORMATION FOR SEQ ID NO: 3561:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3561:

AAATTATGTG AAGTAAAGG AGTACGTCCA TGCAAAATTT AGATAAGAAT TTTCGACaTT 60  
 TATCtCGTAA AGAAAAGTTA CaACAATTGG TTGATAAGCA ATGGTTATCA GAAGAACAAT 120

ATGTCATCGC GCAAGGTGCA TTACCCGTTG GATTATTACC GAATATCATT GTGGACGATA 240  
 AGGCATATGT TGTACCTATG ATGGTGGAAG AGCCTTCAGT TGTCGCTGCA GCTAGTTATG 300  
 5 GTGCAAAGCT AGTGAATCAG ACTGGCGGAT TTAAAACGGT ATCTTCTGAA CGTATTATGA 360  
 TAGGTCAAAT CGTCTTTGAT GGC GTTGACG ATACTGAAAA ATTATCAGCA GACATTAAAG 420  
 10 CTTTAGAAAA GCAAATTCAT AAAATTGCGG ATGAGGCATA TCC 463

(2) INFORMATION FOR SEQ ID NO: 3562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3562:

AATTTAAACC CAATTGTCTG GCAAAACGTT TTCCTTTATA AAAAGATTTA AACGCGTTAA 60  
 TTAATCTTGG TGCnGGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT 120  
 25 TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG 180  
 TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA CTGCTTTATT TTCAAAAAAT 240  
 CAAATGCTCA TTTACAAAAG TAAACTCCGC TTAAATTTTT CTTAATGCAT TGTCTAACAA 300  
 CCGCTTTCTT TAAAAAGAAT AGATTGTCAA GCGCTCGCAT AAGCAATATC ACTTTAACCA 360  
 AAAAATATTT GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA CGTTATTCCg 420  
 35 CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC AGCCGCACCT 480  
 TCCGATACGG CTACCTTGtT ACGACTTCAC CCCAATCATT TGTCCACCT TCGACGGCTA 540  
 GCTCCTAAAA GGTTACTCCA CCGGCTTCGG GTGTTACAAA CTCTCGTGGT GTGACGGGCG 600  
 40 GTGTGTACAA GACCCGGGAA CGTATTCACC GTAGCATGCC TCG 643

(2) INFORMATION FOR SEQ ID NO: 3563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3563:

GATAAATCCA AATAGTGCAC TATAAAAAAT AATATCTACT AAAGTATCTT TATGTAATCC 60

TTCCATACCA TCGTACACTC AGTGGTCCTA AGTTAAATGC CACAGGATCT ATATAGTTAA 180  
 ATACAATACC CATTCAACCT ACTCCTCACT CTTATGACTG TTCTTGATAA TTTCTTCATT 240  
 5 TAATCTTTCA CTAAATTCTT CGGCCGTGTT AATGCCCATG ATATTTAATC GATAGTTCAT 300  
 TGCAGCGACC TCAATAATTA CCGCAACATT TCTACCAGGT CTTACAGGTA TTGGTTTTTT 360  
 10 TTAGTGGnTT TCAGTATCTA AAATACTTAG CGTCTCTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3564:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3564:

TCGTCAGCnC nTGTCGTGAG ACGTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTAAGCT 60  
 TAGTTGCCAT CATTAAAGTTG GGCACCTCTAA GTTGACTGCC GGTGACAAAC CGGAGGAAGG 120  
 25 TGGGGATGAC GTCAAATCAT CATGCCCTT ATGATTTGGG CTACACACGT GCTACAATGG 180  
 ACAATACAAA GGGCAGCGAA ACCGCGAnGT CAAGCAAATC CCATAAAGTT GTTCTCAGTT 240  
 CGGATTGTAG TCTGCAACTC GACTACATGA AGCTGGAATC GCTAGTAATC GTAGATCAGC 300  
 30 ATGCTACGGT GAATACGTTT CCGGGTCTTG TACACACCGC CCGTCACACC ACCGAGAGTTT 360  
 GTAACACCCG AAGCCGGTGG AGTAACTTTT AGGAGCTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3565:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3565:

CAAACCATTT GTAGCTATTT GTAACCTTA TATTGATATT GTTCCTGGAC ATGTTCACTT 60  
 GAGAGAGCTT GCAGATATAG CTAAAGAAGC AATTAGAGAA GCCGGTGCCA TTCCATTTGA 120  
 ATTCAATACA ATTGGTGTG ATGATGGAAT AGCTATGGGA CATATCGGAA TGCGATATTC 180  
 50 TCTACCATCA CGTGAAATTA TTGCAGATGC AGCTGAAACT GTAATTAACG CTCATTGGTT 240  
 TGACGGCGTA TTTTACATTC CTAATTGTGA CAAGATTACA CCCGGTATGA TTTTAGCAGC 300

TGCACATGGA AAAGCATTAA CACTTTCATC AATGTTTGAA

400

(2) INFORMATION FOR SEQ ID NO: 3566:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3566:

AAATTACGTA CatATTTAAA GCTGACGGCA CTATGACTGC AGGAACATCT GCCCCACTTT 60  
 CTGATGGTGC AGGATTTGTA GTTTTAATGT CTGGAGATAA AGTGAAAGAA CTCGGcGTGA 120  
 CACCTATTGC ACGATTCGTT GGTTTTAAGG CAGTAGGCGT TGACCCGAAA ATTATGGGTA 180  
 TTGGGCCTGC ATATGCGATT CCTGAAGTAT TGTCACCTCAG CAATCTATCT GTTGAAGACA 240  
 TTGATTTGAT CGAATTGAAC GAAGCATTTG CTTCTCAAAC GATTGCATCT ATTAAAGAAG 300  
 TAGGTCTAGA TATATCACGT ACGAATGTGA ATGGTGGCGC TATTGCTTka GGTCATCCAT 360  
 TAGGTGCTAC AGGCGCaATG TTAACCGCGC GTTTACTtTAA TGAAATGGGT AGACGTCCCG 420

(2) INFORMATION FOR SEQ ID NO: 3567:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3567:

TACGGGAAGT AGCTCAGCTT GGGTAGAGCA CTTGGTTTGG GACCAAGGGG TCGCAGGTTc 60  
 GAATCCTGTC TTCCCGATAT ACTGTAATTA TTATGGGGGC TTAGCTCAGC TGGGAGAGCG 120  
 CCTGCTTTGC ACGCAGGAGG TCAGCGGTTC GATCCCGCTA GTCTCCACCA TATTATTTAC 180  
 AAATATATA AGGCGGTGTA GCTCAGCTGG CTAGAGCGTA CGGTTcATAC CCGTGAGGTC 240  
 GGGGGTTCGA TCCCTCCAC CGCCACTATT TATTAGTTGT AAAATTATAT TTAGGACCTT 300  
 TAGCTCAGTT GGTTAGAGCT AACGGCTCAT AACCGTTCGG TCGCAGGTTc GAGTCCTGCA 360  
 GGTCcCATAT AATTTTGGAG GAATACCCAG TCCGGCTGAA 400

(2) INFORMATION FOR SEQ ID NO: 3568:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3568:

	TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG CTGCGCTTCT	60
10	TCCACTGGAT GATTACACAG ACCAATCGTT GGCAGTTTGT CCAAACGTTT GCGATTCTGGT	120
	GTTTCAGAAA TCATCGGCAT CGCGTCATTC AATGATTCAT ATGCATCTAA AGCAATAGAA	180
	GATAATGTGT CTGGCACATA TACCCATGCC AACGTATCAG TAGACGTATG ATGTTCTGCT	240
15	ACCGCAAAAA CAGTTGTCTC TGGAnTATAC ACACCTGATT GTTTTAATCC TTGTCTGACA	300
	TTTGACGAT TACATATCAT CGCTAATAAC TTAGCATTnA AAACCGCTTG ATGCGCCACC	360
20	ACAAGCCCCA CATTCAAGT GATGGCATGG nTGTGGGTTh	400

(2) INFORMATION FOR SEQ ID NO: 3569:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3569:

	CCCCGACCTC ACGGGTATGA ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA	60
	GTTTGTAAT AATATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG	120
35	CAGGCGCTCT CCCAGCTGAG CTAAGCCCC ATAATAATTA CAGTATATCG GGAAGACAGG	180
	ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT ACCAAGCTGA GCTACTTCCC	240
	GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC	300
40	TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA	360
	TCGAACCGGT ACGTGATCAC TCACCGCAGA TTTTAAGTCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3570:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 542 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3570:

55

GTTTTTATCC GTTGAGCGAT GGCCnTCCCA TGGGGACCTA CCGGATCACT AAGTCCGTCT 120  
 TTTTCGACCCT GCTTCGACTT GTAGGTCTCG CAGTCAAGCT CCCTTATGCC TTTACACTCT 180  
 5 ATGAATGATT TCCAACCACT CTGAGGGAAC CTTTGAGCGC CTCCGTTACC TTTTAGGAGG 240  
 CGACCGCCCC AGTCAAACCTG CCCGCCTGAC ACTGTCTCCC ACCACGATAA GTGGTGCGGG 300  
 10 TTAGAAAGCC AACACAGCTA GGGTAGTATC CCACCAGCGC CTCCACGTaA GyTAGCGCTC 360  
 ACGTTTCAAA GGCTCCTACC TATCCTGTAC AAGCTGTGCC GAATTTCAAT ATCAGGCTAC 420  
 AGTAAAGCTC CACGGGGTCT TTCCGTCCTG TCGCGGGTAA CCTGCATCTT CACAGGTACT 480  
 15 ATGATTTTAC CGAGTCTCTC GTTGAGACAG TGCCCAAATC GTTACGCCTT TCGTGCGGGT 540  
 CG 542

(2) INFORMATION FOR SEQ ID NO: 3571:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 619 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3571:

30 ATGCCCCGACC ACATGGAGCT TCCAATCCCA TTGCTCTAAC CAATGAGCTA CTGAACCATa 60  
 aTaAAAAATGT AAtGATGGCG GTCTCGACGG GAATCGAACC CGCGATCtCn GCGTGACAGG 120  
 CAGGCGTGTT AACCCCTACA CTACGAGACC TATAAAATAT TGCGGGAGGC GGATTTGAAC 180  
 35 CACCGGACTT CGGGTTATGA GCCCGACGAG CTACCGAACT GCTCCATCCC GCGATAATAA 240  
 AAAATAATGG CGGAGGAAGA GGGATTCTGAA CCCCCGCGGC CCGTTAAGGc CCTGTCTGGTT 300  
 TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCTCTC ATTATTATAG GTAAATCGCT 360  
 40 ATTAATTATA AAATTAAATG GCGGTCTCGA CGGAATCGA ACCCGCGATC TCCTGCGTGA 420  
 CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG AAGAGGGATT 480  
 45 CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC 540  
 TTGGGTATTCT CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTkCGA CCGAACGGTT 600  
 ATGAGCCGTT AGCTCTAAC 619

(2) INFORMATION FOR SEQ ID NO: 3572:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3572:

5	GGTGAAGACA TCACGTATCA AGAAGCATGG GCAGATGAAG AATATCGTGA AGACTTAAAA	60
	GCAGAATTAA TTGATCAAGC GGTTACTTCA TTGAGCCACA AGATTTATTC AGTGCGATGA	120
	TTCGTGAAAT TGAAACGCAA GATTTCGATA TAGAACATCT AGCGACGGCG ATTCGCAAAG	180
10	TTGAAACATC TACATTAGGT GAAGAAAGTG AAAATGACTT TATCGGGCTG TTCAGCGATA	240
	TGGATTGAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA ACGTACTGCT TTAATCTCTA	300
	AAGTCATGGT TAATCTTGAC GACTTACCAT TCGTTCACAG TGACATGGAA ATTGATATGT	360
15	TAGGTGATGC ATATGAATTC CTAATCGGGC GCTTTGCGGC	400

(2) INFORMATION FOR SEQ ID NO: 3573:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3573:

	CAAATCGTAA CTCGCCGGTT CATTCTACAA AAGGCACGCC ATCACCATT AACGGGCTCT	60
30	GACTACTTGT AAGCACACGG TTTCAGGTTC TATTTCACTC CCCTTCCGGG GTGCTTTTCA	120
	CCTTTCCCTC ACGGTACTGG TTTACTATCG GTCACTAGAG AGTATTTAGC CTTAGGAGAT	180
	GGTCCTCCCA GATTCCGACG GAATTTACAG TGCTCCGTCG TACTCAGGAT CCACTCAAGA	240
35	GAGACAACAT TTTCGACTAC AGGATTATTA CCTTCTTTGA TTCATCTTTC CAGATGATTC	300
	GTCTAATGTC GTCCTTTGTA ACTCCGTATA GAGTGTCTTA CAACCCCAAC AAGCAAGCTT	360
40	GTTGGTTTGG GGCTCTTCCC ATTTGCTCG CGGCTACTAA	400

(2) INFORMATION FOR SEQ ID NO: 3574:

(i) SEQUENCE CHARACTERISTICS:

45	(A) LENGTH: 1051 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3574:

55	TCCCTCAAAG ATGGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC ATGTGGCAGC	60
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TTTACTTACT ATCTAGTTTT GAATGTATAA ATTACATTCA TATGTCTGGT GACTATAGCA 180  
 AGGAGGTCAC ACCTGTTCCC ATGCCGAACA CAGAAGTTAA GCTCCTTAGC GTCGATGGTA 240  
 5 GTCGAACTTA CGTTCGCTA GAGTAGAAGC TTGCCAGGCA TAATATTAAT CCACAGTAGC 300  
 TCAGTGGTAG AGCTATCGGC TGTTAACCGA TCGGTCGTAG GTTCGAGTCC TACCTGTGGA 360  
 10 GCCATGGCTC cTtGGTCAAG CGGTAAAGAC ACCGCCCTTT CACGGCGGTA ACACGGGTTC 420  
 GAGTCCCGTA GnAGTCATTA TTTTGGAGAA TTAGCTCAGC TGGGAGAGCA TCTGCCTTAC 480  
 AAGCAGAGGG TCGGCGGTTC GAACCCGTCA TTCTCCACCA TTTTGATTAT TAAATTATAT 540  
 15 GAATAAGCTG GAGGGGTAGC GAAGTGGCTA AACGCGGCGG ACTGTAAATC CGCTcCTTCG 600  
 GGTTCGGCAG TTCGAATCTG CCCCCCTCCA CCATCTATAT ATTGGGCTAT AGCCAAGCGG 660  
 TAAGGCAACG GACTTTGACT CCGTCACTCG TTGGTTCGAA TCCAGCTAGC CCAGCCATTA 720  
 20 GAGCCATTAG CTCAGTTGGT AGAGCATCTG ACTTTTAATC AGAGGGTCAG AGGTTCGAAT 780  
 CCTCTATGGC TCACTACTTG CACTTTCCAT TTTTGGGAAG TGCTTTTTTT TAGGTTCTcC 840  
 ACCAAATGTG GTGGGtATAT AATTAAAGA ACTATTTTAA AAATACAAC TTTAGAGCTT 900  
 25 TTATTATTAG GCGGCCAGTC CATTATTGGG CTTGGTTGTC TTCTTTTTTT CTCCTTTGtA 960  
 CAAGCTGAAA ATCATCATT TACGTGctTA AAGTGTGAAA TTTCTGTAAC CAAAAGAATn 1020  
 30 CACTTGATTA ATTnnATCTA TATAATGCCT C 1051

## (2) INFORMATION FOR SEQ ID NO: 3575:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3575:

GTGGAGCGCT TAGAAGTGAG AATGCAAGTG TGAgTAGCGA AAGACGGGTG AGAATCCCGT 60  
 CCACCGATTG ACTAAGGTTT CCAGAGGAAG GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA 120  
 45 AGCTGAGGCC GACACGTATG GCGATGGATA ACAGGTTGAT ATTCCGTGTAC CACCTATAAT 180  
 CGTTTAAATC GATGGGGGGA CGCATAGGAT AGGCGAcGTG sCGATTGGAT TGCACGTCTA 240  
 50 AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTgATGGGGA 300  
 GAAGACATTG TGTCTTCGAG TCGTTgATTT CACACTGCCG AGAAAAGCCT CTAGATAGAA 360  
 AATAgGTGCC CGTaCCGCAA AaCCGACACA GGTAGTCCAA GATGnGAATT CTAAnGTGAA 420

55

## (2) INFORMATION FOR SEQ ID NO: 3576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3576:

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TTTGTTCCCTT TTTTAATTTA TATATTTAAA ATACACATAT TCAAGAGCTC GAGATATAAG      60
TCAATGTACT AGGCACACAA TTTAATATTG ACAGTAATTA ACCGAACGAA AATGCGCCCC      120
GGGGCCCCCA CATAGAGAAT TTCGAAAAGA AATTCTACAG ACAATGCAAG TTGGCGGGGC      180
CCCAACATAG AAGCTGGCCA ATAGTTAGCT TTCAATAATG TGCAAGTTGG GGTAAGGGCC      240
CCAACACAGA AGCTGGCCAA TAGTCAGCTT TCAATAATGT GCAAGTTGGG GTAAGGGCCC      300
CAACACAGAG AATTTGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGCCCCAACA      360
CAGAAGCTGG GCCAATAGTC AGCTTTTCCA ATAATGTGGC      400

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## (2) INFORMATION FOR SEQ ID NO: 3577:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3577:

```

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT      60
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT      120
ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAC TAACCACTCC      180
TCTTAACCTT CCAGCACCGG GCAGGCGTCA GCCCTATACA TCACCTTACG GTTTAGCAGA      240
GACCTGTGTT TTTGATAAAC AGTCGCTTGG GCCTATTACG TGCGGCTCTT CTGGGCGTTA      300
ACCCTAAAGA GCACCCCTTC TCCCGAAGTT ACGGGGTCAT TTTGCCGAGT TCCTTAACGA      360
GAGTTCGCTC GCTCACCTTA GAATTCTCAT CTTGACTAAC      400

```

## (2) INFORMATION FOR SEQ ID NO: 3578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3578:

5 TAACTTAACA CGACTTCTTA AGTCATTTAG TTTTAATGTT TGATGTGTTT CTGCTAAACC 60  
 AATCTCCCAA GGAACACCGG CATGCTGAAT ACTCGTTTTG GGTGAAGCCC TGTACCACCA 120  
 TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCAGCA TGCAATGGTA 180  
 10 CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT CGCATTTTTTC 240  
 AAATCATGTA TCAGTTGCGC TAAATCTTCT ATTGAATAAA TATCATGATG TGGCGGTGGT 300  
 GAAATCAGAC CGATACCTGG CGTTGGACCC TCTTGTCTTC GCAATCCACG GATATACCTT 360  
 15 AGTACCAGGT AATTGGACCA CCTTCACCAG GCTTTGCACC 400

## (2) INFORMATION FOR SEQ ID NO: 3579:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3579:

25 AGCTACACCG CTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG ATCGAACCGC 60  
 30 TGACCTCCTG CGTGCAAAGC AGGCGCTCTC CCAGCTGAGC TAAGCCCCCA TAATAATTAC 120  
 AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC AAGTGCTCTA 180  
 CCAAGCTGAG CTAATTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC CCATAACCTC 240  
 35 TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT TTTATTGAAA 300  
 ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA TTTTAAGTCC 360  
 TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3580:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3580:

50 ACGTAAATAA CCATAACGAC GTGCCTCAAA GGCATTTGTA GAGACTTTCG CAAATGCGAT 60

TATGCGATCA GCCATTTCTG CAAGGCCACC GCCACTCGGT AATAAGCCAA CACCTGCTTC 180  
 AACAAGACCG ATATATGTTT CACTTGCAGC GACAACAATA GGTGAGTAAA GTACAAGCTC 240  
 5 ACAGCCACCG CCTAAGGCAC GACCTTGAAC AGCTGTGACT ACTGGTTTCA AACTATACTT 300  
 CAAACGATTA AAGCTATAAT GTAATTTATC AATTGATTGT GCACGACATC ATCTACAAGA 360  
 10 CCGTCTTCCA TGCGCCTTTT TCCATTAAGA AAGGGTTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3581:

ATGTCATTGT TGGTACGGCT TTTCCAGAAG GATTACAAGG CCAAACATT GCACGAACGA 60  
 TTGCATTGCG TGCGGATTAT CTGACACGGT ACCGGGTCAA ACAGTGAATC GCTACTGCTC 120  
 25 ATCAGGATTA CAAACCATGC GATTGCAGCC AATCAAATTA TGGCTGGTCA AGGAGATATA 180  
 CTTGTAGCTG GTGCGTTGAA TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA 240  
 ACAATCCAAC CTTACAATAT GATGATATAG GTGCGTCATA TCCTATGGGT TTAAGTCTG 300  
 30 AAAATGTAGC ATCCCAATTT GACGTATCAC GCGAAGATCA AGATGCTTAT GCTGTCAGAA 360  
 GTCATCAACG TGCCTATGAC GCACAACGTG ATGGGTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3582:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60  
 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA GACCTTGCGG 120  
 50 TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT 180  
 AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT 240  
 CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC 300

ATTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGT

400

(2) INFORMATION FOR SEQ ID NO: 3583:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3583:

15	AAGCAGGCGC TCTCCCAGCT GAGCTAAGCC CCCAAATAGG TATTAAATTA ATGGTGGGCC	60
	TAAGTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT GCGCTCTAAC CAGCTGAGCT	120
	ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA ATACAATATG TCACGTTATT	180
20	CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA AAGGAGGTGA TCCAGCCGCA	240
	CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC ATTTGTCCCA CCTTCGACGG	300
	CTAGTCCTTA AAAAGGTTAC TCCACCGGCT TCGGGTGTTA CAACTCTCG TGGTGTGACG	360
25	GGCGGTGTGT ACAAGACCCG GGAACGTATT TCACCGTAGC	400

(2) INFORMATION FOR SEQ ID NO: 3584:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3584:

	ACTTATTTGG CGATATTTTA AGTGATGAAG CTTCAGTGAT TCCTGGTTCA CTTGGTTTAT	60
40	CACCTTCTGC TAGTTTTAGT AACGATGGTC CAAGATTGTA TGAGCCTATT CATGGATCAG	120
	CACCAGATAT TGCAGGTAAA AACGTTGCCA ATCCATTTGG AATGATTCTA TCTTTAGCGA	180
	TGTGTTTACG TGAAAGCTTA AATCAACCAG ATGCTGCAGA TGAATTAGAA CAACATATTT	240
45	ATAGCATGAT TGAACATGGG CAAACGACAG CAGATTTAGG CGGCAAATTG AATACTACTG	300
	ATATTTTCGA AATTCTATCT CAAAAATTGA ATCACTAAGG GGGGAGATGT AAATGGGGTC	360
50	AAACATTATT TGACAAAGTG TGGGACAGAC ATGTGTTATA	400

(2) INFORMATION FOR SEQ ID NO: 3585:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3585:

	ACTGATGACA ATTTTATCTG CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC	60
10	TGTTTTTCGAA ACTAATTTTA CCGCGATATC TGCATCTTTA TTCGCATTTT TCAAATCATG	120
	TATCAGTTGC GCTAAATCTT CTATTGAATA AATATCATGA TGTGGCGGTG GTGAAATCAG	180
	ACCGATACCT GCGGTTGACC CTCTTGTCTT CGCAATCCAC GGATATACCT TAGTACCAGG	240
15	TAATTGACCA CCTTCACCAG GCTTTGCACC TTGCGCAACT TTAATTTGAA TTTCTTTGGG	300
	CATGTTGTAA ATAATCACTA GTTACACCAA AACGCCCAGA AGCAACTTGT TTAATCGCAC	360
	TTACTTTGGT GGCTTCCATC AACTTGTA CTATAACGGT	400

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(2) INFORMATION FOR SEQ ID NO: 3586:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3586:

	TACAAGTATT ACCATTATCT CnAGAGGATT CTAGATAAGG GGCATGGATC ATTTGTCTTC	60
	TTATGAATTT GAGCCAGATA AAGAATCTAT CTTAAGTGTA ATCTTGACCT CAATATGTTG	120
35	AGAGTTTGAT TTACGGAACA ATATTAGACG CAAAAGCAAG TGAGCATGCA ACACGTATGA	180
	CTGCGATGAA AAATGCCACT GATAATGCAA CTGAACTTAT TGATGACTTA TCATTAGAAT	240
	ATAACAGAGC GAGACAAGCA GAAATTACGC AACAAATTAC TGAAATTGTT GGTGGTTCCG	300
40	CAGCGCTTGA ATAATATTTA AnGGAGGAAA ATAGCATGGG AATTGGCCGT GTACTCAAGT	360
	TATGGGTCCT GTAATTGATG TTCGATTGA ACATAACGAG	400

45

(2) INFORMATION FOR SEQ ID NO: 3587:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3587:

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AGGATTGAA CCTGCGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120  
 CCCGTATAAT TAACGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180  
 5 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATGGTG CCGAGGACCG 240  
 GAATCGAACC GGTACGTGAT CACTCACC GC AGGATTTTAA GTCCTGTGCG TCTGCCAGTT 300  
 CCGCCACCCC GGCACTATAA AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC 360  
 10 CTTGGCAAGG TTGTATTCTA CCGCTGAACT ACTTCTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 3588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3588:

TACTATTGAC ATGTGTGAAC CCTATGTCCG ATTATTTTCG GACCTATTTT CTAATGCAGC 60  
 25 TATTATTTTT GACAGATTCC ATATCGTTCA ACATTTAAAT AGAGAACTTA ATAAGTATCG 120  
 TGTACAAGTT ATGAATGAAT ACCGTAATAA AAAAGGACCT GATTATACAA TTTTAAAGAA 180  
 TAACTGGAAA GTCCTATTGA TGGATACTAG TAAACCATA TTTAGTAAAT ACAGATGGAA 240  
 30 TAAATCTTTT AAGGGCTTAT AAACGCTCAT CTGACATTGT AGAATTCATG CTTTCAAAG 300  
 ACATATACT ACACACTCC TACGAACCTG TCCAGGGATT ACGAAAAGAC CTAAGGGTAT 360  
 35 GTAATTGGGC CTAAATTTAT TAATCGTTTA AATTCCGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3589:

AGAGCGAACG GACGAGAAGC TTGCTTCTCT GATGTTAGCn GCGGACGGGT GAGTAACACG 60  
 TGGATAACCT ACCTATAAGA CTGGGATAAC TTCGGGAAAC CGGAGCTAAT ACCGGATAAT 120  
 50 ATTTTGAACC GCATGGTTCA AAAGTGAAAG ACGGTCTTGC TGTCACCTTAT AGATGGATCC 180  
 GCGCTGCATT AGCTAGTTGG TAAGGTAACG GCTTACCAAG GCAACGATGC ATAGCCGACC 240

AGTAGGGAAT CTTCCGCAAT GGGCGAAAGC TGACGGAGCA ACGnCGCGTG AGTGATGAAG 360  
 GTCTTCCGAT CGTAAAACTC TGTATTAGG GAAGAACATA 400

(2) INFORMATION FOR SEQ ID NO: 3590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3590:

GTTAgGAGAG CGTTCTAAGG GCGTTGAAGC ATGATCGTAA GGACATGTGG AGCGCTTAGA 60  
 AGTGAGAATG CCGGTGTGAG TAGCGAAAGA CGGGTGAGAA TCCctCCACC GATTGACTAA 120  
 GGTtTCCAGA GGAAGGCTCG TCCGCTCTGG GTTAGTCGGG TCCTAAGCTG AGGCCGACAg 180  
 gTAaGGCGAT GGATAACAGG TTGATATTCC TGTACCACCT ATAATCGTTT TaATCGATGG 240  
 GGGGACGCAT AGGATAGGCG AAcGTGcGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAg 300  
 TATTAGGCAA ATCCGGTACT CGTTaAGGCT GAGCTGTGAT GGGGAGAAGA CATTGwGTCT 360  
 TCGAGTCGTT GATTTCACAC TGCCGAGAAA AgCCTCTAGA TAGAAAATAG GTGCCCCGTAC 420  
 CGCAAACCGA CACAGGTAAT CCAAGATGAG AATTCTAAGG TGAGCGAGCG AACTCTCGTT 480  
 AAGGAACTCG GCAAAATGAC CCCGTAACT 509

(2) INFORMATION FOR SEQ ID NO: 3591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3591:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60  
 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120  
 TCGAACCGCT GACCTCCTGC GTGCAAAGCA GCGCTCTCC CAGCTGAGCT AAGCCCCCAA 180  
 ATAGGTATTA AATTAATGGT GGGCCTAAGT GGACTCGAAC CACCGACCTC ACGCTTATCA 240  
 GCGTGCGCT CTAACCAGCT GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA 300  
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 360



## (2) INFORMATION FOR SEQ ID NO: 3592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3592:

TGGGnAACGC AACATCCTTT TCCAACCTTAA CATATATTTT GGGACCTTaG CTGGTGGTCT 60  
 GGGCTGTTTC CCTTTCGAAC ACGGACCTTA TCACCCATGT TCTGACTCCC aAGTTAAATT 120  
 AATTGGCATT CGGAGTTTGT CTGAATTTCGG TAACCCGAGA GGGGCCCTC GTCCAAACAG 180  
 TGCTCTACCT CCAATAATCA TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA 240  
 GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA 300  
 ACGTAAGTCG GTTCGGTCct CCATTcAGTG TTACCTGAAC TTCAACCTGa CCAAGGGTAG 360  
 ATCACCTGGT TTCcGsGTsT ACGACCAAAT AsTAAACGCC CTATTCAGAC TCGCTTTTCGC 420  
 TAnGGCTCCA CATTACTGGn 440

## (2) INFORMATION FOR SEQ ID NO: 3593:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3593:

TAAACGAACC AATTTTATTT GGTGCACCAC TAGTATTGAA TCCTGTGTTC TTTATTCCAT 60  
 TTGTATTAGC ACCAATTGTT AACGTATGGA TTTTCAAACCT TTTCGTTGAA GTGTTAGGAA 120  
 TGAATAGTTT TAGTGTGAAT TTACCTTGGA CAACACCAGG TCCATTGGGC ATTATCATGG 180  
 GTACAGGTTT TGGTTTATGG TCATTTCGTAC TAGCTATTAC TTTGATTGTT GTAGATATTA 240  
 TTATnTACTA CCCATTCCCTA AAAGTTTATG ATAGTGAAAT TCTTGATGAA GAAGAAGGAC 300  
 GTAAAGAAAG TAATTCAGAT TTAAAGAAA AAGTTGCAGC AAACCTTTGA TACGAAAAAA 360  
 GCTGATTCAA TTTTAGCGGC AAGTGGTGTA TCAGACGATG 400

## (2) INFORMATION FOR SEQ ID NO: 3594:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3594:

AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60  
 10 TGCCTTCTGa TATGCTATGT ATTCACATAT CGATAACATG ACATAACTCA TGCTGGGTTT 120  
 CCCCATTCGG AAATCTCTGG ATCAAAGCTT aCTaCAGCTC CCCAAAGCAT ATCGTCGTTA 180  
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240  
 15 TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT 300  
 TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAAATAA TTAACTCAT TGTCTGCTAA 360  
 ACGTTTTCTT TTATAAAAAG ATTTAAAcGC GTTAtTAATC CTCTCGCTC 409

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(2) INFORMATION FOR SEQ ID NO: 3595:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3595:

30

AATATAAGCC CTGGATCATA CATGACCTGT ATTTGGGCAA TCCCTTCTGC TACATCTTCT 60  
 GCCCACTCAT TCAATATTTG TTTTGCAATA TCATCACCTT CTTAGCTGC TTCAAACAAT 120  
 35 ACTGGCACAT GTGTGCTTCT CGTAAATCCT CCGGCAATCA TGCGCTTTTT CAATGCACTC 180  
 GTTGCGAGCAC GTTGCTCAAA CGTTGTATTT TCAGTTGGAC GATACAATAA ATACCCAACT 240  
 TCATTTGCCT TATGAAGCTC ACCATTATCA ATATGACCTT GGATTATTCT TGTACGCACC 300  
 40 CCCAATGGCC TGGTACCAAG CGTCCATACA AAAGATCCGT TCTGGCTTGG ATATTGGATG 360  
 GTAATTTCCA ATTCGGCCTA GTTAATGGCA GCGGTTTTAA 400

40

(2) INFORMATION FOR SEQ ID NO: 3596:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 596 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3596:

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CTGCCGAACC CGAAGAGCGG ATTTACAGTC CGCCGCGTTT AGCCACTTCG CTACCCTCCA 120  
 GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG ACGGGTTCGA CCGCCGACCC 180  
 5 TCTGCTTGTA AGGCAGATGC TCTCCAGCT GaGCTAATTC TCCAAAATAA TGA CTCTCTAC 240  
 GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGtGTCT TAACCGCTTG ACCAAGGAGC 300  
 CATGGCTCCA CaGGTAGGAC TCGAACCTAC GACCGATCGG TTAACAGCCG ATAGCTCTAC 360  
 10 CACTGAGCTA CTGTGGaTTA ATATTATGCC TGGcAACGTT CTACTCTAGC GGAACGTAAG 420  
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 480  
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 540  
 15 AGTAAAAGTG ATTTTGCTTC GCAAAACATT TATTTTGATT AAGTCTTCGA TCGATT 596

## (2) INFORMATION FOR SEQ ID NO: 3597:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3597:

TCATCTTGAG GGGGGCTTCA TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 60  
 30 TACCCAGCTA TGCCGTTGGC ACGACAAGTGT GTACACCAGA GGTATGTCCA TCCCGGTCTCT 120  
 CTCGTACTAA GGACAGCTCC TCTCAAATTT CCTACGCCCA CGACGGATAG GGACCGAACT 180  
 GTCTCAGCAG GTTCTGAACC CAGCTCGCGT ACCGCTTTAA TGGGCGAACA GCCCAACCCT 240  
 35 TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT 300  
 CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCCG GGTAGCTTTT ATCGTTGAG 360  
 40 CGATGGCCCT TCCATGCGGA ACCACCGGAT CAATAAAGTC 400

## (2) INFORMATION FOR SEQ ID NO: 3598:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3598:

AACCAACGGC AGCAACTACA TGACCTAATT CTTGTGCTGA CTCTACATTT AGTAGCTCTA 60

CACTTCAATT GTACCAATCA ATCGTTGACG ATCTTGATCG TAACGCCATG TAGCAATACC 180  
 ACGATACTGT CCGTCACGAC TCGCGTATGC ATGCGCACTT GCTTCTGCAC CACGCGTATC 240  
 5 ATTTCTGTGTT GCTAAAACAA CAGCATGTAT GCCATTGATA ACACCTTTAT TATGTGTTGC 300  
 TGCACGATGA ATATCTACTT GGGCCAATAC AGAAGCACGT TCCATcGTTT GcaACCTCTT 360  
 CTCCAGTTCT CTCGCCCCTT GGCTAAATCT TTAACAT 397

(2) INFORMATION FOR SEQ ID NO: 3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3599:

AACCCTTGGG ACCGACTACA GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT 60  
 CCCCCTCGAT GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCggggTA GCTTTTATCC 120  
 25 GTTGAGCGAT GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG 180  
 CTCGACTTGT AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTC 240  
 CAACCATTCT GAGGGAACCT TTGAGCGCCT CCGTTACCTT TTAGGAGGCG ACCGCCCCAG 300  
 30 TCAAAGTGCC CGCTGACAC TGTCTCCAC CACGATAAGT GTGCGGGTTA GAAAGCCAAC 360  
 ACAGCTAGGG TAGTATCCCA CCAGCGCCTC CAACGTAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3600:

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA ATCGCTATCT GAATCTGAGT CGCTATCTGA 60  
 GTCTGAGTCG CTATCTGAAT CTGAGTCGCT GTCTGAATCT GAATCACTGT CTGAGTCTGA 120  
 50 GTCGCTGTCT GAGTCTGAAT CGCTGTCAGA ATCTGAGTCG CTATCTGAGT CTGAATCTGA 180  
 ATCACTGTCT GAGTCCGAAT CGCTATCTGA ATCTGAATCG CTATCTGAGT CTGAGTCGCT 240  
 ATCCGAATCT GAGTCGCTAT CTGAGTCTGA GTCGCTATCC GAGTCTGAAT CGCTGTCTGA 300

GGTCTGGAAT CTGA<sup>n</sup>TCGCT AACTGAAATC TGAGTCGCTA

400

(2) INFORMATION FOR SEQ ID NO: 3601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3601:

15 ATTTAATACC TATTTGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 60  
 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTATTTGTA CATTGAAAAC TAGATAAGTA 120  
 AGTAAAATAT AGATTTTACC AAGCAAACC GAGTGAATAA AGAGTTTTAA ATAAGCTTGA 180  
 20 ATTCATAAGA AATAATCGCT AGTGTTTCGAA AGAACATCCA CAAGATTAAT AACGCGTTTA 240  
 AATCTTTTTA TAAAAGAACG TAAC TTCATG TTAACGTTTG ACTTATAAAA ATGGTGAAAA 300  
 CATAGGTAA GTTATTAAGG GCGCACGGTG GGATGCCTTG GCACTAGAAG CCGATGAAGG 360  
 25 G<sup>n</sup>CGTTACTA ACGACGATAT GCTTTGGGGA GCTGTAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 3602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

GCTGTCTGAG TCGGAATCAC TG<sup>n</sup>GGAGTC AGAATCGCTG TCTGAGTCGG AATCACTGTC 60  
 40 GGAATCTGAA TCGCTATCTG AATCTGAATC GCTATCTGAA TCCGAGTCAC TGTCTGAGTC 120  
 AGAATCG<sup>n</sup>TA TCTGAATCTG AGTCACTGTC GGAATCTGAG TCACTGTCTG AGTCAGAATC 180  
 45 GCTATCTGAA TCCGAGTCAT TGTCTGAGTC GGAATCGCTC GCTGAGTCGG AATCGCTTGC 240  
 TGAATCTGAA TCACTCGCTG AGTCTGAATC ACTTGCTGAA TCTGAATCAC TCGCTGAATC 300  
 TGAACCACTA TCTGATGTAG GAATCACTAC CCGAATCTGA A<sup>n</sup>CGCTATCT GAATAAGAAT 360  
 50 CGCTGCCAGA TCTGAACCTG GGGTCAGAAT CTGAAT 396

(2) INFORMATION FOR SEQ ID NO: 3603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3603:

	TTTCTTATCT GTAATTTTAT CGTAAGATTT TTTCGCAATG AGATTGGAT CGTnTTTGTC	60
10	CACTACAATA TCTAATAGTT TTACTTTAAG TCCAGCATT CAAAAAGTG CTGCCAGTTG	120
	AGCGCCCAATT GTGCCTGCGC CAAGAACGGT TACTTTATTA ATTGTCATAG TGATTCTCTCC	180
	AATTTAGTTG AGGATAAGAT AACCATTAAAG ATAATTGGAA TAACGTGCT ATTTTATAAA	240
15	ATTAATTAAG TATCTTTGAC AGTCATCTTA GCCTCTTATT TAAGGaAAAA GCTTTATGCT	300
	TAAATAAGT CTTTTTTAGT GAAATTAATG CATCTCATAT AATTATTTGC TATTTATACG	360
	AAAGCmGaAT CTCCAGTCaA AGCGCGTCCA ATTACTAAGG CATTAAATTC ATGTGTACCT	420
20	TCGTACGTGT AAATCGCTTC TGCATCAGAG AAGAAACGTG CAATATCATA ATCGTCAGCT	480
	AGTATGCCAT TACCACCTGT AATACCGCGG CCCATAGCTA CtnTCTCAC	529

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(2) INFORMATION FOR SEQ ID NO: 3604:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3604:

35	CACAAGATAA GCATTGTAGA TGTGGATGCT TTAAGTGGC AAGCGATTGG TCGTCCTAAA	60
	ACAGGTACAT ATGCGCTATC TGACCTAGTC GGTTTAGATA TTGCAGTGTC TGTAATTAAA	120
	GGCATGCAAC AAGTACCTGA AGAAACACCT TATTTTCATG ATGTCAAAT TGTAATACG	180
40	TTGTTTGACA ATGGCGCACT CGGACGTAAA ACGAAACAAG GATTTTACAA AAAGGATAAA	240
	GAAACTAAAG CTCGACTTGT TTACGATGTT GAAAAACAAG ATTATGTACC TGTATCGCAA	300
45	CCACAATTAC CAATTTTAAA TGAATTTAAT AAAGACTTAG TGCaTAACCT TGATACCATA	360
	TTCCAATGCG CAAGACGAGC GGGGACTATT TTTATGGGG	399

(2) INFORMATION FOR SEQ ID NO: 3605:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3605:

5 ATCACTTGAG GCTAGCCCTA AAGCTATTTC GGAGAGAACC AGCTATCTCC AGGTTGATT 60  
 GGAATTTCTC CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT 120  
 CCATTGAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 180  
 10 CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 240  
 TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT 300  
 TAACGGGCTC TGGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTCAC TCCCCTTCCG 360  
 15 GGGTGGCTTT TCACCTTTCC CTCACGGTAA TGGGTTCACT 400

## (2) INFORMATION FOR SEQ ID NO: 3606:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3606:

AAATCCTGCG GTGAGTGATC ACTAACCCGG TTCGATTCCG GTCCTCGGCA CCATTTTCAA 60  
 TAAAAACATA TGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGACTACGGA TCAAGAGGTT 120  
 30 ATGGGTTCGA CTCCTATCGG GCGCGTTAAT TATACGGGAA GTAGCTCAGC TTGGTAGAGC 180  
 ACTTGGTTTG GGACCAAGGG GTCGCAGGTT CGAATCCTGT CTTCCCGATA TACTGTAATT 240  
 35 ATTATGGGGG CTTAGCTCAG CTGGGGAGAG CGCTGCTTT GCACGCAGGA GGTCAGCGGT 300  
 TCGATCCCGC TAGTCTCCAC CATATTATTT ACAAATAATA TAAGGCGGTG TAGCTCAGCT 360  
 GGCTAGAGCG TACGGTTCAT ACCCGTGAGG TCGGGGGTTC 400

40 (2) INFORMATION FOR SEQ ID NO: 3607:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3607:

GGGTGTGCTT CTGATATGCT ATGTATTAC ATATCGATAA CATGACATAA CTCATGCTGG 60  
 GTTTCCTTTC CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 120

TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA CATGAAGTTA CGTTCTTTTA 240  
TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCTT TTCGAACACT AGCGATTATT 300  
5 TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCACCTC GGTTTTGCTT GGTAAATCT 360  
ATATTTTACT TACTTATCTA GTTTnCAATG TACAAATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3608:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3608:

20 TAGTTTTCAA TGTACAAATA ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 60  
TGCAAAAnAGC CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA TTAATGGTGG 120  
GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCCTCTT AACCAGCTGA 180  
25 GCTATAGGCC CATTAAATTG AATGAACAAA CATTCAAAC TGAATACAAT ATGTCACGTT 240  
ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300  
GCACCTTCCG ATACGGCTAC CTTGTTACGA CTTACCCCA ATCATTGTGTC CCACCTTCGA 360  
30 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3609:

- (i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3609:

AGGGCACTCT TACTGGGCGT GTTAAATTAC TAAnTTCAAT CAGCAGAAGA ACTAGGACAT 60  
45 GGCGCTTTTA AAATTATTGA AACACATGCA TTAAAGATG TACAAGCAGT ATTGGGTTTT 120  
CATAATGACC CATCGCGTTC GGTAGGTACA TTTGCAATCA AAACAGGGGC AATTACATCA 180  
GCAGTAGATC GTTTTGAGTT TCATATTAAA GCGTGGGTG GTCATGCTGC AAACCAGAAC 240  
50 AATGCAACGA TCCAGTTATT GTGTTGGCGC AATTGATTAA TAGTATTCAA TCCATAGTTA 300  
GTAGAAATCT ATCTGCGTTT GATGAAGCGG TAGTAACAAT TGGACAAATA TCATGTGGTA 360



## (2) INFORMATION FOR SEQ ID NO: 3610:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3610:

```

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT      60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC      120
CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA      180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA      240
TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT      300
TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAAATGA ATTTAACTCA TTGTCTGCTA      360
AACGTTTTGC TTTTATAAAA AGATTTAAAC GCGTTGATTT      400

```

## (2) INFORMATION FOR SEQ ID NO: 3611:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3611:

```

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC      60
CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT      120
GGCAACGTTT TACTCTAGCG GAAnTAAGTT GnACTACCAT CGACGCTAAG GAGCTTAACT      180
TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG      240
TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA      300
TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC ACATGTCACC ATGCTTCCAC      360
CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTAAT      400

```

## (2) INFORMATION FOR SEQ ID NO: 3612:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3612:

5 ACCCAGCTCG CGTACCGCTT TAATGGGCGA ACAGCAATCC CTTGGGACCG ACTACAGCCC 60  
 CAGGATGCGA TGAGCCGACA TCGAGGTGCC AACCTCCCC GTCGATGTGA ACTCTTGGGG 120  
 GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC CTTCCATGCG 180  
 10 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAAGT CTCGCAGTCA 240  
 AGCTCCCTTA TGCCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACCTTTGA 300  
 15 GnGCCTCCGT TACCTTTTAG GAGGCGACCG CCCCAGTCAA ACTGCCCCGCC TGACACTGTC 360  
 TCCCACCACG ATAAGTGThC GGGGGTTAGA AAGCCAACAC 400

## (2) INFORMATION FOR SEQ ID NO: 3613:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 487 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3613:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCaA 60  
 30 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTT ATAAGTCAAA 120  
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 180  
 TTTAAAATAA TTTAACTCAT TGTCTGCTAA ACGTTTTCTT TTATAAAAAG ATTTAAACGC 240  
 35 GTTATTAATC TTGTGAGTGT TCTTTGGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 300  
 TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAAA TCTATATTT ACTTACTTAT 360  
 40 CTAGTTTTCA ATGTACAAAT AATGGTGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC 420  
 TTATCAGGCG TGCGCTCTAA CCAGCTGAGC TATAGGcCCA TTTTTTTGaA TGTTAAATAA 480  
 ACATTCA 487

## (2) INFORMATION FOR SEQ ID NO: 3614:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG 60  
 AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG 120  
 5 CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT 180  
 GGTCCCAAAC CAAGTGnTCT ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT 240  
 AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC TCTATnCAAT TGAGCTACGG 300  
 10 GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA TCGAACCGGT ACGGTGATCA 360  
 CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GChAGTTCCG 400

15 (2) INFORMATION FOR SEQ ID NO: 3615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3615:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC 60  
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC 120  
 30 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCTACTCTA 180  
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 240  
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 300  
 35 TCTTTTCTCG TTTCGTGAGA TTCAAACGTT TTTCACTTCGC CAAGCCATTT TTCTTTGTGT 360  
 TTACTTTTTTA TTTTGACGTT TAGGCATAAA AAAAGAGAC 400

40 (2) INFORMATION FOR SEQ ID NO: 3616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3616:

TnGTGTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT 60  
 ATTCACTCGG TTTTGCTTGG kAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA 120  
 55 CAATTTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 180

AAGATGTTCC GAATATATCC TTAGAAAGGA GGnGATCCAG CCGCACCTTC CGATACGGCT 300  
 ACCTTGTTAC GACTTCACCC CAATCATTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 360  
 5 TTACTIONCCACC GGCTTCGGGT GTTACAACT CTCGTnGGTG TGACGGGCGG TGTGTACAAG 420

## (2) INFORMATION FOR SEQ ID NO: 3617:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3617:

CACTAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCCTTTATTC ACTCGGTTTT 60  
 20 GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT TTCTTTTTTAG 120  
 TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT TAAATAAACA 180  
 25 TTCAAAACTG AATACAATAT GTCACATTAT TCCGCATCTT CTGAAGAAGA TGTTCCGAAT 240  
 ATATCCTTAG AAAGGAGGTG ATCCAGCCGC ACCTTCCGAT ACGGCTACCT TGTTACGACT 300  
 TCAnCCCAAT CATTTGTCCC ACCTTCGACG GCTAGCTCCT AAAAGGTTAC TCCACCGGCT 360  
 30 TCGGGTGTTA CAAACTCTCG TGGTGTGACG GGCGGTGTGT 400

## (2) INFORMATION FOR SEQ ID NO: 3618:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3618:

GATATACGCT ATGGCTGGAG CAGTGTGGCC AAATGGCGGA AGACAAACGT TTAATGCGAT 60  
 45 ATACTTAGCG CAAAATATTG GTGTGGCTGT CGGTGCTGCA ATGGGCGGCT TTGTGCGAGA 120  
 ATTTAGCTTT AACTATATCT TTTTAGCCAA TCTTATTATG TATGTTGTGT TTGCGCTTGT 180  
 CCGGTTAACn AATTTAATAT TGAAATTAAT GCGAAAGTTA AATATCCAAC TCATTTAGAT 240  
 50 ATTACTGGTA AAAAGAATAA AGCAAGATTT ATTTCAATTAG TACTAATTTG TGCAATGTTT 300  
 GCAATTTGTT GGGTTGCATA TATTCAATGG GGAGTCTACA ATCGCTTCAT TTTACACAAT 360  
 55 CTATTAATAT TTCAATGGGC ACAATATAGT GTTTTATGGG 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3619:

```

TCGCACGCCT TCGCCTATCC TACTGCGTCC CCCCATCGAT TAAAACGATT ATAGGTGGTA      60
CAGGnAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTGC GCCTCAGCTT AGGACCCGAC      120
TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC      180
ACCCGTCTTT CGCTACTCAC ACCGGCATTG TCACTTCTAA GCGCTCCACA TGTCTTACG      240
ATCATGCTTC AACGCCCTTA GAACGCTCTC CTACCATTTGT CCAAAGGAAA TCCACAGCTT      300
CGGTAATATG TTTAGCCCCG GTACATTTTC GGCGCAGTGT CACTCGACTA GTGAGCTATT      360
ACGCACTCTT TAAATGATGG CTGCTTCTAA GCCAACATCC      400

```

(2) INFORMATION FOR SEQ ID NO: 3620:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3620:

```

TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA      60
CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTTGA      120
GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT CCACACATAG CTACCCAGCT      180
ATGCCGTTGG CACGACAACT GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA      240
AGGACAGCTC CTCTCAAATT TCCTACGCCC ACGACGGATA GGGACCGAAC TGTCTCACGA      300
CGTTCTGAAC CCAGCTCGCG TACCGCTTTA ATGGGCGAAC AGCCCAACCC TTGGGACCGA      360
CTACAGnCCC AAGGATGCGA TGAGCCGACA TCGAGGTGCC      400

```

(2) INFORMATION FOR SEQ ID NO: 3621:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 475 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3621:

5 CCACACCCGc AAATGGTGag CCATAGcAGG ATTCGgaACC TCTGcACCCT CTGATTAAAA 60  
 GTCAGcATGC TCTACCAACT GaGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 120  
 ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG 180  
 10 TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA 240  
 TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAACTGCC TGGCAACGTT CTA CTCTAGC 300  
 GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA 360  
 15 ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTAATTTA TACATTCAAA 420  
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAACAT TTATTTTGAT TAAGT 475

## (2) INFORMATION FOR SEQ ID NO: 3622:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3622:

30 TGGACGAAAC TTTATATCGA TCAATTTCTA TCGAGTTGGA CAATGCCGAA GCGTGACAAA 60  
 AGTTTTTACC ATGCATGGTT GCATTAGCG CAACATGACC ATAGTTTTAC TAAAGCACAG 120  
 CGCnCAAGTG ATTAAAGGCT TACCCAATGA TCCTGAAATG ACGATAGAGT CAGTATTAAC 180  
 35 TCATTTTTCA ATAGATCAGG AAGACTACCA AGCTTATGTT GAAGGACATC TTTTGCGGTT 240  
 ACCGGGTTGG GCAGGTATGT TGTATTACCG TTCACAACAG CATCACTTTG AACAACTTT 300  
 40 GTTAACGGAT TATTTGGCAA TTCGGTTAGT TGTCGAACAA TTGCTAGTTG GTGGATGAGT 360  
 TTTAAGTCAG TCGCTAAAGA TTGTGGAAAG TAAGATCCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3623:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3623:

55 TAGATGCTTT CASACTTATC CCGTCCACAC ATAGCTACCC AGCTATGCCG TTGGACGACA 60

ATTTCTACG CCCACGACGG ATAGGGACCG AACTGTCTCA CGACGTTCTG AACCCAGCTC 180  
 GCGTACCGCT TTAATGGGCG AACAGCCAAC CCTTGGGACC GACTACAGCC CCAGGATGCG 240  
 5 ATGACCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG GAGATAAGCC 300  
 TGTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC TTCCATGCGG GAACACCGGA 360  
 TCACTAAGTC CGTCTTTCGA CCCTGCTCGA CTTTGTAGGn 400

(2) INFORMATION FOR SEQ ID NO: 3624:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3624:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC 60  
 CCTCTGCTTG TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120  
 25 GGCAACGTTT TACTCTAGCG GAAnTAAGTn GnACTACCAT CGACGCTAAG GAGCTTAACT 180  
 TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240  
 30 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAACATTTAT 300  
 TTTGATTAAG TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC 360  
 TCGAACCTAT TAACCTCATC ATCTTTGAGG GGATCTTATA 400

(2) INFORMATION FOR SEQ ID NO: 3625:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3625:

TTAAAGAACG CTAATAACTG ATCGTAACCA CTATATATAT TGTTGTGACC TCTAACAGCA 60  
 TAATGTCTAA ATGTTTGTGG GATATATTGA AGCAATCCTT TTGCTGGATT GCCCTGTAAA 120  
 50 ACGTTGATGT CTCTAAGCGA ACTAGATTGA GTTATACCTG CATTTCTCCTCC TGATTCGTGT 180  
 TGAATCAAGC TAATGATATT TCCTACGTCA GCCGAAGTAA CATTAAACACC CATTCGTTTT 240  
 GCTGCACGAC GTATATCGCC TGCCCAAGCA GATGCAGCCT TATTAACACC TGAACCACTT 300

CCTGGATGCG ACCCTTGCAT CAnTTGGGAA ATGTAnGTGT

400

(2) INFORMATION FOR SEQ ID NO: 3626:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3626:

15 GATTGTGGTT CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCCTTATT ATTAATGGGC 60  
 TATAGCCAAG CGGTAAGGCA ACGGACTTTG ACTCCGTCAC TCGTTGGTTC GAATCCAGCT 120  
 AGCCCAAGTTA TTGGCGGCAT AGCAAGTGGT AAGGCAGAGG TCTGCAAAAC CTTTATCACC 180  
 20 GGTTCAAATC CGGTTGCCGC CTCCAGGTTT ATGCGGGAGT AGTTCAACTT TTAGAACACG 240  
 TTCCTTCCCG GAAGAGGTAT AGGTGCAAAT CCTATCTTCC GCTCCATAAT TTAATAATAA 300  
 TGCGGGAGTA TTTCAACTCT TAGAATACAT TCCTTCCTGG AATgAGGTAT AGGTGTAAAT 360  
 25 CCTATCTTCC GCTCCATAAT TTAATATTG cGGGAGTAGT TCAACTTTTA GAAACAGCTC 420  
 CTTCCCGGAA CCGAGGTATA GGTGTAAATC CTATCTTCCG C 461

(2) INFORMATION FOR SEQ ID NO: 3627:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3627:

40 TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG 60  
 AACGTAAGTT GGCTnAnATC GACGCTAAGA ACCTTTCTTG ACTTGTGACA ATCGCTTGCT 120  
 45 TCTTTCCTCT TCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAACTCG TTGCGCTCTT 180  
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCGCAAG CCATTTTTCT TTGTGTTTGC 240  
 TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT 300  
 50 CGCATCCATT TTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC GACTACCATC 360  
 GACGCTAAGG GAGCTTAACT TCTGTGTnCG GGCATGGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3628:



- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3628:

10 ATGCTTTTCAG CACTTATCCC GTCCACACAT AGCTACCCAC CTATGCCGTT GGCACGACAA 60  
 CTGGGTACAC CAGAGGTATG TCCATCCCCG TCCTCTCGTA CTAAGGACAG CTCCTCTCAA 120  
 ATTTCTTACG ACCCAGGACG GATAGGGACC GAACTGTCTC ACGACGTTCT GAACCCAGCT 180  
 15 CGCGTACCGC TTTAATGGGC GAACAGCCCA ACCCTTGGGA CCGACTACAG CCCAGGATG 240  
 CGATGAGCCG ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTCTG GGGGAGATAA 300  
 GCCTGTTATC CCCGGGGTAG CTTTATCCG nTGAGCGATG GGCCTTCCAT GCGGnACCAC 360  
 20 CGGnTTACTA AGTCCGTCTT TCGAnCCTGC TCGACTTGTA 400

(2) INFORMATION FOR SEQ ID NO: 3629:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3629:

TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTGAAAGG 60  
 35 ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGT TTTTCATACC AAGTCGCTGC 120  
 CGGCAAAACA ATGTCAGAAT ATAACGGTGT TGCCGTCATT CTGAAGTCTA AAGAGACCAC 180  
 40 TAAATCTAAC TTACCTGTTG TTTCTTCACG CCACGTAATT TCTTCTGGCT TTTTCATCTC 240  
 ATTTGGTGTA GCTAATAACC CTGATTTTGT GCCAAGTAAA TGCTTCATAA AGTATTCTTG 300  
 ACCTTTTGCA GAACTTGAAA TTAAGTTTGA ACGCCATATA AATAATGATT TTGGATGATT 360  
 45 CTnTTTCAAA TCAGGATCTT CTATTGCAAA TGGGGTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3630:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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TTTAAGTTGT nGATTTAAAA TATTAATAAA GTGTAAATTT GACTATTGAn ATTCKrACaA 60  
 ATACATATTA AAATAATATT TGTTGAATTA ATTGAGTTAG GAAATTTATT TTTTAGAAAT 120  
 5 AAAATAATTA AAAATAATTC TTGACTTACA AAAACTTACG AGTTATAATT AAATCTTGTA 180  
 AGTGACAAAC GAACATTGAA AACTGAATGA CAATATGTCA ACGTTAATTC CAAAAACGTA 240  
 10 ACTATAAGTT ACAAACATTA TTTAGTATTT ATGAGCTAAT CAAACATCAT AATTTTTTATG 300  
 GAGAGTTTGA TCCTGGCTCA GGATGAACGC TGGCGGCGTG CCTAATACAT GCAAGTCGAG 360  
 CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 420  
 15 TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATrATATTT 480  
 TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 540  
 TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATA 589

(2) INFORMATION FOR SEQ ID NO: 3631:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

CCAAGTGAAG TAATGGCTCT TCCATGGTGC CGGCCAGAGG ACTTGAACCC CCAACCTACT 60  
 GATTACAAGT CAGTTGCTCT ACCAATTGAG CTAGGCCGGC AATATGTAAG AATAAATGGT 120  
 35 GGAGAATGAC GGGTTCGAAC CGCCGACCCT CTGCTTGTA GGCAGATGCT CTCCCAGCTG 180  
 AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTCG 240  
 40 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 300  
 CTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA 360  
 AAAGTGATTT GCTTCGCAA ACATTTATTT TGATTAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3632:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3632:

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 120  
 AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT 180  
 5 CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA TATnTTACTT 240  
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCGCTGACC 300  
 10 TCCTGGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAh GCCCCCAhAT AGGTATTAAA 360  
 TTAATGGGGG GGCCTAAGTG GACTCGAACC ACCGACCTCA 400

## (2) INFORMATION FOR SEQ ID NO: 3633:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3633:

25 ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT TTAGTATTTA 60  
 TGAGCTAATC AAACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAG GATGAACGCT 120  
 GGCGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT TCTCTGATGT 180  
 30 TAGCGGCGGA CGGGTGAGTA ACACGTGGAT AACCTACCTA TAAGACTGGG ATAACCTCGG 240  
 GAAACCGGAG CTAATACCGG ATAATATTTT GAACCGCATG GTTCAAAAGT GAAAGACGGT 300  
 CTTGCTGTCA CTTATAGATG GATCCGCGCT GCATTAGCTA GTTGGTAAGG TAACGGCTTA 360  
 35 CCAAGGChAC GATGCATAGC CGACCTGAGA nGGTGATCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3634:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3634:

45 TGAGCTAGGC CGGCAATATG TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA 60  
 50 CCCTCTGCTT GTAAGGCAGA TGCTCTCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC 120  
 TGGCAACGTT CTA CTCTAGC GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA 180  
 55 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 240

TATTTTGATT AAGTCTTCGA TCGATTAGTA TTCGTCAGCT CCACATGTCA CCATGCTTCC 360  
 ACCTCGAACC TATTAACCTC ATCATCTTTG AGGGATCTTA 400

(2) INFORMATION FOR SEQ ID NO: 3635:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3635:

TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT TTAGCTCTAC 60  
 TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 120  
 ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTGTAGAC ATAAAAAAAA GAGACCTTGC 180  
 GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCCTGGC AACGTTCTAC TCTAGCGGAA 240  
 CGTAAGTTGG GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT 300  
 CTTTCCTCTT CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTTT 360  
 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3636:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3636:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTAGTCAA GCGCTCGCAT ACTGATTTTC 60  
 AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT ATTTTCTTA ATGCATTGTC 120  
 TAACAACCGC TTCTTTTAAA AAGAATAGAT TGTCAAGCGC TCGCATAAGC AATATCACTT 180  
 TAACCAAAAA ATATTTGAAT GTTAAATAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240  
 ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300  
 GCACCTTnCG ATACGGCTAC CTTGTTACGA CTTACCCCA nTCATTTGTn CCACCTTCGA 360  
 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3637:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3637:

10 AGCGCTCGCA TAAGCAATAT CACTTTAACC AAAAAATATT TGAATGTTA AATAACATT 60  
 CAAACTGnA ATACAATATG TCACATTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA 120  
 TATCCTTAGA AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT 180  
 15 CACCCCAATC ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTACT CCACCGGCTT 240  
 CGGGTGTTAC AACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC 300  
 20 ACGTAGCAT GCTGATCTAC GATTACTAGC GATTCCAGCT TCATGTAGTC GAGTTGCAGA 360  
 CTACAATCCG AACTGAGAAC CACTTATGGG ATTGCCTnAC 400

## (2) INFORMATION FOR SEQ ID NO: 3638:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3638:

35 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAGTAAGT CGAnCTACCA 60  
 TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA 120  
 TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAAC TAGATAGTAA GTAAAAGTGA 180  
 40 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 240  
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTGA GGGATCTTAT 300  
 AACCGAAGTT GGGGAAATCT CATCTTGAGG GGGGCTTCAT GCTTAGATGC TTTCAGCACT 360  
 45 TATCCCGTCC ACACATAGCT ACCCAGCTAT GCCGTTGGCA 400

## (2) INFORMATION FOR SEQ ID NO: 3639:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 551 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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ATGTCTCTAA CGCCTTTAAT AGTATTGAAC ACAATTGGGA AAAAGCAGC GATAAAAATA 60  
 ATCGCAATCG CTGGCAAACCT ACCAATACCA AACCATAGAA CAACAAATGG TGCCCATGCT 120  
 5 ATCGGAGATA TCGGCCTAAT CAATTGAAAT AGCGGTTCTGA TAGCGTTGTA TAGCCAACGA 180  
 TTCCTTCCAA GCAAGAAGCC CAATGGAATA GCAACCAACA ATGCGACAAC AAAGCCCGCT 240  
 ACAAATCTCC ATAAACTAAT TGCTAAATGT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 300  
 10 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 360  
 ATAaTGACCA TTTCCCAaT GCCTAAGAAA aTAATAAATG TGATAATAGG TAATATAAAT 420  
 15 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 480  
 AGTCATCCAT ATGCAGGTGG ATTAAACAAA TGATGTTGTT TTACCAngTC GTAATTTCTT 540  
 GATAGCCGGA T 551

(2) INFORMATION FOR SEQ ID NO: 3640:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3640:

CACTAAACTA AATTAATGAA GTGCCTTATG TATAAAAATT ATAACCTGAT CCAACTTACA 60  
 CTACCAATAG AAACCTTCTGT TAGAATTCCT CAAATTGATA TTTCGCGATA TGTTAATGAA 120  
 35 ATTGTTGAAA CGATACCTGA TAGCGAATTC GATAAATTCA GACATCATCG TGGCGCAACA 180  
 TCCTATCATC CAAAATGAT GTTAAAAATC ACCTTATATG CATATACTCA ATCTGTATTT 240  
 TCTGGTCGTA GAATAGAGAA ATTACTTCAT GACAGTATTC GAATGATGTG GTTAGCTCAA 300  
 40 AATCAAACAC CTTCTTATAA AACTATTAAT CGTATTAGAG TGAATCCTAA TACTGATGCG 360  
 TTAATTGAAT CTTTATTTAT CCAGTTTCAT AGTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3641:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3641:

GATTGTCCTT TGGcAATGGT AGGAGAGCGT TCTAAGGGCG TTGAAGCATG ATCGTAAGGA 120  
 CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CGAAAGACGG GTGAGAATCC 180  
 5 CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC 240  
 CTAAGCTGAG GCCGACAGnG TagGCGATGG ATAACAGGTT GATATTCCTG TACCACCTAT 300  
 AATCGTTTTA ATCGATGGGG GGrCGCATAG GATAGGCGAA CGTTGCGATT GGATTGCACG 360  
 10 TCTAAGCAGT AAGGCTGGAG TATTAGGCAA ATCCGGTA 398

## (2) INFORMATION FOR SEQ ID NO: 3642:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3642:

TAATGTCTAC ACTTTGCTTG CGATCATTCA TTTTAAAGCC AGACTTTTTTA TAATCTTGTA 60  
 25 CAAATGCTTG CGCTACATCC TTGTGTTGAT CAAGCAATTC CCCTCTCAGT ACTAGCACAC 120  
 AGCAATACGC ATCAGGtATA ACGTCATCAC CATGTTTCAA AGTCTTACCT TTGCCTAACT 180  
 TTTCACCCAG TGCACCGAAT GGTTCGGCTA CAGAATACCC TGTaATTCTG TGTTCACTCA 240  
 30 ATGCGGCTGG CATTTCTGCT GGCGACATTT CATGATAGCT AAAATGCCCC GGTTTAATCT 300  
 TTAATTGTTT ACGTAATTCC TCAAGTAAAA GATAATGTGt TGAATAACgA TGTGGtATAC 360  
 CAAATGGKa ATCATCGCCA TTAtTATTAA ATTCaTTTAA GTGCATACCT TTTTGTCCCA 420  
 35 TAATGACATT GCCTTCATG 439

## (2) INFORMATION FOR SEQ ID NO: 3643:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3643:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60  
 50 TCTATATTTT ACTTACTTAT CTAGTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120  
 TCGAACCGTG ACCTCCTGCG TGCAAAGCAG GCGCTCTCCC AGCTGAGCTA AGCCCCAAA 180

GCGTGCGCTC TAACCAGCTG AGCTATAGGC CCATTAATTT GAATGAACAA ACATTCAAAA 300  
 CTGAATACAA TATGTCACGT TATTCGCGAT CTTCTGAAGA AGATGTTCCG AATATATCCT 360  
 5 TAGAAAGGAG GTGATCCAGC CGCACCTTnC GATACGGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3644:

GCGAAACTGT ACGGAGCAAC GCCGCGTGAG TGATGAAGGT CTTCGGATCG TAAAACTCTG 60  
 TTATTAGGGA AGAACATATG TGTAAGTAAC TGTGCACATC TTGACGGTAC CTAATCAGAA 120  
 AGCCACGGCT AACaCGTGCC AGCAGCCGCG GTAATACGTA GGTGGCAAGC GTTATCCGGA 180  
 ATTATTGGGC GTAAAGCGCG CGTAGGnGTT TTTTAAGTCT GATGTGAAAG CCCACGGnTC 240  
 25 AACCGTGGAG GGTCATTGGA AACTGGAAAA CTTGAGTGCA GAAGAGGAAA GTGGAATTCC 300  
 ATGTGTAGCG GTGAAATGCG CAGAGATATG GAGGAACACC AGTGGCGAAG GCGACTTTCT 360  
 GGTCTGTAAC TGACGCTGAT GTGCGAAACG TGGGGATCA 399

(2) INFORMATION FOR SEQ ID NO: 3645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3645:

TATTATACTT TACATTTCTC GTTTCGTCAG ATTCAAACGT TTTCACITTCG CCAAGCCATC 60  
 TTTCTTTGTG TTTGCTTTTA TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT 120  
 45 CAATGCGGCT CATCGCATCC ACTTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 180  
 TnCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 240  
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATnAT ACATTCAAAA CTAGATAGTA 300  
 50 AGTAAAAGTG GATTTTGCTT CGCAAAACAT TTATTTTGGA TTAAGTCTTC GATCGGATTA 360  
 GTATTCGTCA GCTCCACATG TCACCATGGC TTCCACCTCG 400



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3646:

AGATAAGTAA GTAAATATA GATTTTACCA AGCAAAACCG AGTGAATAAA GAGTTTTTAAA 60  
 TAAGCTTGAA TTCATAAATA ATCGCTAGTG TTCGAAAGAC ACGAnCAAGA TTAATAACGC 120  
 GTTTAAATCT TTTTATAAAA GAACGTAACT TCATGTTAAC GTTTGACTTA TAAAAATGGT 180  
 GGAAACATAG ATTAAGTTAT TAAGGGCGCA CCGTGATGC CTTGGCACTA GAAGCCrATG 240  
 AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA GTAAGCTTTG ATCCAGAGAT 300  
 TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT CGATATGTGA ATACATAGCA 360  
 TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA GAAAGAAAAT 420  
 TCGATTCCCT TAGTAGCGGC GAGCAnAACG GGAAGAGCCC AAACCAACAA GCTTGCTtGg 480  
 GGGTnTGtAG GACACTCTAT ACGGATTACA AAGGACGACA TTAGACGAAT CATCTGGaAA 540  
 GATGAATCAA AGAAGGTAAT AATCCTGTAG TCGAAAATGT TGTCTCTCTT GAGTGGATCC 600  
 TGaGTACGAC GGAGCACGTG AAATCCGTC GGAATCTGGG GAGGaCCATC TCCTAAGGCT 660  
 AAATACTCTC TAGTGACCGA TAGTGGAACC aGTaCCGTGA GGGAAAGGTg AAAAGCACCC 720  
 gGAAGGnAGT TGAAATaGAA ctGGAAACCG TGTGCTTA 758

## (2) INFORMATION FOR SEQ ID NO: 3647:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3647:

ACAAACTCCG AATGCCAATT AATTAACTT GGGAGTCAGA ACATGGGTGA TAAGGTCCGT 60  
 GTTCGAAAGG GAAACAGCCC AGACCACCAG CTAAGGTCCC AAAATATATG TTAAGTGGAA 120  
 AAGGATGTGG CGTTGCCCAG ACAACTAGGA TGTTGGCTTA GAAGCAGCCA TCATTTAAAG 180  
 AGTGCGTAAT AGCTCACTAG TCGAGTGACA CTGCGCCGAA AATGTACCGG GGCTAAACAT 240  
 ATTACCGAAG CTGTGGATTG TCCTTTGGn TGGGTAAGGA GAGCGTTCTA AGGGCGTTGA 300

AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAAGGTT

400

(2) INFORMATION FOR SEQ ID NO: 3648:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 521 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3648:

GTCATTGGAA ACTGGAAAAC TTGAGTGCAG AAGAGGAAAG TGGAATTCCA TGTGTAGCGG 60  
 TGAAATGCGC AGAGATATGG AGGAACACCA GTGGnCGAAG GCGACTTTCT GGTCTGTAAC 120  
 TGACGCTGAT GTGCGAAACG TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC 180  
 GTAAACGATG AGTGCTAAGT GTTAGGGGGT TTCCGCCCTT TAGTGCTGCA GCTAACGCAT 240  
 TAAGCACTCC GCCTGGGGAG TACGACCGCA AnGTTGAAAC TCAAAGGAAT TGACGGGGAC 300  
 CCGCACAAGC GgTGGaGCAT GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC 360  
 TTGACATCCT TTGACAACTC TAGAGATAGA GCcTTCCCTT TCGGGGGACA AAGTGACAAG 420  
 TGGTGATGG TGTCGTCAAC TCCTGTCGTT GAGATGTTGG GGTAAnTCCC CGCAAnGAGC 480  
 GCACCCTTAA GCCTTAGTTT nCATCATTAA GTTGGGCACT C 521

(2) INFORMATION FOR SEQ ID NO: 3649:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3649:

CCAAAGTTCA TCTTTTACGA ATGAGAAATA GGTGTTGCAT ATTCAATGGT CTCATCTTGT 60  
 TTATAAAAGC CACCATCTAA ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC 120  
 ATACGTGTTT TAACACGTTC GTATCCCATT GCATCCCATA ATTGGAATGG ACCAAGTTTC 180  
 CAGTTGAACC CCCAGACAAG CGCACGGTCT ATGTCTCGGA AATCATCGGT AGCTTTAGGT 240  
 ACATTGATAG CAGAGTAATA GAAATTATTA CGTAATGTCT CCCATAAAAA TAGTCCCGCT 300  
 TCGTCTTGcG CATTGAATAT GGTATCAAkG TTATGCACTA aGTCTTTATT AAATTCATTT 360  
 AAAATTGGTA ATTGTGGTTG CGATACAGGT ACATAATCTT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3650:

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10 GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTTCGAA CCCCCGCGGn CCGTTAAGGC      60
    CCTGTCCGGT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG      120
15 GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC      180
    TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG      240
    AAGAGGGATT CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT      300
20 TCAGCCGGAC TTGGGTATTC CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTGCGA      360
    CCGAACGGTT ATGGAGCCGT TAGCTCTAAn CAACTTGAGC      400
  
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(2) INFORMATION FOR SEQ ID NO: 3651:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3651:

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35 TGGCGCTGTG CTTTAGTAAA ACTATGGTCA TGTGCGCTA AATGCAACCA TGCATGGTAA      60
    AAACTTTGCT CACGCTTCGG CATTGTCCAA CTCGATAGAA ATTGATCGAT ATAAAGTTTC      120
    GTCCATTTAA TCATTTGACG ATTCACCTGT TCGCTAAGTG GCTCACCTTG TTCATCTATT      180
40 ATTGCATCAC TCATCGGACG TACATCATAG TGATGATATG ATTCAGCCAT ATCACGTTTT      240
    GATTTTTCTA ATAGTAGATC AGCAACAACA TCAACATTTG AATGATTCAT ATATGATGGC      300
    AGGTACGTCT TTTAATGTTT TAATGTTATC AATATAAAGA TGATGTAGTG TTGCGGGATA      360
45 TGTAGTGAnG TTCAAGTAAC ATATCAGTAA CAAGTTGATT      400
  
```

(2) INFORMATION FOR SEQ ID NO: 3652:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3652:

CATTGTCCAA AGGACAATCC ACAGCTTCGG TAATATGTTT AGCCCCGGTA CATTTCGGC 60  
 5 GCAGTGTAC TCGACTAGTG AGCTATTACG CACTCTTTAA ATGATGGCTG CTTCTAAGCC 120  
 AACATCCTAG TTGTCTGGGC AACGCCACAT CCTTTTCCAC TTAACATATA TTTTGGGACC 180  
 TTAGCTGGTG GTCTGGGCTG TTTCCCTTTC GAACACGGAC CTTATCACCC ATGTTCTGAC 240  
 10 TCCCAAGTTA AATTAATTGG CATTCCGAGT TTGTCTGAAT TCGGTAACCC GAGAGGGGCC 300  
 CCTCGTCCAA ACAGTGCTCT ACCTCCAATA ATCATCACTT GAGGGCTAGC CCTAAAGCTA 360  
 ATTTCCGAGA GAACCAGCTA TCTCCAGGTT CGATGGAATT 400

## (2) INFORMATION FOR SEQ ID NO: 3653:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3653:

GGTTCGGTCC TCCATTCACT GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG 60  
 TTTCGGGTCT ACGACCAAAT ACTAAACGCC CTATTCAGAC TCGCTTTCGC TACGGCTCCA 120  
 30 CATTTACTGC TTAACCTTGC ATCAAATCGT AACTCGnCGG TTCATTCTAC AAAAGGCACG 180  
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTAC 240  
 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 300  
 35 AGAGTATTTA GCCTTAGGAG ATGGTCTCTC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 360  
 CGTACTCAAG nATCCACTCA AGAGAGACAA CATTTCGAC 400

## (2) INFORMATION FOR SEQ ID NO: 3654:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3654:

AAAGGTCCTA AATATAATTT TACAACTAAT AAATAGTGGC GGTGGAGGGG ATCGAACCCC 60  
 CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC TTATATAGTT 120

GCGCTCTCCC AGCTGAGCTA AGCCCCATA ATAATTACAG TATATCGGGA AGACAGGATT 240  
 CGAACCTGCG ACCCCTTGGT CCCAAACCAA GTGCTCTACC AAGCTGAGCT ACTTCCCGTA 300  
 5 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGnTCT 360  
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3655:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3655:

20 TATTGAAGCC TGAGTCAACA CGTACGCAA TCGATCAAAT CATCGATGAA GCGAAACATA 60  
 CAATTTTAAA TCTGTATGTG TGAATCCAAC ACATGTTAAA TATGCAGCAG AGCnnCTAGC 120  
 TGATTCAGAG GTGCTCGTTT GTACGGTAAT AGGATTCCCA TTAGGTGCGT CGACAACTGC 180  
 25 AACGAAAGCA TTTGAAACAG AAGATGCAAT TCAAAATGGT GCAGATGAAA TTGACATGGT 240  
 CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 300  
 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGGAT TATTGAGACG GTATTGTTGG 360  
 30 GACCATGACG AAATTGTAAA AGCGAGTGGG ATTAACCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3656:

- (i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 530 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3656:

GATGAGTCGC TGnCTGATCT GAACGCTGTC TGAGnCCGAA CGCTACTGAA CTGAGTCGCT 60  
 45 GTCTGAGTCT GAATCGCTAT CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 120  
 GTCTGAGTCG CTGTCTGAGT CTGAATCGCT ATCTGAATCT GAGTCGCTGT CTGAGTCTGA 180  
 GTCGCTATCT GAGTCTGAGT CGCTGTCTGA ATCTGAGTCG CTGTCTGAAT CTGAATCGCT 240  
 50 GTCTGAGTCT GAATCGCTAT CTGAGTCTGA ATCGCTATCT GAGTCTGAAT CACTGTCTGA 300  
 GTCCGAGTCA CTGTCTGAAT CTGACTCACT ATCTGATTCT GAGTCGCTAT CTGATTCTGA 360

ATCTGAACCT GAGTCGCTGT CTGAGCCTGA AGTCACTGGT CTGAATCCGA ATCCGGATCC 480  
 GGGTCTGGGG CTTGGGTTCC GGTTCCTGGGT CTGGGACTTG GGTTCCTGGGA 530

(2) INFORMATION FOR SEQ ID NO: 3657:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3657:

GTTTTAACTA CGCAAGACAT CGAAGAAGCT GACGGTGTCA TAATTGCAGC TGATAAACAA 60  
 GTTGATCTGT CCCGATTGTG TGGTAAACGG TTGATTAAATG AAAATGTTTCG CGAAGGGATT 120  
 CATAATCCGA GAGGTCTAAT TCAACGTATC ATTAATCAAG ATGCGCCTAT TTATCAATCT 180  
 GAAACAAATT ATCATTTCGAA AGATCGCGGT AAGTCTAAAA ATGGTATTCA AATGGTGTAT 240  
 CAACATTTAA TGAACGGTGT ATCGTTTATG GTTCCTTTTA TCGTAGTTGG TGGACTCCTT 300  
 ATCGCCATCG CGCTGGACTC TAGGCGGTGA ACGACATCAA AAGGATTAGT CATCCCAGAT 360  
 GGATTCATTT TGGGAAATCC ATTGGAAAAC ATTGGGTAGT 400

(2) INFORMATION FOR SEQ ID NO: 3658:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 668 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3658:

GAAGAAGTTT ATGAAACGGT TATGAATAAG CCATACACTA GATATCCAGT GTACGAGGGA 60  
 GATATTGATA ACATTATTGG GGTGTTTCAT TCTAAATATC TGTTGGCTTG GAGTAATAAA 120  
 AAAGAAAATC AAATTACAAA CTATTCAGCT AAGCCATTAT TTGTGAATGA ACACAATAAA 180  
 GCTGAATGGG TATTACGTAA GATGACTATT TCTAGAAAAC ATTTAGCAAT TGTGTTGGAC 240  
 GAATTTGGTG GTECTGAAGC GATAGTGTCA CATGAAGACT TAATTGAAGA ATTATTAGGT 300  
 ATGGaAATTG AAGATGAGAT GGaTAAAAAG GAAAAAGAAA AACTTTCTCA ACAGCAAATT 360  
 CmATTTCAAC AACGGAAAAA TCGCmACGTA TCTATATAAG GnGCGAACAG CTATGTGGTA 420  
 ATAAGAATCG ACTTACTCAA ATGTTAAGTA TTGAATATCC AATTATACAA GCAGGTATGG 480

TAGGCGCGGT TACTTTAATA CGCAGCAATT GGAAGATGAA ATAGATTATG GTACGCCAAT 600  
 TAACGTCAAA TTCTTTTGGC GTAAATGTCT TTGGTACCAA GTCAACAATC ATATACCACT 660  
 5 AGTCAAAT 668

## (2) INFORMATION FOR SEQ ID NO: 3659:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3659:

AAAAGAATGG TAAGTTGAAT AAAGTATTGA AATCAATTGC CAATATCTTT ATACCGTTGA 60  
 20 TTCCTGnATT TATTGGAGCT GGATTAATTG GTGGTATTGC AGCAGTACTG AGTAACTTAA 120  
 TGGTGGCAGG CTATATTTCA GGTGCTTGGG TTACGCAACT TATAACAGTA TTTAATGTCA 180  
 TTAAAGACGG TATGTTAGCA TACTTAGCTA TTTTCACTGG TATTAATGCG GCTAAAGAAT 240  
 25 TTGGTGGCAG ACCAGGACTT GGTGGCGTGA TTGGTGGTAC AACGTTATTA ACGGGTATTG 300  
 CTGGTAAAAA TATTTTAATG AATGTCTTCA CTGGAGAACC ATTGCAACCT GGACAANGTG 360  
 GGATTATTGG CGTTATTTTG CCGTTTGGAA TTTAAGTAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3660:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3660:

CTGAGCTAAT GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GAACCCCCAA CCTACTGATT 60  
 ACAAGTCAGT TGCTCTACCA ATTGAGCTAG GCCGGCAATA TGTAAGAATA AATGGTGGAG 120  
 45 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 180  
 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTCGGACT 240  
 ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 300  
 50 GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AAAGTAGATA GTAAGTAAAA 360  
 GTGATTTTGn TTTTCGAAAA CATTTATTTT GGATTAAGTC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3661:

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10  TGATGTTTGA TTAGCTCATA AATACTAAAT AATGTTTGTA ACTTATAGTT ACGTTTTTTG      60
    GAATTAACGT TGACATATTG TCATTCAGTT TTCAATGTTC ATTTTCTTA CCGACAAGAA      120
    TTAATTATAC ATTTTATTAA CATTTAAGTC AATAACTTTT TTTATCTTGT CCATTTTATT      180
15  TTTTAACCAA AATTTGATTA AAAAAGTCC TGGCAACGTT CTAAGCTAGC GGAACGTAAG      240
    TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA      300
    CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA      360
20  AGTAAAAGTG ATTTTGCTTC GCAACATTT ATTTTGATTA      400
  
```

(2) INFORMATION FOR SEQ ID NO: 3662:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 742 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3662:

```

35  CGCTCAACGT CTGCCTTCGT AATGGCTTTT GTAGAAATTC TAACTAAATA ATTTGGAATG      60
    CTATCATTGA TTGTTTCAAC AGCTTGATGC TTTTGTTCAA GCTTTTGTAT CAATTTTTTA      120
    TCGTCTTTTG TAATTTTCGG AATGTCTTCA AACATTGATA AGACAATCTG ACCCACATTT      180
40  TGTAATTCTT TTTGAGTTTC TTGTAATGCA ACACCAGGTG CGTGATAAAC AAGATCTTTG      240
    TTTAAGTGCT GAGGTTTATA GTCATCAGCA ATATCTTTAC CTGGGACAAG CTTTGTAACA      300
    ATCCATGCTA AACCTGCTAC AAATGGTAAT TGAATCAAAG TATTTGTTAT GTTGAAGATA      360
45  CCATGTGATA CTGCAATCGT CATCGCTGGT TTTAAGTGCC ATAAATCTTG TAACAAACTA      420
    ATCAAATGAA TCACAACTGG CAAGAAAATT GTGAAGATAA TTACCCCGAT TAAGTTAAAG      480
    ATGACGTGTA CAAGCGCCGC ACGTTTGTGA GCGATTGAGC CGGCTAAACT AGCTAAGATA      540
50  GCTGTAATCG TGGTACCAAT GTTATCGCCT AGTAACACAG GGAATGCTGC GTTTAAGCTA      600
    ATTAAATCTT GTTGATAAAA TTCTTGTAAG ATACCAATCG TCGCACTTGA ACTTTGAACT      660
  
```



AGCATTAAAT TGGCTTnAAA TC

742

## (2) INFORMATION FOR SEQ ID NO: 3663:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3663:

ATGAATTCAA GCTTATTTAA AACTCTTTAT TCACTCGGTT TTGCTTGGTA AAATCTATAT 60  
 TTTACTTACT TATCTAGTTT TCAATGTACA ATTTCTTTTT AGTCAAGCGC TCGCATACTG 120  
 CTTTATTTTC AAAAAATCAA ATGCTCATTT AAAAAAGTAA ACTCCGCTTT AATTTTCTTT 180  
 AATGCATTGT CTAACAACCG CTTTCTTTAA AAAGAATAGA TTGTCAAGCG CTCGCATAAG 240  
 CAATATCACT TTAACCAAAA AATATTTGAA TGTAAATAA ACATTCAnAA CTGAATACAA 300  
 TATGTCACGT nATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT TAGAAAGGAG 360  
 GTGATCCAGC CGCACCTTCC GATACGGGCT ACCTnGtnAC 400

## (2) INFORMATION FOR SEQ ID NO: 3664:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 636 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3664:

AACTAATAGT TCACTTTTAC TTTTCTTTT TTCAATTATTA TCCATTATTT TTTCACCGCC 60  
 AAAACGAATT TCATGATGTT AATTAAATG TTCTATGACA AAATTAAGCA ACGATGTTtT 120  
 ATATTTATTT CCAACTATGT CTAGATTAAA TTTCTAAAAA TAkACATCAT TTAAAAGGAG 180  
 CTTGGGACAT AAATCAATGT CCTAGGGTCT ATAATATTAT AKTGCTAGTA GTTGACTGAA 240  
 TGAAAATGCG CTTGCAACAA GCTTTTTTCA ACTCTAGTCA GGGGCCCCAA CACAGAGAAT 300  
 TTCGAAAAGA AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA CAGAGAATTT 360  
 CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGTGGG CCCCACACA GAGAATTTcG 420  
 AAAAGAAATt CTACAGGCAA TGCGAGTTGG GGTGTGGGCC CCAACATAGA GAAATGGaTT 480  
 CCCAaTTTCT ACAGACAATG CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC 540

TACAATAATG nGCAAGTTGG CGGGGnCCCC AACACA

636

(2) INFORMATION FOR SEQ ID NO: 3665:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 404 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3665:

TATCATTTC	TGTTGCTAAA	ACAACAGCAT	GTATGCCATT	CATAACACCT	TTATTATGTG	60
TTGCTGCACG	ATGAATATCT	ACTTGGGCCA	ATACAGAAGC	ACGTTCCATT	CGTTTGGCAA	120
CCTCTTCTCC	AGTTCTCTCG	CCCCTTGCTA	AATCTTTAAC	ATCAATTTTCG	CCTTGAACTT	180
TAACAACGGA	CGCTGTTGCA	TGATTGGATA	AAATACTCAT	TAAAATGTCG	CTTTGGGAAA	240
tTCATTTTTT	AAAAATGCAG	TTATGGCCTC	TAAAATCGTA	TTAAGCATAT	TAGCGCCCAT	300
AGCATCTTTC	GTATCAACAA	ATACTTTTAA	AGATAGTAAC	TGtTGcTCAG	GrAATGTakC	360
mAtCGCTATA	CGtTGgTAAC	CACCACCACG	CGCTTTAATA	GGAA		404

(2) INFORMATION FOR SEQ ID NO: 3666:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3666:

GTGGTTCCAG	TAGCAATTAT	TGAACGATAT	TAGGCTATCT	AGTCGGCATA	TTTGTA AAAC	60
AAGATCCAAT	TAAATATCAA	CAGGAATAAC	GAATAATATA	AAAGAGGTG	GGACATAAAT	120
CCCTAAAAAA	ACAGCAGTAA	GATAATTTTC	AATTAGAAAA	TATCTTACTG	CTGTTCTCTA	180
TTTATACAAT	ACTTCGTATT	GAATGGCTTC	GCTTTCCTAG	GGTGCCGTCT	CAGCCTCGGT	240
CTTCGACTGG	CACTGCTCCC	TCAGGAGTCT	CGCCATTAAAT	ACTACGTATT	AACGTGTAAT	300
TTTACTTTGA	AATACTTTAA	AAAAATAAGA	CACTTTGCCC	AACTTGCACA	TAAATGTAAA	360
ATTCAATAAA	ATAAATTTCT	GTGTTGGATC	CCTnCGTATA			400

(2) INFORMATION FOR SEQ ID NO: 3667:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3667:

	CCAACAAATC TGTCTGTCGC ATCGCCTTTG TCGTTCCAAA TAAATATGTA CAAACGAATC	60
10	CACCAGCATA CGCnCCAAGT AATCCTGCAA TATAACCTAA ATACATATTA TCTGAGATTA	120
	ATGGTAATAG TGACACACCA CTTGGGCCTA TTGCTTTGGC ACCAATATGT CCAATTCCAC	180
	CTATTACAGC GCCACCAATA CCACCACCAA TACAAGCAGT TAAGAAAGGT CGACCTAATG	240
15	GCAAAGTCAC ACCATAGATT AATGGTTCTC CGATACCTAG GGAAACCAAC TGGCAATGCA	300
	CCTTTTAAAG TATTACGTAA TGTTGTGTTG CGGTTTACAT CTTACCCAAA GTGCTAATGC	360
20	GGGCACCTAC TTGGTCCCAG CACCAGCCAT CGCTGCAATT	400

(2) INFORMATION FOR SEQ ID NO: 3668:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3668:

	ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG CTATGTATTC ACATATCGAT	60
	AACATGACAT AACTCATGAC TGGGTTTCCC CATTCGGAAA TCTCTGGATC AAAGCTTACT	120
35	TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG	180
	CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA AACGCGTTAT	240
40	TAATCTTGTG AGTGTTCTTT CGAACACTAG CGATTATTC TTATGAATTC AAGCTTATTT	300
	AAAACCTTTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT	360
	TTTCAATGTA CAATTTCTTT TTAGTCAAGC GCTCGCATAA	400

45

(2) INFORMATION FOR SEQ ID NO: 3669:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3669:

GAGCGCTACT TACTGGnAGG CGCTGGTGGG ATACTACCCT AGCTGTGTTG GCTTTCTAAC 120  
 CCGCACCCT TATCGTGGTG GGAGACAGTG TCAGGCGGGC AGTTTGACTG GGGCGGTCGC 180  
 5 CTCCTAAAAG GTAACGGAGG CGCTCAAAGG TTCCCTCAGA ATGGTTGGAA ATCATTCTATA 240  
 GAGTGTAAG GCATAAGGGA GCTTGACTGC GAGACCTACA AGTCGAGCAn GGTCGAAAGA 300  
 10 CGGACTTAGT GATCCGGTGG TTCCGCATGG AAGGGCCATC GCTCAACGGA TAAAAGCTAC 360  
 CCCGGGGGAT AACAGGCTTA TCTCCCCCAA GAGTTCACAT 400

## (2) INFORMATION FOR SEQ ID NO: 3670:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3670:

ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATCTTTC 60  
 25 TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTTG CGGTCTCAAT 120  
 GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTC 180  
 30 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 240  
 CTTGCTATAG TCACCAGACA TATGAATGTA AATTATACAT TCAAACTAG ATAGTAAGTA 300  
 AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAACT CTTCCGATCG ATTAGTATTC 360  
 35 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCCGAACCT 400

## (2) INFORMATION FOR SEQ ID NO: 3671:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3671:

CACCCGAAGA TATTGCTCAG ACAAAGTCAT CATATACAGG AAAGTATTTA AAAGAAGTAC 60  
 50 TTGAACGAGA TAAACAAAAT ACTGAAGATA AATAAGATTA AAAGAAGTGA AGGATGTTAT 120  
 AAATTTATCC TTCGCTTCTT TTTATTAATT TAGTAATGAA TAGTAGAAAG AAAAGATGCG 180  
 TAAAAAGAAT TATGTAAAGA TAGGGTCAAT CTAGAGTAGT TAAACATAAA TCGAACTGGG 240

TTAGCCACAG CTATTGTGTA CTTAAAAATA GGAATGCATG AGTGCACCA nAGGnAGAAT 360  
 ACTAATTTCC AAAGAAAAAG TATTCCTTAT GTTGGGGCCC 400

(2) INFORMATION FOR SEQ ID NO: 3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3672:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAG ATTCCATTCC AGAAAGAACG 60  
 TAAATTTAAT cCTGATTTAG CmCCaGGGAC aGAAAAAGTA mCmAGaGAAG GACaAAAAGG 120  
 TGAGAAGACA ATaACGACAC CAACACTAAA AAATCCATTA ACTGGAGTAA TTATTAGTAA 180  
 AGGTGAACCA AAAGAAGAAA TCACAAAAGA TCCGATTAAT GAATTAACAG AATACGGACC 240  
 AGAAACGATA ACACCAGGTC ATCGAGACGA ATTTGATCCG AAGTTACCAA CAGGAGAGAA 300  
 AGAAGAAGTT CCAGGTAAAC CAGGAATTAA GAATCCAGAA ACAGGAGACG TaGTTAGACC 360  
 ACCGGTCGAT AGCGTAACAA AATATGGACC TGTAAGGA GACTCGATTG TAGAAAAAGA 420  
 AGAGATTCCA TTCAAAACGT AAATTTAATC CGGATTTAGC A 461

(2) INFORMATION FOR SEQ ID NO: 3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3673:

CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAATCTA 60  
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA 120  
 ACCGCTGACC TCCTGCGTGC AAAGCAGGCG CTCTCCAGC TGAGCTAAGC CCCCAAAnAG 180  
 GTATTAAATT AATGGGGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG 240  
 TGCCTCTAA CCAGCTGAGC TATAGGCCCA TTAATTTGAA TGAACAAACA TTCAAACTG 300  
 AATACAATAT GTCACGTTAT TCCGCATCTT CnGAAGAAGA TGTTCCGAAT ATATCCTTAG 360  
 AAAGGAGGTG ATCCAGCCGC ACCTTCCGAn ACGGCTACCT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

ACATGAAGAC TTAATTGAAG AATTATTAGG TATGGAAATT GAAGATGAGA TGGATAAAAA	60
GGAAAAAGAA AAACCTTCTC AACAGCAAAT TCAATTTCAA CAACGGAAAA ATCGCAACGT	120
ATCTATATAA GGAGCGAACA GCTATGTGGG AATAAGAATC GACTTACTCA AATGTTAAGT	180
ATTGAATATC CAATTATACA AGCAGGTATG GCAGGAAGTA CGACACCGAA ATTAGTTGCA	240
TCAGTAAGTA AACAGTGGTG GGTTAGGCAC AATAGGCGCG GTTACTTTAA TACGCGCCAA	300
TTGGAnGATG GAnATnGATT ATGTACGCCA TTAACGTCAA ATTCTTTTGG CGTAAATGTC	360
TTTGTACCAA GTCAACAATC ATATACCAGT AGTCCAAATT	400

(2) INFORMATION FOR SEQ ID NO: 3675:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3675:

AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA ACCGCCGACC	60
CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAAGTGCCTG	120
GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG GAGCTTAACT	180
TCTGTGTTCT GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG	240
TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA	300
TTTTGATTAA GTCCTCGTCG TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT	360
CGGACCTATT AACCTCATCA ACCTTGAGGG nTCTTATAAA	400

(2) INFORMATION FOR SEQ ID NO: 3676:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG ACATGTGGAG 60  
 5 CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC CCGTCCACCG 120  
 ATTGACTAAG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC CTAAGCTGAG 180  
 GCCGACAGCG TAGGCGATGG ATAACAGTTG ATATTCCTGT ACCACCTATA ATCGTTTTAA 240  
 10 TCGATGGGGG GACGCATAGG ATAnGCGAAAn GTGCGATTGG ATTGCACGTC TAAGCAGTAA 300  
 GGCTGAGTAT TAGGCAAATC CGGTACTCGT TAAGGCTGAG CTGTGATnGG GAGAAGACAT 360  
 15 TGAGTCTTCG AGTCGTTGAT TTCACACTGC CGAGAAAAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3677:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3677:

AAAGCGCCAC ATGGTGCCAA GTCTGGAGTT AATCCAGCAA TTGCTTGTTT TAAGCTATTA 60  
 TATTTTTCTT CTACTTTTGT TTTTCTGCG GCAATTTGTT GGTGAGTCGC ATCACCATTG 120  
 30 TTAATAACAT TTTGTGCATT TGTTGATTCT GTTTGACCCG CACGTTTAGC ATTTTCATAT 180  
 GCTTGGATTG ATGATTGTGT CATACCATCA GTAGTTACTG ATTTATTGAT TTCTTCATCA 240  
 35 AGTTTCGTCT TAGCAGTTTT TAAAGCACTA TTATCAGCTA AAGGTACTAA TTGGATTAAT 300  
 TGCTTGCGTT AATCGCTCAT TGACACGATT TACATTTGTT AACGCAGATT GCACTTCTTG 360  
 TACTGTTCTT AATGGGCTTT TGGAATAATA GCATTAGCGC 400

## (2) INFORMATION FOR SEQ ID NO: 3678:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3678:

ACAGTCAATT GnTCTACCAA TTGAGCTAGG CCGGTTAAGA AATGGTTCCA GGACAGAGTC 60  
 GAATGCCGAC ACATGGAGCT TCAATCCATT GCTCTAACCA ACTGAGCTAC TGAACCATAA 120

AGGCGTGTTA ACCGCTACAC TACGAGACCT ATAAAATATT GCGGGAGGCG GATTTGAACC 240  
 ACCGTACTTC GGGTTATGAG CCCGACGAGC TACCGAACTG CTCCATCCCG CGATAATAAA 300  
 5 AAATAATGGC GGAGGAAGAG GGATTCTGAAC CCCC GCGGCC CGTTAAGGCC tGTCGGTTTT 360  
 CAAGACCGAT CCCTTCAGCC GGA CT TGGGT ATTCTCCAT TATTATAGGT AAATCGCTAT 420  
 TAATTATAAA ATTAAATGGC GGTCTCGACG GGAATCGAAC CCGCGATCTC tGCGTGACAG 480  
 10 GCAGGCGTGT TAAyCGCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 540  
 ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGGACTT 600  
 15 GGGGTATTCC TCCAAAATTA TATGGGACCT TGCAGGACTC GAACCTGC 648

## (2) INFORMATION FOR SEQ ID NO: 3679:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3679:

CTGATCCCGT TGTGCTTCAC ACCCGATAGA TAGGGATTTA CAGATAAATT CAGGTCTCTT 60  
 CCACGTCATA TTTGGACCCA TCGAAAATTC GGGTTCTCAA ATCATCGAAC ATAACAAAAG 120  
 30 AAGCTAAGCA ACATGTAGGC CGTTGTCACT TAACTTCTTG TTTTTCGAT GACAGCTTCT 180  
 ATTTAGAGAA TGTCATGATT ATTTTATATT CACTTCAATG TTATCAATAT TAGTGCCATC 240  
 35 TATGACATCT GCCATGCGAT TTTCTTGTA TTTTTGTGC AATTCAAACG TGTACTTTCC 300  
 ACCGTTTTTC ATTTTAATAA CAATTTTACC TGAACCAACG TTACCGTACA GATTATTTTT 360  
 TTCAATAAGT TGTTTTCTCA ATTTAAAATC AAGTTCTTTC 400

## (2) INFORMATION FOR SEQ ID NO: 3680:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3680:

TCAATGCGGC TCATCGCATT CATTTCTTGT CTAGCAACGT TCTACTCTAG CGGAANTAAAG 60  
 TTAGCTACCA TCCTCGCTAA GAACCTTTCT TGACTTGTGA CAATCGCTTG CTCTTTTCTT 120



TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240  
 TTGACGTTTT AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA 300  
 CTCTAGCGGA AGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC TTGTGACAAT 360  
 CGCTTGGCTT CTnTCCTCTC CTTCGGnTCT CGGCTTACTC 400

(2) INFORMATION FOR SEQ ID NO: 3681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3681:

TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 60  
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTAC 120  
 TTTTATTTTT GACGTTTTAG ACATAAAAAA AGAGACCTCA CGGTCTCAAC TTGCCTGGCA 180  
 ACGTTCTACT CTAGCGGAAC GTAAGTTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT 240  
 TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT 300  
 AAACTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 360  
 TTTTCTTTG TGGTTTACTT TTTATTTTGA CGGTTTAGGC 400

(2) INFORMATION FOR SEQ ID NO: 3682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3682:

TTGAACATGT TGAATCTAAT GAAATTCTTG TTCGTCGTCT AGTTGAAGAG AACGGCGTTG 60  
 AGCATGAAGG TGAATTAGAT CGCTATCCAT TAGCTAAATT TAAACGTTCA AACTCAGGTA 120  
 CATGTTACAA CCAACGTCCA ATCGTTGCAG TTGGAGATGT TGTGAGTAT AACGAGATTT 180  
 TAGCAGATGG ACCATCTATG GAATTAGGAG AAATGGCATT AGGTAGAAAC GTATAGTTGG 240  
 TTTCATGACT TGGGACGGTT ACAACTATGA GGATGCCGTT ATCATGAGTG AAAGACTTGT 300  
 GAAAGATGAC GTGTATACTT CTATTCATAT TGAAGAGTAT GAATCAGAAG CACGTGATAC 360

## (2) INFORMATION FOR SEQ ID NO: 3683:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3683:

```

TTGGAATTTT TCCGCTACCC TCAGTTCATC CGCTCACTTT TCAACGTAAG TCGGTTCCGGT      60
CCTCCATTCA GTGTTACCTG AACTTCAACC TGACCAAGGG TAGATCACCT GGTTCGGGT      120
CTACGACCAA ATACTAAACG CCCTATTCAG ACTCGCTTTC GCTACGGCTC CACATTTACT      180
GCTTAACCTT GCATCAAATC GTAATCGCC GGTTCATTCT ACAAAGGCA CGCCATCACC      240
CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTC ACTCCCCTTC      300
CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGGTTTAC TATCGGTCAC TAnGAGAGTA      360
TTTAAGCCTT AnGAGATGGT CCTCCAGAT TCCCAGACGGG      400

```

## (2) INFORMATION FOR SEQ ID NO: 3684:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3684:

```

GATnTATGAT GAAAACTAT CTGACTGCTG TTTCACTTTT TATAAGACTT CTGAATGTCT      60
TCACTTATAC TTCTAGTCAC AGATtnAAAT AATCAAAAGT GCACATTATT AAAATATCAA      120
TTTCACACTC AATGCGGCTC ATCGCATTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG      180
GAACGTAAGT TAGCTACCAT CCTCGCTAAG AACCTTTcTT GACTTgTGAC AATCGCTTGC      240
TTCTTTCCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC GTTGCCTCTT      300
TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTT TTTGTGTTTA      360
CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA CTTGCCTGGG      420
CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTCTTGA      480
CTTGTGACAA TCGCTTGCTT CTnTCCTCTC CTTCGGCTCT CGGTTACT      528

```

## (2) INFORMATION FOR SEQ ID NO: 3685:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3685:

10 AAATTATGGT CGATTGCGAA TGATTTAAGA GGGAnCATGG ATGCGAGTGA ATTCCGTAAT 60  
 TACATTTTAG GCTTGATTTT CTATCGCTTC TTATCTGAAA AAGCCGAACA AGAATATGCA 120  
 GATGCCTTGT CAGGTGAAGA CATCACGTAT CAAGAAGCAT GGGCAGATGA AGAATATCGT 180  
 15 GAAGACTTAA AAGCAGAATT AATTGATCAA GTCGGTTACT TCATTGAGCC ACAAGATTTA 240  
 TTCAGTGCGA TGATTTCGTGA AATTGAAACG CAAGATTTTCG ATATAGAGCA TCTAGCGACG 300  
 GCGATTGCGA AAGTTGAAAC ATCTACATTA GGTGAnGAAA GTGAAAATGn CTTTATCGGG 360  
 20 CTGTTTCAGCG ATATGGATTT GAGTTCAACG CGGCTAGGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3686:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 403 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3686:

TTAAATTATT GGTCTATCGG TTCTTGGGGT GGCCATGGTA TCTGTTCACT CTTCCGTGGT 60  
 35 GCAGTTGCGA CAACTATGGG TTGGAGATGG ATTTTCATCT TCTCAATTAT CGTTGCCGTA 120  
 CTTTCAATGT TACTCATCAA AGGGACGCCT GAAACGAAAT CAGAAATTAC CAATACACAT 180  
 AAATTTGACG TTGCAGGGCT AATTGTTCTA GTAGTTATGT TGCTAAGTTT AAACGTTGTC 240  
 40 ATTACTAAAG GTGCAGCACT TGGTTACACA TCATTATGGT TCTTTGGTTT GATTGCAATC 300  
 GTAATTGTAG CATTCTTTAT TTTCTTAAAT GTTGAGAAAA AAGTAGATAA TCCACTTATT 360  
 45 GATTTTAAAT TATTgAAAAT AAACCATATA CAGGTGCAAC GGT 403

## (2) INFORMATION FOR SEQ ID NO: 3687:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 449 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

TATGAGCCCG ACGAGCTACC GAACTGCTCC ATCCCGCGAT AATAAAAAAT AATGGCGGAG 60  
 GAAGAGGGAT TCGAACCCCC GCGGCCCGTT AAGGnCCTGT CGGTTTTCAA GACCGATCCC 120  
 5 TTCAGCCGGA CTTGGGTATT CCTCCATTAT TATAGGTAAA TCGCTATTAA TTATAAAATT 180  
 AAATGGCGGT CTCGACGGGA ATCGAACCCG CGATCTCCTG CGTGACAGGC AGGCGTGTTA 240  
 ACCGCTACAC TACGAGACCA TTAGTAAAC GGAGGAAGAG GGATTGGAAC CCCC GCGAGC 300  
 10 CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC CGGACTTGGG TATTCCTCCA 360  
 AAATTATATG GACCTTGCA GACTCGAACC TGC GACCGAA CGGTATGAGC CGTAGCnCTA 420  
 ACCACTGGGC TAAAGTCCTA ATATAATTT 449

(2) INFORMATION FOR SEQ ID NO: 3688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3688:

AAAACGTCGT AATATGCAAA TTGAAGGTGC CAAGGTTGTT ATTCAAGGTT TChATAATGC 60  
 CGGAAGTTTC TTAGCTAAAT TCTTATATGA TTTAGGTGCA AAAATTGTAG GTATCTCTGA 120  
 30 TGCTTACGGT GCATTACAG ATCCAAATGG CTTAGATATA GATTATTTAT TAGACCGTCG 180  
 AGATAGTTTT GGTACGGTAA CAAATTTATT TGAAGAAACA ATCTCAAATA AAGAATTGTT 240  
 TGAATTAGAT TGTGACATTT TAGTACCAGC GGCTATTTCA AACCAAATTA CAGAAGACAA 300  
 35 TGCACATGAT ATTAAAGCTA GTATCGTTGT TGAAGCTGCT AATGGACCTA CAACACCAGA 360  
 AGCAACACGT ATTTTAACTG AACGTGGTAT ATTATTAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3689:

CACGCTTATC AGGCGTGCGC TCTAACCAGC TGAGCTATAG GCCCATTAAT TTGAATGAAC 60  
 AAACATTCAA AACTGAATAC AATATGTCAC GTTATTCGC ATCTTCTGAA GAAGATGTTT 120